

Martin J Aryee

List of Publications by Year in descending order

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Version: 2024-02-01

82
papers

30,709
citations

41344
49
h-index

58581
82
g-index

98
all docs

98
docs citations

98
times ranked

51632
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. <i>Lancet</i> , The, 2012, 380, 2224-2260.	13.7	9,397
2	Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369.	4.1	3,192
3	GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. <i>Nature Biotechnology</i> , 2015, 33, 187-197.	17.5	1,757
4	Engineered CRISPR-Cas9 nucleases with altered PAM specificities. <i>Nature</i> , 2015, 523, 481-485.	27.8	1,388
5	Differential methylation of tissue- and cancer-specific CpG island shores distinguishes human induced pluripotent stem cells, embryonic stem cells and fibroblasts. <i>Nature Genetics</i> , 2009, 41, 1350-1353.	21.4	1,076
6	Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. <i>Nature Biotechnology</i> , 2013, 31, 142-147.	17.5	874
7	Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. <i>Nature Biotechnology</i> , 2014, 32, 569-576.	17.5	852
8	CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPRâ€“Cas9 nuclease off-targets. <i>Nature Methods</i> , 2017, 14, 607-614.	19.0	601
9	Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. <i>Nature Biotechnology</i> , 2016, 34, 869-874.	17.5	566
10	Comprehensive methylome map of lineage commitment from haematopoietic progenitors. <i>Nature</i> , 2010, 467, 338-342.	27.8	554
11	Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. <i>Nature Biotechnology</i> , 2011, 29, 1117-1119.	17.5	547
12	Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16.	28.9	545
13	Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. <i>Nature Genetics</i> , 2010, 42, 668-675.	21.4	539
14	Global Causes of Diarrheal Disease Mortality in Children <5 Years of Age: A Systematic Review. <i>PLoS ONE</i> , 2013, 8, e72788.	2.5	524
15	Engineered CRISPRâ€“Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. <i>Nature Biotechnology</i> , 2019, 37, 276-282.	17.5	439
16	Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. <i>Nature</i> , 2019, 569, 433-437.	27.8	434
17	Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. <i>Cell</i> , 2019, 178, 160-175.e27.	28.9	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. <i>Epigenetics</i> , 2013, 8, 290-302.	2.7	353

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19	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22.	28.9	345
20	EWS-FLI1 Utilizes Divergent Chromatin Remodeling Mechanisms to Directly Activate or Repress Enhancer Elements in Ewing Sarcoma. <i>Cancer Cell</i> , 2014, 26, 668-681.	16.8	334
21	Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. <i>Nature Biotechnology</i> , 2019, 37, 916-924.	17.5	315
22	Reversible switching between epigenetic states in honeybee behavioral subcastes. <i>Nature Neuroscience</i> , 2012, 15, 1371-1373.	14.8	305
23	Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. <i>Science Translational Medicine</i> , 2010, 2, 49ra67.	12.4	292
24	In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018, 561, 416-419.	27.8	274
25	High levels of AAV vector integration into CRISPR-induced DNA breaks. <i>Nature Communications</i> , 2019, 10, 4439.	12.8	257
26	Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015, 12, 230-232.	19.0	248
27	A DNA hypermethylation module for the stem/progenitor cell signature of cancer. <i>Genome Research</i> , 2012, 22, 837-849.	5.5	236
28	CRISPR DNA base editors with reduced RNA off-target and self-editing activities. <i>Nature Biotechnology</i> , 2019, 37, 1041-1048.	17.5	236
29	DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. <i>Science Translational Medicine</i> , 2013, 5, 169ra10.	12.4	231
30	Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014, 11, 309-311.	19.0	205
31	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903.	12.8	198
32	Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580.	27.8	195
33	Activities and specificities of <scp>CRISPR</scp>/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. <i>Plant Biotechnology Journal</i> , 2019, 17, 362-372.	8.3	192
34	Dissecting hematopoietic and renal cell heterogeneity in adult zebrafish at single-cell resolution using RNA sequencing. <i>Journal of Experimental Medicine</i> , 2017, 214, 2875-2887.	8.5	168
35	A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. <i>Nature Biotechnology</i> , 2020, 38, 861-864.	17.5	168
36	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461.	17.5	150

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37	Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693.	21.4	147
38	hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. <i>Nature Methods</i> , 2018, 15, 155-156.	19.0	139
39	Large-Scale Topological Changes Restrained Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23.	28.9	126
40	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7.	6.4	122
41	Genome-Wide DNA Methylation Scan in Major Depressive Disorder. <i>PLoS ONE</i> , 2012, 7, e34451.	2.5	120
42	Estimating Diarrhea Mortality among Young Children in Low and Middle Income Countries. <i>PLoS ONE</i> , 2012, 7, e29151.	2.5	114
43	Alterations in Nucleolar Structure and Gene Expression Programs in Prostatic Neoplasia Are Driven by the MYC Oncogene. <i>American Journal of Pathology</i> , 2011, 178, 1824-1834.	3.8	113
44	<i>MET</i> Exon 14 Skipping in Non-Small Cell Lung Cancer. <i>Oncologist</i> , 2016, 21, 481-486.	3.7	94
45	GeMes, Clusters of DNA Methylation under Genetic Control, Can Inform Genetic and Epigenetic Analysis of Disease. <i>American Journal of Human Genetics</i> , 2014, 94, 485-495.	6.2	93
46	An improved empirical bayes approach to estimating differential gene expression in microarray time-course data: BETR (Bayesian Estimation of Temporal Regulation). <i>BMC Bioinformatics</i> , 2009, 10, 409.	2.6	87
47	DNA methylation shows genome-wide association of <i>NFIX</i> , <i>RAPGEF2</i> and <i>MSRB3</i> with gestational age at birth. <i>International Journal of Epidemiology</i> , 2012, 41, 188-199.	1.9	71
48	Defining CRISPR-Cas9 genome-wide nuclease activities with CIRCLE-seq. <i>Nature Protocols</i> , 2018, 13, 2615-2642.	12.0	69
49	Accurate genome-scale percentage DNA methylation estimates from microarray data. <i>Biostatistics</i> , 2011, 12, 197-210.	1.5	67
50	diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. <i>Bioinformatics</i> , 2018, 34, 672-674.	4.1	57
51	Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <i>Nature Communications</i> , 2018, 9, 2905.	12.8	56
52	OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. <i>Cancer Discovery</i> , 2017, 7, 288-301.	9.4	53
53	Subset Quantile Normalization Using Negative Control Features. <i>Journal of Computational Biology</i> , 2010, 17, 1385-1395.	1.6	52
54	Lysine Demethylase KDM4A Associates with Translation Machinery and Regulates Protein Synthesis. <i>Cancer Discovery</i> , 2015, 5, 255-263.	9.4	51

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55	Open-source guideseq software for analysis of GUIDE-seq data. <i>Nature Biotechnology</i> , 2016, 34, 483-483.	17.5	49
56	STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10.	16.8	49
57	Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , 2020, 119, 1905-1916.	0.5	45
58	Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021, 16, 4004-4030.	12.0	34
59	Inconsistency and features of single nucleotide variants detected in whole exome sequencing versus transcriptome sequencing: A case study in lung cancer. <i>Methods</i> , 2015, 83, 118-127.	3.8	33
60	The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. <i>Epigenetics</i> , 2017, 12, 793-803.	2.7	31
61	Reverse Transcriptase Inhibition Disrupts Repeat Element Life Cycle in Colorectal Cancer. <i>Cancer Discovery</i> , 2022, 12, 1462-1481.	9.4	30
62	Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. <i>Gastroenterology</i> , 2018, 155, 2016-2018.e11.	1.3	29
63	Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021, 39, 1086-1094.	17.5	28
64	Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. <i>Molecular Cell</i> , 2016, 64, 1088-1101.	9.7	27
65	High-specificity bioinformatics framework for epigenomic profiling of discordant twins reveals specific and shared markers for ACPA and ACPA-positive rheumatoid arthritis. <i>Genome Medicine</i> , 2016, 8, 124.	8.2	27
66	Defining genome-wide CRISPR-Cas genome-editing nuclease activity with GUIDE-seq. <i>Nature Protocols</i> , 2021, 16, 5592-5615.	12.0	27
67	Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018, 15, 238-239.	19.0	25
68	Magnetic Resonance Spectroscopy-based Metabolomic Biomarkers for Typing, Staging, and Survival Estimation of Early-Stage Human Lung Cancer. <i>Scientific Reports</i> , 2019, 9, 10319.	3.3	23
69	Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. <i>JCI Insight</i> , 2017, 2, e91078.	5.0	23
70	Therapeutic Implications of GIPC1 Silencing in Cancer. <i>PLoS ONE</i> , 2010, 5, e15581.	2.5	22
71	Screening human lung cancer with predictive models of serum magnetic resonance spectroscopy metabolomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	20
72	EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. <i>Nature Communications</i> , 2022, 13, 2267.	12.8	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.	2.7	17
74	Augmenting and directing long-range CRISPR-mediated activation in human cells. Nature Methods, 2021, 18, 1075-1081.	19.0	17
75	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	1.4	14
76	CRISPR-Cas9 treatment partially restores amyloid- β 42/40 in human fibroblasts with the Alzheimer's disease PSEN1 M146L mutation. Molecular Therapy - Nucleic Acids, 2022, 28, 450-461.	5.1	13
77	Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma. Communications Biology, 2022, 5, 213.	4.4	10
78	A (fire)cloud-based DNA methylation data preprocessing and quality control platform. BMC Bioinformatics, 2019, 20, 160.	2.6	7
79	A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. Genetic Epidemiology, 2014, 38, 714-721.	1.3	3
80	Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. Methods in Molecular Biology, 2019, 1935, 187-202.	0.9	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.	1.3	0