

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 | Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. <i>Blood</i> , 2022, 139, 2534-2546. | 0.6 | 14 |
| 2 | CRISPR-Cas9 treatment partially restores amyloid- β 42/40 in human fibroblasts with the Alzheimer's disease PSEN1 M146L mutation. <i>Molecular Therapy - Nucleic Acids</i> , 2022, 28, 450-461. | 2.3 | 13 |
| 3 | Genome-wide DNA methylation patterns reveal clinically relevant predictive and prognostic subtypes in human osteosarcoma. <i>Communications Biology</i> , 2022, 5, 213. | 2.0 | 10 |
| 4 | Reverse Transcriptase Inhibition Disrupts Repeat Element Life Cycle in Colorectal Cancer. <i>Cancer Discovery</i> , 2022, 12, 1462-1481. | 7.7 | 30 |
| 5 | EWSR1-ATF1 dependent 3D connectivity regulates oncogenic and differentiation programs in Clear Cell Sarcoma. <i>Nature Communications</i> , 2022, 13, 2267. | 5.8 | 18 |
| 6 | Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. <i>Nature Biotechnology</i> , 2021, 39, 451-461. | 9.4 | 150 |
| 7 | Extended-representation bisulfite sequencing of gene regulatory elements in multiplexed samples and single cells. <i>Nature Biotechnology</i> , 2021, 39, 1086-1094. | 9.4 | 28 |
| 8 | STAG2 loss rewires oncogenic and developmental programs to promote metastasis in Ewing sarcoma. <i>Cancer Cell</i> , 2021, 39, 827-844.e10. | 7.7 | 49 |
| 9 | Smart-RRBS for single-cell methylome and transcriptome analysis. <i>Nature Protocols</i> , 2021, 16, 4004-4030. | 5.5 | 34 |
| 10 | Augmenting and directing long-range CRISPR-mediated activation in human cells. <i>Nature Methods</i> , 2021, 18, 1075-1081. | 9.0 | 17 |
| 11 | Defining genome-wide CRISPR-Cas genome-editing nuclease activity with GUIDE-seq. <i>Nature Protocols</i> , 2021, 16, 5592-5615. | 5.5 | 27 |
| 12 | 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, . | 3.3 | 20 |
| 13 | Large-Scale Topological Changes Restrain Malignant Progression in Colorectal Cancer. <i>Cell</i> , 2020, 182, 1474-1489.e23. | 13.5 | 126 |
| 14 | Data-Driven Polymer Model for Mechanistic Exploration of Diploid Genome Organization. <i>Biophysical Journal</i> , 2020, 119, 1905-1916. | 0.2 | 45 |
| 15 | A dual-deaminase CRISPR base editor enables concurrent adenine and cytosine editing. <i>Nature Biotechnology</i> , 2020, 38, 861-864. | 9.4 | 168 |
| 16 | Activities and specificities of CRISPR/Cas9 and Cas12a nucleases for targeted mutagenesis in maize. <i>Plant Biotechnology Journal</i> , 2019, 17, 362-372. | 4.1 | 192 |
| 17 | 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. | 1.6 | 23 |
| 18 | CRISPR DNA base editors with reduced RNA off-target and self-editing activities. <i>Nature Biotechnology</i> , 2019, 37, 1041-1048. | 9.4 | 236 |

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|----|---|------|-----------|
| 19 | High levels of AAV vector integration into CRISPR-induced DNA breaks. <i>Nature Communications</i> , 2019, 10, 4439. | 5.8 | 257 |
| 20 | Droplet-based combinatorial indexing for massive-scale single-cell chromatin accessibility. <i>Nature Biotechnology</i> , 2019, 37, 916-924. | 9.4 | 315 |
| 21 | Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. <i>Cell Reports</i> , 2019, 27, 3228-3240.e7. | 2.9 | 122 |
| 22 | Stromal Microenvironment Shapes the Intratumoral Architecture of Pancreatic Cancer. <i>Cell</i> , 2019, 178, 160-175.e27. | 13.5 | 367 |
| 23 | Transcriptome-wide off-target RNA editing induced by CRISPR-guided DNA base editors. <i>Nature</i> , 2019, 569, 433-437. | 13.7 | 434 |
| 24 | Epigenetic evolution and lineage histories of chronic lymphocytic leukaemia. <i>Nature</i> , 2019, 569, 576-580. | 13.7 | 195 |
| 25 | Reply. <i>Gastroenterology</i> , 2019, 156, 1933-1934. | 0.6 | 0 |
| 26 | Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019, 10, 1903. | 5.8 | 198 |
| 27 | Interrogation of human hematopoiesis at single-cell and single-variant resolution. <i>Nature Genetics</i> , 2019, 51, 683-693. | 9.4 | 147 |
| 28 | A (fire)cloud-based DNA methylation data preprocessing and quality control platform. <i>BMC Bioinformatics</i> , 2019, 20, 160. | 1.2 | 7 |
| 29 | Engineered CRISPR-Cas12a variants with increased activities and improved targeting ranges for gene, epigenetic and base editing. <i>Nature Biotechnology</i> , 2019, 37, 276-282. | 9.4 | 439 |
| 30 | Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. <i>Cell</i> , 2019, 176, 1325-1339.e22. | 13.5 | 345 |
| 31 | Preprocessing and Computational Analysis of Single-Cell Epigenomic Datasets. <i>Methods in Molecular Biology</i> , 2019, 1935, 187-202. | 0.4 | 2 |
| 32 | hichipper: a preprocessing pipeline for calling DNA loops from HiChIP data. <i>Nature Methods</i> , 2018, 15, 155-156. | 9.0 | 139 |
| 33 | diffloop: a computational framework for identifying and analyzing differential DNA loops from sequencing data. <i>Bioinformatics</i> , 2018, 34, 672-674. | 1.8 | 57 |
| 34 | Integrated Single-Cell Analysis Maps the Continuous Regulatory Landscape of Human Hematopoietic Differentiation. <i>Cell</i> , 2018, 173, 1535-1548.e16. | 13.5 | 545 |
| 35 | Response to "Unexpected mutations after CRISPR-Cas9 editing in vivo". <i>Nature Methods</i> , 2018, 15, 238-239. | 9.0 | 25 |
| 36 | Detection and Analysis of Circulating Epithelial Cells in Liquid Biopsies From Patients With Liver Disease. <i>Gastroenterology</i> , 2018, 155, 2016-2018.e11. | 0.6 | 29 |

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|----|--|------|-----------|
| 37 | Defining CRISPR-Cas9 genome-wide nuclease activities with CIRCLE-seq. <i>Nature Protocols</i> , 2018, 13, 2615-2642. | 5.5 | 69 |
| 38 | In vivo CRISPR editing with no detectable genome-wide off-target mutations. <i>Nature</i> , 2018, 561, 416-419. | 13.7 | 274 |
| 39 | Enhancer histone-QTLs are enriched on autoimmune risk haplotypes and influence gene expression within chromatin networks. <i>Nature Communications</i> , 2018, 9, 2905. | 5.8 | 56 |
| 40 | OTX2 Activity at Distal Regulatory Elements Shapes the Chromatin Landscape of Group 3 Medulloblastoma. <i>Cancer Discovery</i> , 2017, 7, 288-301. | 7.7 | 53 |
| 41 | CIRCLE-seq: a highly sensitive in vitro screen for genome-wide CRISPR-Cas9 nuclease off-targets. <i>Nature Methods</i> , 2017, 14, 607-614. | 9.0 | 601 |
| 42 | 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. | 4.2 | 168 |
| 43 | The early pregnancy placenta foreshadows DNA methylation alterations of solid tumors. <i>Epigenetics</i> , 2017, 12, 793-803. | 1.3 | 31 |
| 44 | Diverse repetitive element RNA expression defines epigenetic and immunologic features of colon cancer. <i>JCI Insight</i> , 2017, 2, e91078. | 2.3 | 23 |
| 45 | Survival in Quiescence Requires the Euchromatic Deployment of Clr4/SUV39H by Argonaute-Associated Small RNAs. <i>Molecular Cell</i> , 2016, 64, 1088-1101. | 4.5 | 27 |
| 46 | 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. | 3.6 | 27 |
| 47 | <i>MET</i> Exon 14 Skipping in Non-Small Cell Lung Cancer. <i>Oncologist</i> , 2016, 21, 481-486. | 1.9 | 94 |
| 48 | Open-source guideseq software for analysis of GUIDE-seq data. <i>Nature Biotechnology</i> , 2016, 34, 483-483. | 9.4 | 49 |
| 49 | Genome-wide specificities of CRISPR-Cas Cpf1 nucleases in human cells. <i>Nature Biotechnology</i> , 2016, 34, 869-874. | 9.4 | 566 |
| 50 | Lysine Demethylase KDM4A Associates with Translation Machinery and Regulates Protein Synthesis. <i>Cancer Discovery</i> , 2015, 5, 255-263. | 7.7 | 51 |
| 51 | Engineered CRISPR-Cas9 nucleases with altered PAM specificities. <i>Nature</i> , 2015, 523, 481-485. | 13.7 | 1,388 |
| 52 | 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. | 1.9 | 33 |
| 53 | GUIDE-seq enables genome-wide profiling of off-target cleavage by CRISPR-Cas nucleases. <i>Nature Biotechnology</i> , 2015, 33, 187-197. | 9.4 | 1,757 |
| 54 | Coverage recommendations for methylation analysis by whole-genome bisulfite sequencing. <i>Nature Methods</i> , 2015, 12, 230-232. | 9.0 | 248 |

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|----|--|-----|-----------|
| 55 | A Novel Method for Detecting Association Between DNA Methylation and Diseases Using Spatial Information. <i>Genetic Epidemiology</i> , 2014, 38, 714-721. | 0.6 | 3 |
| 56 | 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. | 2.6 | 93 |
| 57 | Dimeric CRISPR RNA-guided FokI nucleases for highly specific genome editing. <i>Nature Biotechnology</i> , 2014, 32, 569-576. | 9.4 | 852 |
| 58 | 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. | 7.7 | 334 |
| 59 | Minfi: a flexible and comprehensive Bioconductor package for the analysis of Infinium DNA methylation microarrays. <i>Bioinformatics</i> , 2014, 30, 1363-1369. | 1.8 | 3,192 |
| 60 | Epigenome-wide association studies without the need for cell-type composition. <i>Nature Methods</i> , 2014, 11, 309-311. | 9.0 | 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. <i>Epigenetics</i> , 2013, 8, 290-302. | 1.3 | 353 |
| 62 | DNA Methylation Alterations Exhibit Intraindividual Stability and Interindividual Heterogeneity in Prostate Cancer Metastases. <i>Science Translational Medicine</i> , 2013, 5, 169ra10. | 5.8 | 231 |
| 63 | Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. <i>Nature Biotechnology</i> , 2013, 31, 142-147. | 9.4 | 874 |
| 64 | Global Causes of Diarrheal Disease Mortality in Children ≤ 5 Years of Age: A Systematic Review. <i>PLoS ONE</i> , 2013, 8, e72788. | 1.1 | 524 |
| 65 | 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. | 0.9 | 71 |
| 66 | A DNA hypermethylation module for the stem/progenitor cell signature of cancer. <i>Genome Research</i> , 2012, 22, 837-849. | 2.4 | 236 |
| 67 | 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. <i>Lancet</i> , The, 2012, 380, 2224-2260. | 6.3 | 9,397 |
| 68 | Reversible switching between epigenetic states in honeybee behavioral subcastes. <i>Nature Neuroscience</i> , 2012, 15, 1371-1373. | 7.1 | 305 |
| 69 | Estimating Diarrhea Mortality among Young Children in Low and Middle Income Countries. <i>PLoS ONE</i> , 2012, 7, e29151. | 1.1 | 114 |
| 70 | Genome-Wide DNA Methylation Scan in Major Depressive Disorder. <i>PLoS ONE</i> , 2012, 7, e34451. | 1.1 | 120 |
| 71 | Donor cell type can influence the epigenome and differentiation potential of human induced pluripotent stem cells. <i>Nature Biotechnology</i> , 2011, 29, 1117-1119. | 9.4 | 547 |
| 72 | 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. | 1.9 | 113 |

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|----|---|------|-----------|
| 73 | Accurate genome-scale percentage DNA methylation estimates from microarray data. <i>Biostatistics</i> , 2011, 12, 197-210. | 0.9 | 67 |
| 74 | Adaptation of the CHARM DNA methylation platform for the rat genome reveals novel brain region-specific differences. <i>Epigenetics</i> , 2011, 6, 1378-1390. | 1.3 | 17 |
| 75 | Comprehensive methylome map of lineage commitment from haematopoietic progenitors. <i>Nature</i> , 2010, 467, 338-342. | 13.7 | 554 |
| 76 | Androgen-induced TOP2B-mediated double-strand breaks and prostate cancer gene rearrangements. <i>Nature Genetics</i> , 2010, 42, 668-675. | 9.4 | 539 |
| 77 | Therapeutic Implications of GIPC1 Silencing in Cancer. <i>PLoS ONE</i> , 2010, 5, e15581. | 1.1 | 22 |
| 78 | Personalized Epigenomic Signatures That Are Stable Over Time and Covary with Body Mass Index. <i>Science Translational Medicine</i> , 2010, 2, 49ra67. | 5.8 | 292 |
| 79 | Subset Quantile Normalization Using Negative Control Features. <i>Journal of Computational Biology</i> , 2010, 17, 1385-1395. | 0.8 | 52 |
| 80 | 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. | 1.2 | 87 |
| 81 | 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. | 9.4 | 1,076 |
| 82 | Circularization for In vitro Reporting of Cleavage Effects (CIRCLE-seq). <i>Protocol Exchange</i> , 0, , . | 0.3 | 1 |