Martin J Aryee

List of Publications by Year
in descending order

82	30,709	41344	49	58581	82
papers	citations		h-index		g-index

98	98	98	51632
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	1.4	14
2	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.	5.1	13
3	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma. Communications Biology, 2022, 5, 213.	4.4	10
4	Reverse Transcriptase Inhibition Disrupts Repeat Element Life Cycle in Colorectal Cancer. Cancer Discovery, 2022, 12, 1462-1481.	9.4	30
5	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. Nature Communications, 2022, 13, 2267.	12.8	18
6	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	17.5	150
7	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. Nature Biotechnology, 2021, 39, 1086-1094.	17.5	28
8	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. Cancer Cell, 2021, 39, 827-844.e10.	16.8	49
9	Smart-RRBS for single-cell methylome and transcriptome analysis. Nature Protocols, 2021, 16, 4004-4030.	12.0	34
10	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	19.0	17
11	Defining genome-wide CRISPRâ€“Cas genome-editing nuclease activity with GUIDE-seq. Nature Protocols, 2021, 16, 5592-5615.	12.0	27
12	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, .	7.1	20
13	Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. Cell, 2020, 182, 1474-1489.e23.	28.9	126
14	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. Biophysical Journal, 2020, 119, 1905-1916.	0.5	45
15	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. Nature Biotechnology, 2020, 38, 861-864.	17.5	168
16	Activities and specificities of <scp>CRISPR</scp>/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. Plant Biotechnology Journal, 2019, 17, 362-372.	8.3	192
17	Magnetic Resonance Spectroscopy-based Metabolomic Biomarkers for Typing, Staging, and Survival Estimation of Early-Stage Human Lung Cancer. Scientific Reports, 2019, 9, 10319.	3.3	23
18	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. Nature Biotechnology, 2019, 37, 1041-1048.	17.5	236

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19	High levels of AAV vector integration into CRISPR-induced DNA breaks. Nature Communications, 2019, 10, 4439.	12.8	257
20	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. Nature Biotechnology, 2019, 37, 916-924.	17.5	315
21	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	6.4	122
22	Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. Cell, 2019, 178, 160-175.e27.	28.9	367
23	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. Nature, 2019, 569, 433-437.	27.8	434
24	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. Nature, 2019, 569, 576-580.	27.8	195
25	Reply. Gastroenterology, 2019, 156, 1933-1934.	1.3	0
26	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	12.8	198
27	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	21.4	147
28	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. BMC Bioinformatics, 2019, 20, 160.	2.6	7
29	Engineered CRISPRâ€“Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. Nature Biotechnology, 2019, 37, 276-282.	17.5	439
30	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	28.9	345
31	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. Methods in Molecular Biology, 2019, 1935, 187-202.	0.9	2
32	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. Nature Methods, 2018, 15, 155-156.	19.0	139
33	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. Bioinformatics, 2018, 34, 672-674.	4.1	57
34	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. Cell, 2018, 173, 1535-1548.e16.	28.9	545
35	Response to â€œUnexpected mutations after CRISPRâ€“Cas9 editing in vivoâ€• Nature Methods, 2018, 15, 238-239.	19.0	25
36	Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. Gastroenterology, 2018, 155, 2016-2018.e11.	1.3	29

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37	Defining CRISPRâ€“Cas9 genome-wide nuclease activities with CIRCLE-seq. Nature Protocols, 2018, 13, 2615-2642.	12.0	69
38	In vivo CRISPR editing with no detectable genome-wide off-target mutations. Nature, 2018, 561, 416-419.	27.8	274
39	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. Nature Communications, 2018, 9, 2905.	12.8	56
40	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. Cancer Discovery, 2017, 7, 288-301.	9.4	53
41	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPRâ€“Cas9 nuclease off-targets. Nature Methods, 2017, 14, 607-614.	19.0	601
42	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. Journal of Experimental Medicine, 2017, 214, 2875-2887.	8.5	168
43	The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. Epigenetics, 2017, 12, 793-803.	2.7	31
44	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. JCI Insight, 2017, 2, e91078.	5.0	23
45	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. Molecular Cell, 2016, 64, 1088-1101.	9.7	27
46	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.	8.2	27
47	MET Exon 14 Skipping in Non-Small Cell Lung Cancer. Oncologist, 2016, 21, 481-486.	3.7	94
48	Open-source guideseq software for analysis of GUIDE-seq data. Nature Biotechnology, 2016, 34, 483-483.	17.5	49
49	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. Nature Biotechnology, 2016, 34, 869-874.	17.5	566
50	Lysine Demethylase KDM4A Associates with Translation Machinery and Regulates Protein Synthesis. Cancer Discovery, 2015, 5, 255-263.	9.4	51
51	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. Nature, 2015, 523, 481-485.	27.8	1,388
52	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.	3.8	33
53	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. Nature Biotechnology, 2015, 33, 187-197.	17.5	1,757
54	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. Nature Methods, 2015, 12, 230-232.	19.0	248

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55	A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. Genetic Epidemiology, 2014, 38, 714-721.	1.3	3
56	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.	6.2	93
57	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. Nature Biotechnology, 2014, 32, 569-576.	17.5	852
58	EWS-FLI1ÂUtilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. Cancer Cell, 2014, 26, 668-681.	16.8	334
59	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. Bioinformatics, 2014, 30, 1363-1369.	4.1	3,192
60	Epigenome-wide association studies without the need for cell-type composition. Nature Methods, 2014, 11, 309-311.	19.0	205
61	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.	2.7	353
62	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. Science Translational Medicine, 2013, 5, 169ra10.	12.4	231
63	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. Nature Biotechnology, 2013, 31, 142-147.	17.5	874
64	Global Causes of Diarrheal Disease Mortality in Children <5 Years of Age: A Systematic Review. PLoS ONE, 2013, 8, e72788.	2.5	524
65	DNA methylation shows genome-wide association ofNFIX,RAPGEF2andMSRB3with gestational age at birth. International Journal of Epidemiology, 2012, 41, 188-199.	1.9	71
66	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. Genome Research, 2012, 22, 837-849.	5.5	236
67	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.	13.7	9,397
68	Reversible switching between epigenetic states in honeybee behavioral subcastes. Nature Neuroscience, 2012, 15, 1371-1373.	14.8	305
69	Estimating Diarrhea Mortality among Young Children in Low and Middle Income Countries. PLoS ONE, 2012, 7, e29151.	2.5	114
70	Genome-Wide DNA Methylation Scan in Major Depressive Disorder. PLoS ONE, 2012, 7, e34451.	2.5	120
71	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. Nature Biotechnology, 2011, 29, 1117-1119.	17.5	547
72	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.	3.8	113

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73	Accurate genome-scale percentage DNA methylation estimates from microarray data. Biostatistics, 2011, 12, 197-210.	1.5	67
74	Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. Epigenetics, 2011, 6, 1378-1390.	2.7	17
75	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. Nature, 2010, 467, 338-342.	27.8	554
76	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. Nature Genetics, 2010, 42, 668-675.	21.4	539
77	Therapeutic Implications of GIPC1 Silencing in Cancer. PLoS ONE, 2010, 5, e15581.	2.5	22
78	Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. Science Translational Medicine, 2010, 2, 49ra67.	12.4	292
79	Subset Quantile Normalization Using Negative Control Features. Journal of Computational Biology, 2010, 17, 1385-1395.	1.6	52
80	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.	2.6	87
81	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.	21.4	1,076
82	Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). Protocol Exchange, 0, , .	0.3	1