Martin J Aryee

List of Publications by Year in Descending Order

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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.

90 papers	22,364 citations	47 h-index	98 g-index
98 ext. papers	27,318 ext. citations	21.9 avg, IF	6.49 L-index

#	Paper	IF	Citations
90	A Congenital Anemia Reveals Distinct Targeting Mechanisms for Master Transcription Factor GATA1.. *Blood*, **2022**,	2.2	2
89	CRISPR-Cas9 treatment partially restores amyloid-β42/40 in human fibroblasts with the Alzheimer's disease M146L mutation.. *Molecular Therapy - Nucleic Acids*, **2022**, 28, 450-461	10.7	1
88	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma.. *Communications Biology*, **2022**, 5, 213	6.7	1
87	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma.. *Nature Communications*, **2022**, 13, 2267	17.4	1
86	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,	11.5	3
85	Defining genome-wide CRISPR-Cas genome-editing nuclease activity with GUIDE-seq. *Nature Protocols*, **2021**, 16, 5592-5615	18.8	0
84	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. *Nature Biotechnology*, **2021**, 39, 1086-1094	44.5	4
83	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. *Cancer Cell*, **2021**, 39, 827-844.e10	24.3	7
82	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. *Nature Biotechnology*, **2021**, 39, 451-461	44.5	59
81	Smart-RRBS for single-cell methylome and transcriptome analysis. *Nature Protocols*, **2021**, 16, 4004-4030	18.8	7
80	Augmenting and directing long-range CRISPR-mediated activation in human cells. *Nature Methods*, **2021**, 18, 1075-1081	21.6	1
79	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. *Biophysical Journal*, **2020**, 119, 1905-1916	2.9	19
78	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. *Nature Biotechnology*, **2020**, 38, 861-864	44.5	72
77	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. *Cell*, **2020**, 182, 1474-1489.e23	56.2	41
76	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. *Nature Biotechnology*, **2019**, 37, 1041-1048	44.5	146
75	High levels of AAV vector integration into CRISPR-induced DNA breaks. *Nature Communications*, **2019**, 10, 4439	17.4	119
74	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. *Nature Biotechnology*, **2019**, 37, 916-924	44.5	152

73	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. *Cell Reports*, **2019**, 27, 3228-3240.e7	10.6	70
72	Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. *Cell*, **2019**, 178, 160-175.e27	56.2	211
71	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. *Nature*, **2019**, 569, 433-437	50.4	270
70	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. *Nature*, **2019**, 569, 576-580	50.4	104
69	Reply. *Gastroenterology*, **2019**, 156, 1933-1934	13.3	
68	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. *Nature Communications*, **2019**, 10, 1903	17.4	97
67	Interrogation of human hematopoiesis at single-cell and single-variant resolution. *Nature Genetics*, **2019**, 51, 683-693	36.3	77
66	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. *BMC Bioinformatics*, **2019**, 20, 160	3.6	4
65	Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. *Nature Biotechnology*, **2019**, 37, 276-282	44.5	235
64	Activities and specificities of CRISPR/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. *Plant Biotechnology Journal*, **2019**, 17, 362-372	11.6	125
63	Magnetic Resonance Spectroscopy-based Metabolomic Biomarkers for Typing, Staging, and Survival Estimation of Early-Stage Human Lung Cancer. *Scientific Reports*, **2019**, 9, 10319	4.9	14
62	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. *Cell*, **2019**, 176, 1325-1339.e22	56.2	174
61	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. *Methods in Molecular Biology*, **2019**, 1935, 187-202	1.4	1
60	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. *Nature Methods*, **2018**, 15, 155-156	21.6	72
59	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. *Bioinformatics*, **2018**, 34, 672-674	7.2	28
58	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. *Cell*, **2018**, 173, 1535-1548.e16	56.2	292
57	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". *Nature Methods*, **2018**, 15, 238-239	21.6	25
56	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. *Nature Communications*, **2018**, 9, 2905	17.4	36

55	Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. *Gastroenterology*, **2018**, 155, 2016-2018.e11	13.3	19
54	Defining CRISPR-Cas9 genome-wide nuclease activities with CIRCLE-seq. *Nature Protocols*, **2018**, 13, 2615-2642	13.8	46
53	In vivo CRISPR editing with no detectable genome-wide off-target mutations. *Nature*, **2018**, 561, 416-419	50.4	202
52	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. *Cancer Discovery*, **2017**, 7, 288-301	24.4	32
51	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPR-Cas9 nuclease off-targets. *Nature Methods*, **2017**, 14, 607-614	21.6	397
50	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. *Journal of Experimental Medicine*, **2017**, 214, 2875-2887	16.6	82
49	The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. *Epigenetics*, **2017**, 12, 793-803	5.7	27
48	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. *JCI Insight*, **2017**, 2, e91078	9.9	13
47	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. *Nature Biotechnology*, **2016**, 34, 869-74	44.5	415
46	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. *Molecular Cell*, **2016**, 64, 1088-1101	17.6	20
45	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	14.4	20
44	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. *Oncologist*, **2016**, 21, 481-6	5.7	67
43	Open-source guideseq software for analysis of GUIDE-seq data. *Nature Biotechnology*, **2016**, 34, 483	44.5	34
42	Lysine demethylase KDM4A associates with translation machinery and regulates protein synthesis. *Cancer Discovery*, **2015**, 5, 255-63	24.4	31
41	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. *Nature*, **2015**, 523, 481-5	50.4	1061
40	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. *Methods*, **2015**, 83, 118-27	4.6	22
39	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. *Nature Biotechnology*, **2015**, 33, 187-197	44.5	1275
38	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. *Nature Methods*, **2015**, 12, 230-2, 1 p following 232	21.6	171

37	GeMes, clusters of DNA methylation under genetic control, can inform genetic and epigenetic analysis of disease. *American Journal of Human Genetics*, **2014**, 94, 485-95	11	76
36	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. *Nature Biotechnology*, **2014**, 32, 569-76	44.5	738
35	EWS-FLI1 utilizes divergent chromatin remodeling mechanisms to directly activate or repress enhancer elements in Ewing sarcoma. *Cancer Cell*, **2014**, 26, 668-681	24.3	223
34	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. *Bioinformatics*, **2014**, 30, 1363-9	7.2	1941
33	Epigenome-wide association studies without the need for cell-type composition. *Nature Methods*, **2014**, 11, 309-11	21.6	171
32	A novel method for detecting association between DNA methylation and diseases using spatial information. *Genetic Epidemiology*, **2014**, 38, 714-21	2.6	3
31	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	5.7	266
30	DNA methylation alterations exhibit intraindividual stability and interindividual heterogeneity in prostate cancer metastases. *Science Translational Medicine*, **2013**, 5, 169ra10	17.5	190
29	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nature Biotechnology*, **2013**, 31, 142-7	44.5	691
28	Global causes of diarrheal disease mortality in children . *PLoS ONE*, **2013**, 8, e72788	3.7	421
27	A comparative risk assessment of burden of disease and injury attributable to 67 risk factors and risk factor clusters in 21 regions, 1990-2010: a systematic analysis for the Global Burden of Disease Study 2010. *Lancet, The*, **2012**, 380, 2224-60	40	7625
26	Reversible switching between epigenetic states in honeybee behavioral subcastes. *Nature Neuroscience*, **2012**, 15, 1371-3	25.5	237
25	DNA methylation shows genome-wide association of NFIX, RAPGEF2 and MSRB3 with gestational age at birth. *International Journal of Epidemiology*, **2012**, 41, 188-99	7.8	60
24	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. *Genome Research*, **2012**, 22, 837-49	9.7	196
23	Estimating diarrhea mortality among young children in low and middle income countries. *PLoS ONE*, **2012**, 7, e29151	3.7	92
22	Genome-wide DNA methylation scan in major depressive disorder. *PLoS ONE*, **2012**, 7, e34451	3.7	113
21	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. *Nature Biotechnology*, **2011**, 29, 1117-9	44.5	443
20	Alterations in nucleolar structure and gene expression programs in prostatic neoplasia are driven by the MYC oncogene. *American Journal of Pathology*, **2011**, 178, 1824-34	5.8	82

19	Accurate genome-scale percentage DNA methylation estimates from microarray data. *Biostatistics*, **2011**, 12, 197-210	3.7	62
18	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. *Epigenetics*, **2011**, 6, 1378-90	5.7	17
17	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. *Nature*, **2010**, 467, 338-42	50.4	484
16	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. *Nature Genetics*, **2010**, 42, 668-75	36.3	436
15	Therapeutic implications of GIPC1 silencing in cancer. *PLoS ONE*, **2010**, 5, e15581	3.7	18
14	Personalized epigenomic signatures that are stable over time and covary with body mass index. *Science Translational Medicine*, **2010**, 2, 49ra67	17.5	254
13	Subset quantile normalization using negative control features. *Journal of Computational Biology*, **2010**, 17, 1385-95	1.7	44
12	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	3.6	75
11	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, 1350-3	36.3	936
10	Genome-wide specificity profiles of CRISPR-Cas Cpf1 nucleases in human cells		2
9	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data		1
8	Unexpected mutations after CRISPR-Cas9 editing in vivo are most likely pre-existing sequence variants and not nuclease-induced mutations		6
7	Varying-Censoring Aware Matrix Factorization for Single Cell RNA-Sequencing		4
6	hichipper: A preprocessing pipeline for assessing library quality and DNA loops from HiChIP data		3
5	Interrogation of human hematopoiesis at single-cell and single-variant resolution		7
4	In vivo CRISPR-Cas gene editing with no detectable genome-wide off-target mutations		5
3	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4
2	Feature Selection and Dimension Reduction for Single Cell RNA-Seq based on a Multinomial Model		24

List of Publications

1	Global-scale CRISPR gene editor specificity profiling by ONE-seq identifies population-specific, variant off-target effects	2