

Sebastian Moran

List of Publications by Citations

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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.

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

#	Paper	IF	Citations
87	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016 , 166, 740-754	56.2	892
86	Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011 , 6, 692-702	5.7	767
85	Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10522-7	11.5	563
84	Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. <i>Epigenomics</i> , 2016 , 8, 389-99	4.4	352
83	DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013 , 23, 1363-72	9.7	272
82	Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology, The</i> , 2016 , 17, 1386-1395	21.7	251
81	A prognostic DNA methylation signature for stage I non-small-cell lung cancer. <i>Journal of Clinical Oncology</i> , 2013 , 31, 4140-7	2.2	210
80	DNA methylation map of human atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014 , 7, 692-700		157
79	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016 , 17, 11	18.3	141
78	Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , 2018 , 67, 1995-2005	19.2	119
77	MAX inactivation in small cell lung cancer disrupts MYC-SWI/SNF programs and is synthetic lethal with BRG1. <i>Cancer Discovery</i> , 2014 , 4, 292-303	24.4	118
76	A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015 , 9, 555-68	7.9	117
75	DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013 , 34, 102-8	4.6	117
74	Whole-exome sequencing identifies MDH2 as a new familial paraganglioma gene. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	114
73	Epigenetic prediction of response to anti-PD-1 treatment in non-small-cell lung cancer: a multicentre, retrospective analysis. <i>Lancet Respiratory Medicine, the</i> , 2018 , 6, 771-781	35.1	107
72	Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016 , 6, e718	8.6	101
71	Gene amplification of the histone methyltransferase SETDB1 contributes to human lung tumorigenesis. <i>Oncogene</i> , 2014 , 33, 2807-13	9.2	94

70	H3K4me1 marks DNA regions hypomethylated during aging in human stem and differentiated cells. <i>Genome Research</i> , 2015 , 25, 27-40	9.7	89
69	Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , 2016 , 7, 3084-97	3.3	88
68	Aberrant DNA methylation profiles in the premature aging disorders Hutchinson-Gilford Progeria and Werner syndrome. <i>Epigenetics</i> , 2013 , 8, 28-33	5.7	84
67	GENE-13. AN INTEGRATED GENOMIC ANALYSIS OF ANAPLASTIC MENINGIOMA IDENTIFIES PROGNOSTIC MOLECULAR SIGNATURES. <i>Neuro-Oncology</i> , 2017 , 19, vi95-vi95	1	78
66	Epigenetic activation of a cryptic TBC1D16 transcript enhances melanoma progression by targeting EGFR. <i>Nature Medicine</i> , 2015 , 21, 741-50	50.5	75
65	Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021 , 12, 498	17.4	74
64	The DNA methylation drift of the atherosclerotic aorta increases with lesion progression. <i>BMC Medical Genomics</i> , 2015 , 8, 7	3.7	73
63	Effects of APOE- ϵ 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> , 2018 , 14, 902-912	1.2	64
62	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> , 2016 , 2, 82-92	6	63
61	Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. <i>Carcinogenesis</i> , 2015 , 36, 1453-63	4.6	62
60	Linkage of DNA methylation quantitative trait loci to human cancer risk. <i>Cell Reports</i> , 2014 , 7, 331-338	10.6	60
59	Whole-genome bisulfite DNA sequencing of a DNMT3B mutant patient. <i>Epigenetics</i> , 2012 , 7, 542-50	5.7	59
58	Precision medicine based on epigenomics: the paradigm of carcinoma of unknown primary. <i>Nature Reviews Clinical Oncology</i> , 2017 , 14, 682-694	19.4	57
57	Non-CpG island promoter hypomethylation and miR-149 regulate the expression of SRPX2 in colorectal cancer. <i>International Journal of Cancer</i> , 2013 , 132, 2303-15	7.5	57
56	Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. <i>Acta Neuropathologica</i> , 2019 , 138, 1053-1074	14.3	55
55	A comprehensive DNA methylation profile of epithelial-to-mesenchymal transition. <i>Cancer Research</i> , 2014 , 74, 5608-19	10.1	54
54	A DNA methylation map of human cancer at single base-pair resolution. <i>Oncogene</i> , 2017 , 36, 5648-5657	9.2	52
53	Gene amplification-associated overexpression of the RNA editing enzyme ADAR1 enhances human lung tumorigenesis. <i>Oncogene</i> , 2016 , 35, 4407-13	9.2	52

52	Validation of DNA methylation profiling in formalin-fixed paraffin-embedded samples using the Infinium HumanMethylation450 Microarray. <i>Epigenetics</i> , 2014 , 9, 829-33	5.7	49
51	KAT6B Is a Tumor Suppressor Histone H3 Lysine 23 Acetyltransferase Undergoing Genomic Loss in Small Cell Lung Cancer. <i>Cancer Research</i> , 2015 , 75, 3936-45	10.1	48
50	Targeted Exome Sequencing of Krebs Cycle Genes Reveals Candidate Cancer-Predisposing Mutations in Pheochromocytomas and Paragangliomas. <i>Clinical Cancer Research</i> , 2017 , 23, 6315-6324	12.9	47
49	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017 , 23, 3203-3213	12.9	45
48	Genomic Profiling of Patient-Derived Xenografts for Lung Cancer Identifies B2M Inactivation Impairing Immunorecognition. <i>Clinical Cancer Research</i> , 2017 , 23, 3203-3213	12.9	45
47	DNMT3A mutations mediate the epigenetic reactivation of the leukemogenic factor MEIS1 in acute myeloid leukemia. <i>Oncogene</i> , 2016 , 35, 3079-82	9.2	41
46	Arachidonic and oleic acid exert distinct effects on the DNA methylome. <i>Epigenetics</i> , 2016 , 11, 321-34	5.7	40
45	The NCI-60 Methylome and Its Integration into CellMiner. <i>Cancer Research</i> , 2017 , 77, 601-612	10.1	34
44	MicroRNA-654-5p suppresses ovarian cancer development impacting on MYC, WNT and AKT pathways. <i>Oncogene</i> , 2019 , 38, 6035-6050	9.2	34
43	Variable maternal methylation overlapping the nc886/vtRNA2-1 locus is locked between hypermethylated repeats and is frequently altered in cancer. <i>Epigenetics</i> , 2014 , 9, 783-90	5.7	33
42	Identification of an episinature of human colorectal cancer associated with obesity by genome-wide DNA methylation analysis. <i>International Journal of Obesity</i> , 2019 , 43, 176-188	5.5	32
41	Epigenetic Homogeneity Within Colorectal Tumors Predicts Shorter Relapse-Free and Overall Survival Times for Patients With Locoregional Cancer. <i>Gastroenterology</i> , 2016 , 151, 961-972	13.3	30
40	Identification of a new locus and validation of previously reported loci showing differential methylation associated with smoking. The REGICOR study. <i>Epigenetics</i> , 2015 , 10, 1156-65	5.7	30
39	Molecular portrait of high alpha-fetoprotein in hepatocellular carcinoma: implications for biomarker-driven clinical trials. <i>British Journal of Cancer</i> , 2019 , 121, 340-343	8.7	29
38	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , 2018 , 8, 13537	4.9	29
37	DNA methylation dynamics in human carotid plaques after cerebrovascular events. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 1835-42	9.4	28
36	Genome-wide DNA methylation profiling predicts relapse in childhood B-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2013 , 160, 406-9	4.5	28
35	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> , 2018 , 10, 53	7.7	27

34	White matter microstructure is altered in cognitively normal middle-aged APOE- ϵ homozygotes. <i>Alzheimer's Research and Therapy</i> , 2018 , 10, 48	9	27
33	Obesity and menopause modify the epigenomic profile of breast cancer. <i>Endocrine-Related Cancer</i> , 2017 , 24, 351-363	5.7	23
32	Prenatal adverse environment is associated with epigenetic age deceleration at birth and hypomethylation at the hypoxia-responsive EP300 gene. <i>Clinical Epigenetics</i> , 2019 , 11, 73	7.7	23
31	A multi-omic study reveals BTG2 as a reliable prognostic marker for early-stage non-small cell lung cancer. <i>Molecular Oncology</i> , 2018 , 12, 913-924	7.9	23
30	DNA methylation signal has a major role in the response of human breast cancer cells to the microenvironment. <i>Oncogenesis</i> , 2017 , 6, e390	6.6	22
29	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> , 2017 , 386, 196-207	9.9	22
28	Circular RNA CpG island hypermethylation-associated silencing in human cancer. <i>Oncotarget</i> , 2018 , 9, 29208-29219	3.3	22
27	Genomic and Molecular Screenings Identify Different Mechanisms for Acquired Resistance to MET Inhibitors in Lung Cancer Cells. <i>Molecular Cancer Therapeutics</i> , 2017 , 16, 1366-1376	6.1	19
26	Copy number rather than epigenetic alterations are the major dictator of imprinted methylation in tumors. <i>Nature Communications</i> , 2017 , 8, 467	17.4	18
25	Caveolin-1 is down-regulated in alveolar rhabdomyosarcomas and negatively regulates tumor growth. <i>Oncotarget</i> , 2014 , 5, 9744-55	3.3	18
24	EGLN2 DNA methylation and expression interact with HIF1A to affect survival of early-stage NSCLC. <i>Epigenetics</i> , 2019 , 14, 118-129	5.7	17
23	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> , 2018 , 38, 250-261	7.3	17
22	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> , 2016 , 25, 4819-4834	5.6	16
21	Characterization of parent-of-origin methylation using the Illumina Infinium MethylationEPIC array platform. <i>Epigenomics</i> , 2018 , 10, 941-954	4.4	13
20	Epigenetic loss of the RNA decapping enzyme NUDT16 mediates C-MYC activation in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2017 , 31, 1622-1625	10.7	12
19	Profiling of oxBS-450K 5-hydroxymethylcytosine in human placenta and brain reveals enrichment at imprinted loci. <i>Epigenetics</i> , 2018 , 13, 182-191	5.7	12
18	The Altered Transcriptome and DNA Methylation Profiles of Docetaxel Resistance in Breast Cancer PDX Models. <i>Molecular Cancer Research</i> , 2019 , 17, 2063-2076	6.6	12
17	SIPA1L3 methylation modifies the benefit of smoking cessation on lung adenocarcinoma survival: an epigenomic-smoking interaction analysis. <i>Molecular Oncology</i> , 2019 , 13, 1235-1248	7.9	11

16	Epigenetic modifications in lysine demethylases associate with survival of early-stage NSCLC. <i>Clinical Epigenetics</i> , 2018 , 10, 41	7.7	11
15	Epigenetic mechanisms involved in melanoma pathogenesis and chemoresistance. <i>Annals of Translational Medicine</i> , 2015 , 3, 209	3.2	11
14	Whole genome grey and white matter DNA methylation profiles in dorsolateral prefrontal cortex. <i>Synapse</i> , 2017 , 71, e21959	2.4	10
13	APOE- ϵ risk variant for Alzheimer's disease modifies the association between cognitive performance and cerebral morphology in healthy middle-aged individuals. <i>NeuroImage: Clinical</i> , 2019 , 23, 101818	5.3	10
12	Identification of 20 novel loci associated with ischaemic stroke. Epigenome-wide association study. <i>Epigenetics</i> , 2020 , 15, 988-997	5.7	9
11	Sensitization of retinoids and corticoids to epigenetic drugs in MYC-activated lung cancers by antitumor reprogramming. <i>Oncogene</i> , 2017 , 36, 1287-1296	9.2	7
10	Interactive effect of age and APOE- ϵ allele load on white matter myelin content in cognitively normal middle-aged subjects. <i>NeuroImage: Clinical</i> , 2019 , 24, 101983	5.3	6
9	Deep analysis of acquired resistance to FGFR1 inhibitor identifies MET and AKT activation and an expansion of mutant cells. <i>Oncotarget</i> , 2018 , 9, 31549-31558	3.3	6
8	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> , 2019 , 37, 476-488	5.8	5
7	Infinium DNA Methylation Microarrays on Formalin-Fixed, Paraffin-Embedded Samples. <i>Methods in Molecular Biology</i> , 2018 , 1766, 83-107	1.4	3
6	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> , 2021 , 39, 866-881	5.8	3
5	Mechanisms of resistance to a PI3K inhibitor in gastrointestinal stromal tumors: an approach to identify novel druggable targets. <i>Cancer Management and Research</i> , 2019 , 11, 6229-6244	3.6	2
4	Journal club: epigenetic profiling to classify cancer of unknown primary - AuthorsWepley. <i>Lancet Oncology, The</i> , 2017 , 18, e131	21.7	1
3	Distinct Associations of BMI and Fatty Acids With DNA Methylation in Fasting and Postprandial States in Men. <i>Frontiers in Genetics</i> , 2021 , 12, 665769	4.5	1
2	Technologies for Deciphering Epigenomic DNA Patterns. <i>Advances in Experimental Medicine and Biology</i> , 2017 , 978, 477-488	3.6	
1	[P2B44]: BRAIN MORPHOMETRICAL CORRELATES UNDERLYING COGNITIVE PERFORMANCE IN A GENETICALLY ENRICHED SAMPLE OF HEALTHY INDIVIDUALS AT RISK FOR ALZHEIMER'S DISEASE 2017 , 13, P753-P754		