

# Sebastian Moran

## 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.

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|-------------------|-------------------------|----------------|-----------------|
| 87<br>papers      | 6,762<br>citations      | 41<br>h-index  | 82<br>g-index   |
| 89<br>ext. papers | 8,487<br>ext. citations | 9.2<br>avg, IF | 5.41<br>L-index |

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 87 | A synthetic mRNA cell reprogramming method using CYCLIN D1 promotes DNA repair, generating improved genetically stable human induced pluripotent stem cells. <i>Stem Cells</i> , <b>2021</b> , 39, 866-881                      | 5.8  | 3         |
| 86 | Distinct Associations of BMI and Fatty Acids With DNA Methylation in Fasting and Postprandial States in Men. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 665769  | 4.5  | 1         |
| 85 | Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , <b>2021</b> , 12, 498   | 17.4 | 74        |
| 84 | Identification of 20 novel loci associated with ischaemic stroke. Epigenome-wide association study. <i>Epigenetics</i> , <b>2020</b> , 15, 988-997  | 5.7  | 9         |
| 83 | Interactive effect of age and APOE- $\epsilon$ allele load on white matter myelin content in cognitively normal middle-aged subjects. <i>NeuroImage: Clinical</i> , <b>2019</b> , 24, 101983                                    | 5.3  | 6         |
| 82 | EGLN2 DNA methylation and expression interact with HIF1A to affect survival of early-stage NSCLC. <i>Epigenetics</i> , <b>2019</b> , 14, 118-129  | 5.7  | 17        |
| 81 | Prenatal adverse environment is associated with epigenetic age deceleration at birth and hypomethylation at the hypoxia-responsive EP300 gene. <i>Clinical Epigenetics</i> , <b>2019</b> , 11, 73                               | 7.7  | 23        |
| 80 | APOE- $\epsilon$ risk variant for Alzheimer's disease modifies the association between cognitive performance and cerebral morphology in healthy middle-aged individuals. <i>NeuroImage: Clinical</i> , <b>2019</b> , 23, 101818 | 5.3  | 10        |
| 79 | SIPA1L3 methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic-smoking interaction analysis. <i>Molecular Oncology</i> , <b>2019</b> , 13, 1235-1248                              | 7.9  | 11        |
| 78 | Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. <i>Acta Neuropathologica</i> , <b>2019</b> , 138, 1053-1074  | 14.3 | 55        |
| 77 | Mechanisms of resistance to a PI3K inhibitor in gastrointestinal stromal tumors: an approach to identify novel druggable targets. <i>Cancer Management and Research</i> , <b>2019</b> , 11, 6229-6244                           | 3.6  | 2         |
| 76 | Molecular portrait of high alpha-fetoprotein in hepatocellular carcinoma: implications for biomarker-driven clinical trials. <i>British Journal of Cancer</i> , <b>2019</b> , 121, 340-343                                      | 8.7  | 29        |
| 75 | The Altered Transcriptome and DNA Methylation Profiles of Docetaxel Resistance in Breast Cancer PDX Models. <i>Molecular Cancer Research</i> , <b>2019</b> , 17, 2063-2076  | 6.6  | 12        |
| 74 | MicroRNA-654-5p suppresses ovarian cancer development impacting on MYC, WNT and AKT pathways. <i>Oncogene</i> , <b>2019</b> , 38, 6035-6050   | 9.2  | 34        |
| 73 | Global Proteomic and Methylome Analysis in Human Induced Pluripotent Stem Cells Reveals Overexpression of a Human TLR3 Affecting Proper Innate Immune Response Signaling. <i>Stem Cells</i> , <b>2019</b> , 37, 476-488         | 5.8  | 5         |
| 72 | Identification of an epistatue of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis. <i>International Journal of Obesity</i> , <b>2019</b> , 43, 176-188                                  | 5.5  | 32        |
| 71 | A multi-omic study reveals BTG2 as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , <b>2018</b> , 12, 913-924   | 7.9  | 23        |

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|----|---|------|-----|
| 70 | Epigenetic modifications in lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 41  | 7.7  | 11  |
| 69 | Infinium DNA Methylation Microarrays on Formalin-Fixed, Paraffin-Embedded Samples. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1766, 83-107   | 1.4  | 3   |
| 68 | Effects of APOE- $\epsilon$ allele load on brain morphology in a cohort of middle-aged healthy individuals with enriched genetic risk for Alzheimer's disease. <i>Alzheimer's and Dementia</i> , <b>2018</b> , 14, 902-912  | 1.2  | 64  |
| 67 | Higher prevalence of cerebral white matter hyperintensities in homozygous APOE-e4 allele carriers aged 45-75: Results from the ALFA study. <i>Journal of Cerebral Blood Flow and Metabolism</i> , <b>2018</b> , 38, 250-261 | 7.3  | 17  |
| 66 | Profiling of oxBS-450K 5-hydroxymethylcytosine in human placenta and brain reveals enrichment at imprinted loci. <i>Epigenetics</i> , <b>2018</b> , 13, 182-191   | 5.7  | 12  |
| 65 | A new approach to epigenome-wide discovery of non-invasive methylation biomarkers for colorectal cancer screening in circulating cell-free DNA using pooled samples. <i>Clinical Epigenetics</i> , <b>2018</b> , 10, 53     | 7.7  | 27  |
| 64 | White matter microstructure is altered in cognitively normal middle-aged APOE- $\epsilon$ homozygotes. <i>Alzheimer's Research and Therapy</i> , <b>2018</b> , 10, 48   | 9    | 27  |
| 63 | Epigenetic prediction of response to anti-PD-1 treatment in non-small-cell lung cancer: a multicentre, retrospective analysis. <i>Lancet Respiratory Medicine</i> , <b>2018</b> , 6, 771-781                                | 35.1 | 107 |
| 62 | Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , <b>2018</b> , 67, 1995-2005                                | 19.2 | 119 |
| 61 | Deep analysis of acquired resistance to FGFR1 inhibitor identifies MET and AKT activation and an expansion of mutant cells. <i>Oncotarget</i> , <b>2018</b> , 9, 31549-31558  | 3.3  | 6   |
| 60 | Circular RNA CpG island hypermethylation-associated silencing in human cancer. <i>Oncotarget</i> , <b>2018</b> , 9, 29208-29219   | 3.3  | 22  |
| 59 | An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , <b>2018</b> , 8, 13537  | 4.9  | 29  |
| 58 | Characterization of parent-of-origin methylation using the Illumina Infinium MethylationEPIC array platform. <i>Epigenomics</i> , <b>2018</b> , 10, 941-954   | 4.4  | 13  |
| 57 | Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , <b>2017</b> , 71, e21959  | 2.4  | 10  |
| 56 | Journal club: epigenetic profiling to classify cancer of unknown primary - AuthorsWepley. <i>Lancet Oncology</i> , <b>2017</b> , 18, e131   | 21.7 | 1   |
| 55 | Genomic and Molecular Screenings Identify Different Mechanisms for Acquired Resistance to MET Inhibitors in Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , <b>2017</b> , 16, 1366-1376                           | 6.1  | 19  |
| 54 | Obesity and menopause modify the epigenomic profile of breast cancer. <i>Endocrine-Related Cancer</i> , <b>2017</b> , 24, 351-363   | 5.7  | 23  |
| 53 | Technologies for Deciphering Epigenomic DNA Patterns. <i>Advances in Experimental Medicine and Biology</i> , <b>2017</b> , 978, 477-488   | 3.6  |     |

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|----|--|------|-----|
| 52 | A DNA methylation map of human cancer at single base-pair resolution. <i>Oncogene</i> , <b>2017</b> , 36, 5648-5657  | 9.2  | 52  |
| 51 | Epigenetic loss of the RNA decapping enzyme NUDT16 mediates C-MYC activation in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , <b>2017</b> , 31, 1622-1625   | 10.7 | 12  |
| 50 | Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 3203-3213   | 12.9 | 45  |
| 49 | The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , <b>2017</b> , 77, 601-612  | 10.1 | 34  |
| 48 | Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies B2M Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 3203-3213   | 12.9 | 45  |
| 47 | DNA methylation signal has a major role in the response of human breast cancer cells to the microenvironment. <i>Oncogenesis</i> , <b>2017</b> , 6, e390   | 6.6  | 22  |
| 46 | Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. <i>Nature Communications</i> , <b>2017</b> , 8, 467  | 17.4 | 18  |
| 45 | Targeted Exome Sequencing of Krebs Cycle Genes Reveals Candidate Cancer-Predisposing Mutations in Pheochromocytomas and Paragangliomas. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 6315-6324  | 12.9 | 47  |
| 44 | Precision medicine based on epigenomics: the paradigm of carcinoma of unknown primary. <i>Nature Reviews Clinical Oncology</i> , <b>2017</b> , 14, 682-694   | 19.4 | 57  |
| 43 | Sensitization of retinoids and corticoids to epigenetic drugs in MYC-activated lung cancers by antitumor reprogramming. <i>Oncogene</i> , <b>2017</b> , 36, 1287-1296  | 9.2  | 7   |
| 42 | DNA methylation profiling identifies PTRF/Cavin-1 as a novel tumor suppressor in Ewing sarcoma when co-expressed with caveolin-1. <i>Cancer Letters</i> , <b>2017</b> , 386, 196-207   | 9.9  | 22  |
| 41 | [P2B44]: BRAIN MORPHOMETRICAL CORRELATES UNDERLYING COGNITIVE PERFORMANCE IN A GENETICALLY ENRICHED SAMPLE OF HEALTHY INDIVIDUALS AT RISK FOR ALZHEIMER'S DISEASE <b>2017</b> , 13, P753-P754  |      |     |
| 40 | GENE-13. AN INTEGRATED GENOMIC ANALYSIS OF ANAPLASTIC MENINGIOMA IDENTIFIES PROGNOSTIC MOLECULAR SIGNATURES. <i>Neuro-Oncology</i> , <b>2017</b> , 19, vi95-vi95   | 1    | 78  |
| 39 | DNMT3A mutations mediate the epigenetic reactivation of the leukemogenic factor MEIS1 in acute myeloid leukemia. <i>Oncogene</i> , <b>2016</b> , 35, 3079-82   | 9.2  | 41  |
| 38 | Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , <b>2016</b> , 17, 1386-1395  | 21.7 | 251 |
| 37 | Epigenetic Homogeneity Within Colorectal Tumors Predicts Shorter Relapse-Free and Overall Survival Times for Patients With Locoregional Cancer. <i>Gastroenterology</i> , <b>2016</b> , 151, 961-972   | 13.3 | 30  |
| 36 | Metformin pharmacogenomics: a genome-wide association study to identify genetic and epigenetic biomarkers involved in metformin anticancer response using human lymphoblastoid cell lines. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 4819-4834 | 5.6  | 16  |
| 35 | Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , <b>2016</b> , 6, e718  | 8.6  | 101 |

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|----|---|------|-----|
| 34 | Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. <i>Epigenomics</i> , <b>2016</b> , 8, 389-99   | 4.4  | 352 |
| 33 | Gene amplification-associated overexpression of the RNA editing enzyme ADAR1 enhances human lung tumorigenesis. <i>Oncogene</i> , <b>2016</b> , 35, 4407-13   | 9.2  | 52  |
| 32 | Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , <b>2016</b> , 17, 11   | 18.3 | 141 |
| 31 | Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , <b>2016</b> , 7, 3084-97  | 3.3  | 88  |
| 30 | A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , <b>2016</b> , 166, 740-754   | 56.2 | 892 |
| 29 | Arachidonic and oleic acid exert distinct effects on the DNA methylome. <i>Epigenetics</i> , <b>2016</b> , 11, 321-34   | 5.7  | 40  |
| 28 | The ALFA project: A research platform to identify early pathophysiological features of Alzheimer's disease. <i>Alzheimer's and Dementia: Translational Research and Clinical Interventions</i> , <b>2016</b> , 2, 82-92 | 6    | 63  |
| 27 | Whole-exome sequencing identifies MDH2 as a new familial paraganglioma gene. <i>Journal of the National Cancer Institute</i> , <b>2015</b> , 107,   | 9.7  | 114 |
| 26 | DNA methylation dynamics in human carotid plaques after cerebrovascular events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2015</b> , 35, 1835-42   | 9.4  | 28  |
| 25 | The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. <i>BMC Medical Genomics</i> , <b>2015</b> , 8, 7  | 3.7  | 73  |
| 24 | Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. <i>Carcinogenesis</i> , <b>2015</b> , 36, 1453-63  | 4.6  | 62  |
| 23 | KAT6B Is a Tumor Suppressor Histone H3 Lysine 23 Acetyltransferase Undergoing Genomic Loss in Small Cell Lung Cancer. <i>Cancer Research</i> , <b>2015</b> , 75, 3936-45  | 10.1 | 48  |
| 22 | A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , <b>2015</b> , 9, 555-68   | 7.9  | 117 |
| 21 | H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , <b>2015</b> , 25, 27-40  | 9.7  | 89  |
| 20 | Epigenetic activation of a cryptic TBC1D16 transcript enhances melanoma progression by targeting EGFR. <i>Nature Medicine</i> , <b>2015</b> , 21, 741-50  | 50.5 | 75  |
| 19 | Identification of a new locus and validation of previously reported loci showing differential methylation associated with smoking. The REGICOR study. <i>Epigenetics</i> , <b>2015</b> , 10, 1156-65                    | 5.7  | 30  |
| 18 | Epigenetic mechanisms involved in melanoma pathogenesis and chemoresistance. <i>Annals of Translational Medicine</i> , <b>2015</b> , 3, 209   | 3.2  | 11  |
| 17 | DNA methylation map of human atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , <b>2014</b> , 7, 692-700  |      | 157 |

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| 16 | MAX inactivation in small cell lung cancer disrupts MYC-SWI/SNF programs and is synthetic lethal with BRG1. <i>Cancer Discovery</i> , <b>2014</b> , 4, 292-303                                 | 24.4 | 118 |
| 15 | Linkage of DNA methylation quantitative trait loci to human cancer risk. <i>Cell Reports</i> , <b>2014</b> , 7, 331-338  | 10.6 | 60  |
| 14 | Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. <i>Oncogene</i> , <b>2014</b> , 33, 2807-13  | 9.2  | 94  |
| 13 | Validation of DNA methylation profiling in formalin-fixed paraffin-embedded samples using the Infinium HumanMethylation450 Microarray. <i>Epigenetics</i> , <b>2014</b> , 9, 829-33            | 5.7  | 49  |
| 12 | A comprehensive DNA methylation profile of epithelial-to-mesenchymal transition. <i>Cancer Research</i> , <b>2014</b> , 74, 5608-19  | 10.1 | 54  |
| 11 | Variable maternal methylation overlapping the nc886/vtRNA2-1 locus is locked between hypermethylated repeats and is frequently altered in cancer. <i>Epigenetics</i> , <b>2014</b> , 9, 783-90 | 5.7  | 33  |
| 10 | Caveolin-1 is down-regulated in alveolar rhabdomyosarcomas and negatively regulates tumor growth. <i>Oncotarget</i> , <b>2014</b> , 5, 9744-55   | 3.3  | 18  |
| 9  | A prognostic DNA methylation signature for stage I non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , <b>2013</b> , 31, 4140-7  | 2.2  | 210 |
| 8  | Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , <b>2013</b> , 160, 406-9                     | 4.5  | 28  |
| 7  | Aberrant DNA methylation profiles in the premature aging disorders Hutchinson-Gilford Progeria and Werner syndrome. <i>Epigenetics</i> , <b>2013</b> , 8, 28-33                                | 5.7  | 84  |
| 6  | DNA methylation contributes to natural human variation. <i>Genome Research</i> , <b>2013</b> , 23, 1363-72   | 9.7  | 272 |
| 5  | Non-CpG island promoter hypomethylation and miR-149 regulate the expression of SRPX2 in colorectal cancer. <i>International Journal of Cancer</i> , <b>2013</b> , 132, 2303-15                 | 7.5  | 57  |
| 4  | DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , <b>2013</b> , 34, 102-8                           | 4.6  | 117 |
| 3  | Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 10522-7                      | 11.5 | 563 |
| 2  | Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , <b>2012</b> , 7, 542-50   | 5.7  | 59  |
| 1  | Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , <b>2011</b> , 6, 692-702  | 5.7  | 767 |