

# Susan J Clark

## List of Publications by Citations

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176  
papers

14,901  
citations

60  
h-index

120  
g-index

186  
ext. papers

17,482  
ext. citations

9.6  
avg. IF

6.25  
L-index

#	Paper	IF	Citations
176	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , <b>2013</b> , 496, 498-503	50.4	2550
175	miRNA-dependent gene silencing involving Ago2-mediated cleavage of a circular antisense RNA. <i>EMBO Journal</i> , <b>2011</b> , 30, 4414-22	13	636
174	Bisulfite genomic sequencing: systematic investigation of critical experimental parameters. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, E65-5	20.1	543
173	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , <b>2016</b> , 17, 208	18.3	517
172	De novo identification of differentially methylated regions in the human genome. <i>Epigenetics and Chromatin</i> , <b>2015</b> , 8, 6	5.8	441
171	Transcriptional gene silencing promotes DNA hypermethylation through a sequential change in chromatin modifications in cancer cells. <i>Cancer Research</i> , <b>2004</b> , 64, 3871-7	10.1	357
170	Epigenetic remodeling in colorectal cancer results in coordinate gene suppression across an entire chromosome band. <i>Nature Genetics</i> , <b>2006</b> , 38, 540-9	36.3	323
169	Detection and measurement of PCR bias in quantitative methylation analysis of bisulphite-treated DNA. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 4422-6	20.1	317
168	Coordinated epigenetic repression of the miR-200 family and miR-205 in invasive bladder cancer. <i>International Journal of Cancer</i> , <b>2011</b> , 128, 1327-34	7.5	301
167	DNA methylation: bisulphite modification and analysis. <i>Nature Protocols</i> , <b>2006</b> , 1, 2353-64	18.8	278
166	Identification and resolution of artifacts in bisulfite sequencing. <i>Methods</i> , <b>2002</b> , 27, 101-7	4.6	242
165	CpNpG methylation in mammalian cells. <i>Nature Genetics</i> , <b>1995</b> , 10, 20-7	36.3	242
164	DNA methylation and gene silencing in cancer: which is the guilty party?. <i>Oncogene</i> , <b>2002</b> , 21, 5380-7	9.2	233
163	Methyl-CpG-binding domain proteins: readers of the epigenome. <i>Epigenomics</i> , <b>2015</b> , 7, 1051-73	4.4	230
162	Epigenetics and human obesity. <i>International Journal of Obesity</i> , <b>2015</b> , 39, 85-97	5.5	226
161	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 726-37	44.5	204
160	Genomic profiling of CpG methylation and allelic specificity using quantitative high-throughput mass spectrometry: critical evaluation and improvements. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, e119	20.1	200

159	Detailed methylation analysis of the glutathione S-transferase pi (GSTP1) gene in prostate cancer. <i>Oncogene</i> , <b>1999</b> , 18, 1313-24	9.2	193
158	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , <b>2016</b> , 26, 719-31	9.7	186
157	Comparison of methyl-DNA immunoprecipitation (MeDIP) and methyl-CpG binding domain (MBD) protein capture for genome-wide DNA methylation analysis reveal CpG sequence coverage bias. <i>Epigenetics</i> , <b>2011</b> , 6, 34-44	5.7	164
156	Epigenetics in prostate cancer: biologic and clinical relevance. <i>European Urology</i> , <b>2011</b> , 60, 753-66	10.2	164
155	Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells. <i>Oncogene</i> , <b>2002</b> , 21, 1048-61	9.2	159
154	Moving AHEAD with an international human epigenome project. <i>Nature</i> , <b>2008</b> , 454, 711-5	50.4	158
153	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. <i>Nature Cell Biology</i> , <b>2010</b> , 12, 235-46	23.4	153
152	Regional activation of the cancer genome by long-range epigenetic remodeling. <i>Cancer Cell</i> , <b>2013</b> , 23, 9-22	24.3	150
151	DNA methylation changes in ovarian cancer: implications for early diagnosis, prognosis and treatment. <i>Gynecologic Oncology</i> , <b>2008</b> , 109, 129-39	4.9	150
150	Reconfiguration of nucleosome-depleted regions at distal regulatory elements accompanies DNA methylation of enhancers and insulators in cancer. <i>Genome Research</i> , <b>2014</b> , 24, 1421-32	9.7	149
149	Sp1 binding is inhibited by (m)Cp(m)CpG methylation. <i>Gene</i> , <b>1997</b> , 195, 67-71	3.8	149
148	Mining cancer methylomes: prospects and challenges. <i>Trends in Genetics</i> , <b>2014</b> , 30, 75-84	8.5	146
147	Hypermethylation of E-cadherin in leukemia. <i>Blood</i> , <b>2000</b> , 95, 3208-3213	2.2	136
146	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. <i>Genome Research</i> , <b>2012</b> , 22, 1120-7	9.7	128
145	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. <i>Genome Research</i> , <b>2012</b> , 22, 307-21	9.7	124
144	Organization of human histone genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1982</b> , 79, 1795-9	11.5	124
143	MicroRNA alterations and associated aberrant DNA methylation patterns across multiple sample types in oral squamous cell carcinoma. <i>PLoS ONE</i> , <b>2011</b> , 6, e27840	3.7	122
142	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , <b>2015</b> , 6, 5899	17.4	118

141	Low O6-methylguanine-DNA methyltransferase (MGMT) expression and response to temozolomide in aggressive pituitary tumours. <i>Clinical Endocrinology</i> , <b>2009</b> , 71, 226-33	3.4	105
140	Circulating microRNAs are associated with docetaxel chemotherapy outcome in castration-resistant prostate cancer. <i>British Journal of Cancer</i> , <b>2014</b> , 110, 2462-71	8.7	103
139	Evaluation of affinity-based genome-wide DNA methylation data: effects of CpG density, amplification bias, and copy number variation. <i>Genome Research</i> , <b>2010</b> , 20, 1719-29	9.7	100
138	Bisulfite sequencing in preimplantation embryos: DNA methylation profile of the upstream region of the mouse imprinted H19 gene. <i>Genomics</i> , <b>1998</b> , 51, 182-90	4.3	100
137	Action at a distance: epigenetic silencing of large chromosomal regions in carcinogenesis. <i>Human Molecular Genetics</i> , <b>2007</b> , 16 Spec No 1, R88-95	5.6	95
136	Analysis of histone gene expression during the cell cycle in HeLa cells by using cloned human histone genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1982</b> , 79, 749-53	11.5	86
135	Prognostic and diagnostic significance of DNA methylation patterns in high grade serous ovarian cancer. <i>Gynecologic Oncology</i> , <b>2012</b> , 124, 582-8	4.9	82
134	Epigenetic and phenotypic changes result from a continuous pre and post natal dietary exposure to phytoestrogens in an experimental population of mice. <i>BMC Physiology</i> , <b>2008</b> , 8, 17	0	80
133	DNA methylation profile of the mouse skeletal alpha-actin promoter during development and differentiation. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 164-72	4.8	78
132	Epigenetic-induced repression of microRNA-205 is associated with MED1 activation and a poorer prognosis in localized prostate cancer. <i>Oncogene</i> , <b>2013</b> , 32, 2891-9	9.2	77
131	DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. <i>Nature Communications</i> , <b>2015</b> , 6, 7758	17.4	75
130	Concordant epigenetic silencing of transforming growth factor-beta signaling pathway genes occurs early in breast carcinogenesis. <i>Cancer Research</i> , <b>2007</b> , 67, 11517-27	10.1	72
129	Increased DNA methyltransferase expression in leukaemia. <i>Leukemia</i> , <b>1998</b> , 12, 311-6	10.7	71
128	Mapping the regulatory sequences controlling 93 breast cancer-associated miRNA genes leads to the identification of two functional promoters of the Hsa-mir-200b cluster, methylation of which is associated with metastasis or hormone receptor status in advanced breast cancer. <i>Oncogene</i> , <b>2012</b> , 31, 4182-95	9.2	69
127	A distinct sequence (ATAAA) <sub>n</sub> separates methylated and unmethylated domains at the 5' end of the GSTP1 CpG island. <i>Journal of Biological Chemistry</i> , <b>2000</b> , 275, 24893-9	5.4	68
126	Multiple H4 histone mRNAs of HeLa cells are encoded in different genes. <i>Nature</i> , <b>1982</b> , 298, 195-8	50.4	68
125	Conversion-specific detection of DNA methylation using real-time polymerase chain reaction (ConLight-MSP) to avoid false positives. <i>Methods</i> , <b>2002</b> , 27, 114-20	4.6	67
124	Transient and Permanent Reconfiguration of Chromatin and Transcription Factor Occupancy Drive Reprogramming. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 834-845.e6	18	64

123	ELF5 suppresses estrogen sensitivity and underpins the acquisition of antiestrogen resistance in luminal breast cancer. <i>PLoS Biology</i> , <b>2012</b> , 10, e1001461	9.7	63
122	Methylated Glutathione S-transferase 1 (mGSTP1) is a potential plasma free DNA epigenetic marker of prognosis and response to chemotherapy in castrate-resistant prostate cancer. <i>British Journal of Cancer</i> , <b>2014</b> , 111, 1802-9	8.7	62
121	Discovery pipeline for epigenetically deregulated miRNAs in cancer: integration of primary miRNA transcription. <i>BMC Genomics</i> , <b>2011</b> , 12, 54	4.5	62
120	Breast cancer epigenetics: normal human mammary epithelial cells as a model system. <i>Journal of Molecular Medicine</i> , <b>2008</b> , 86, 1315-28	5.5	62
119	Cytosine methylation: quantitation by automated genomic sequencing and GENESCAN analysis. <i>BioTechniques</i> , <b>1996</b> , 21, 126-33	2.5	62
118	Permissive transcriptional activity at the centromere through pockets of DNA hypomethylation. <i>PLoS Genetics</i> , <b>2006</b> , 2, e17	6	61
117	Impact of the genome on the epigenome is manifested in DNA methylation patterns of imprinted regions in monozygotic and dizygotic twins. <i>PLoS ONE</i> , <b>2011</b> , 6, e25590	3.7	61
116	Enduring epigenetic landmarks define the cancer microenvironment. <i>Genome Research</i> , <b>2018</b> , 28, 625-638	9.7	60
115	Epigenetic inactivation of a cluster of genes flanking MLH1 in microsatellite-unstable colorectal cancer. <i>Cancer Research</i> , <b>2007</b> , 67, 9107-16	10.1	58
114	Long-range epigenetic silencing at 2q14.2 affects most human colorectal cancers and may have application as a non-invasive biomarker of disease. <i>British Journal of Cancer</i> , <b>2009</b> , 100, 1534-9	8.7	57
113	Aberrant de novo methylation of the p16INK4A CpG island is initiated post gene silencing in association with chromatin remodelling and mimics nucleosome positioning. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 3098-109	5.6	56
112	Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. <i>Epigenetics and Chromatin</i> , <b>2017</b> , 10, 16	5.8	53
111	Cancer-specific region of hypermethylation identified within the HIC1 putative tumour suppressor gene in acute myeloid leukaemia. <i>Leukemia</i> , <b>1999</b> , 13, 877-83	10.7	52
110	Methylation-capture and Next-Generation Sequencing of free circulating DNA from human plasma. <i>BMC Genomics</i> , <b>2014</b> , 15, 476	4.5	51
109	Repitools: an R package for the analysis of enrichment-based epigenomic data. <i>Bioinformatics</i> , <b>2010</b> , 26, 1662-3	7.2	51
108	DNA methylation changes in leukaemia. <i>Seminars in Cancer Biology</i> , <b>2002</b> , 12, 347-57	12.7	51
107	Acetylated histone variant H2A.Z is involved in the activation of neo-enhancers in prostate cancer. <i>Nature Communications</i> , <b>2017</b> , 8, 1346	17.4	50
106	Androgen receptor expression predicts breast cancer survival: the role of genetic and epigenetic events. <i>BMC Cancer</i> , <b>2012</b> , 12, 132	4.8	48

105	Alterations in the p16(INK4a) and p53 tumor suppressor genes of hTERT-immortalized human fibroblasts. <i>Oncogene</i> , <b>2004</b> , 23, 3116-21	9.2	47
104	Methylation sequencing from limiting DNA: embryonic, fixed, and microdissected cells. <i>Methods</i> , <b>2002</b> , 27, 108-13	4.6	46
103	Methylation of a CpG island within the promoter region of the KAI1 metastasis suppressor gene is not responsible for down-regulation of KAI1 expression in invasive cancers or cancer cell lines. <i>Cancer Letters</i> , <b>2000</b> , 157, 169-76	9.9	46
102	Long-range regulators of the lncRNA HOTAIR enhance its prognostic potential in breast cancer. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 3269-3283	5.6	46
101	Epigenetic reprogramming at estrogen-receptor binding sites alters 3D chromatin landscape in endocrine-resistant breast cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 320	17.4	45
100	A bioengineered microenvironment to quantitatively measure the tumorigenic properties of cancer-associated fibroblasts in human prostate cancer. <i>Biomaterials</i> , <b>2013</b> , 34, 4777-85	15.6	45
99	Epigenetic deregulation across chromosome 2q14.2 differentiates normal from prostate cancer and provides a regional panel of novel DNA methylation cancer biomarkers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2011</b> , 20, 148-59	4	45
98	ELF5 Drives Lung Metastasis in Luminal Breast Cancer through Recruitment of Gr1+ CD11b+ Myeloid-Derived Suppressor Cells. <i>PLoS Biology</i> , <b>2015</b> , 13, e1002330	9.7	44
97	Integrative genome-wide expression and promoter DNA methylation profiling identifies a potential novel panel of ovarian cancer epigenetic biomarkers. <i>Cancer Letters</i> , <b>2012</b> , 318, 76-85	9.9	42
96	Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. <i>Nature Communications</i> , <b>2019</b> , 10, 416	17.4	41
95	Methyl-CpG-binding protein MBD2 plays a key role in maintenance and spread of DNA methylation at CpG islands and shores in cancer. <i>Oncogene</i> , <b>2017</b> , 36, 1328-1338	9.2	40
94	Protocol matters: which methylome are you actually studying?. <i>Epigenomics</i> , <b>2010</b> , 2, 587-98	4.4	39
93	Cytosines adjacent to methylated CpG sites can be partially resistant to conversion in genomic bisulfite sequencing leading to methylation artifacts. <i>Analytical Biochemistry</i> , <b>1998</b> , 264, 129-32	3.1	39
92	Hypermethylation of the prostacyclin synthase (PTGIS) promoter is a frequent event in colorectal cancer and associated with aneuploidy. <i>Oncogene</i> , <b>2005</b> , 24, 7320-6	9.2	39
91	Prostate cancer epigenetic biomarkers: next-generation technologies. <i>Oncogene</i> , <b>2015</b> , 34, 1609-18	9.2	38
90	Sequencing 5-methylcytosine residues in genomic DNA. <i>BioEssays</i> , <b>1994</b> , 16, 431-6	4.1	38
89	Lineage specific methylation of the Elf5 promoter in mammary epithelial cells. <i>Stem Cells</i> , <b>2011</b> , 29, 1611-8	5.8	37
88	Multiple links between 5-methylcytosine content of mRNA and translation. <i>BMC Biology</i> , <b>2020</b> , 18, 40	7.3	37

87	MicroRNA profiling of the pubertal mouse mammary gland identifies miR-184 as a candidate breast tumour suppressor gene. <i>Breast Cancer Research</i> , <b>2015</b> , 17, 83	8.3	36
86	BCL-2 hypermethylation is a potential biomarker of sensitivity to antimitotic chemotherapy in endocrine-resistant breast cancer. <i>Molecular Cancer Therapeutics</i> , <b>2013</b> , 12, 1874-85	6.1	36
85	Sequence-specific methylation of the mouse H19 gene in embryonic cells deficient in the Dnmt-1 gene. <i>Genesis</i> , <b>1998</b> , 22, 111-21		35
84	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. <i>Cancer Cell</i> , <b>2019</b> , 35, 297-314.e8	24.3	34
83	DNA methylation: bisulphite modification and analysis. <i>Journal of Visualized Experiments</i> , <b>2011</b> ,	1.6	34
82	Epigenetic architecture and miRNA: reciprocal regulators. <i>Epigenomics</i> , <b>2010</b> , 2, 823-40	4.4	34
81	Visualization of Biomedical Data. <i>Annual Review of Biomedical Data Science</i> , <b>2018</b> , 1, 275-304	5.6	34
80	Headloop suppression PCR and its application to selective amplification of methylated DNA sequences. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, e127	20.1	32
79	Direct cloning of polymerase chain reaction products in an XcmI T-vector. <i>Analytical Biochemistry</i> , <b>1994</b> , 216, 235-6	3.1	32
78	Chromatin remodeler mutations in human cancers: epigenetic implications. <i>Epigenomics</i> , <b>2014</b> , 6, 397-414	4.4	31
77	Mutation and methylation analysis of TP53 in adrenal carcinogenesis. <i>European Journal of Surgical Oncology</i> , <b>2005</b> , 31, 549-54	3.6	31
76	Disruption of the 3D cancer genome blueprint. <i>Epigenomics</i> , <b>2017</b> , 9, 47-55	4.4	27
75	DNA methylation profile of triple negative breast cancer-specific genes comparing lymph node positive patients to lymph node negative patients. <i>Scientific Reports</i> , <b>2016</b> , 6, 33435	4.9	27
74	Guidelines for whole genome bisulphite sequencing of intact and FFPE DNA on the Illumina HiSeq X Ten. <i>Epigenetics and Chromatin</i> , <b>2018</b> , 11, 24	5.8	27
73	ZNF300P1 encodes a lincRNA that regulates cell polarity and is epigenetically silenced in type II epithelial ovarian cancer. <i>Molecular Cancer</i> , <b>2014</b> , 13, 3	42.1	27
72	Collagen and calcium-binding EGF domains 1 is frequently inactivated in ovarian cancer by aberrant promoter hypermethylation and modulates cell migration and survival. <i>British Journal of Cancer</i> , <b>2010</b> , 102, 87-96	8.7	27
71	BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. <i>Genome Biology</i> , <b>2014</b> , 15, R35	18.3	25
70	Epigenome remodelling in breast cancer: insights from an early in vitro model of carcinogenesis. <i>Breast Cancer Research</i> , <b>2012</b> , 14, 215	8.3	24



69	Hypermethylation of the Inhibin $\beta$ Subunit Gene in Prostate Carcinoma. <i>Molecular Endocrinology</i> , <b>2002</b> , 16, 213-220		24
68	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , <b>2012</b> , 22, 2489-96	9.7	23
67	Monozygotic twins and triplets discordant for amyotrophic lateral sclerosis display differential methylation and gene expression. <i>Scientific Reports</i> , <b>2019</b> , 9, 8254	4.9	21
66	Multiplex bisulfite PCR resequencing of clinical FFPE DNA. <i>Clinical Epigenetics</i> , <b>2015</b> , 7, 28	7.7	21
65	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , <b>2015</b> , 7, 52	7.7	21
64	A blueprint for an international cancer epigenome consortium. A report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , <b>2012</b> , 72, 6319-24	10.1	21
63	Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. <i>Nature Communications</i> , <b>2020</b> , 11, 54	17.4	21
62	Alterations in Three-Dimensional Organization of the Cancer Genome and Epigenome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , <b>2016</b> , 81, 41-51	3.9	21
61	NGSANE: a lightweight production informatics framework for high-throughput data analysis. <i>Bioinformatics</i> , <b>2014</b> , 30, 1471-2	7.2	20
60	MicroRNA-196a is regulated by ER and is a prognostic biomarker in ER+ breast cancer. <i>British Journal of Cancer</i> , <b>2019</b> , 120, 621-632	8.7	20
59	Serum Free Methylated Glutathione S-transferase 1 DNA Levels, Survival, and Response to Docetaxel in Metastatic, Castration-resistant Prostate Cancer: Post Hoc Analyses of Data from a Phase 3 Trial. <i>European Urology</i> , <b>2019</b> , 76, 306-312	10.2	19
58	Mother-child transmission of epigenetic information by tunable polymorphic imprinting. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, E11970-E11977	11.5	19
57	Genome-wide DNA methylation profiling in triple-negative breast cancer reveals epigenetic signatures with important clinical value. <i>Molecular and Cellular Oncology</i> , <b>2016</b> , 3, e1038424	1.2	16
56	Isolation of a clone containing human histone genes. <i>Nucleic Acids Research</i> , <b>1981</b> , 9, 1583-90	20.1	16
55	Epigenomics of mammary gland development. <i>Breast Cancer Research</i> , <b>2018</b> , 20, 100	8.3	16
54	Macrophage development and activation involve coordinated intron retention in key inflammatory regulators. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 6513-6529	20.1	15
53	Lack of genetic and epigenetic changes in CDKN2A in melanocytic nevi. <i>Journal of Investigative Dermatology</i> , <b>2001</b> , 117, 383-4	4.3	14
52	Integrated epigenomic analysis stratifies chromatin remodellers into distinct functional groups. <i>Epigenetics and Chromatin</i> , <b>2019</b> , 12, 12	5.8	13



51	Telomere-driven karyotypic complexity concurs with p16INK4a inactivation in TP53-competent immortal endothelial cells. <i>Cancer Research</i> , <b>2006</b> , 66, 10691-700	10.1	12
50	Alterations in the methylome of the stromal tumour microenvironment signal the presence and severity of prostate cancer. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 48	7.7	11
49	Smoke-Induced Changes to the Epigenome Provide Fertile Ground for Oncogenic Mutation. <i>Cancer Cell</i> , <b>2017</b> , 32, 278-280	24.3	11
48	Epigenetic markers of ovarian cancer. <i>Advances in Experimental Medicine and Biology</i> , <b>2008</b> , 622, 35-51	3.6	11
47	Development and protective efficacy of a recombinant-DNA derived fimbrial vaccine against enterotoxigenic colibacillosis in neonatal piglets. <i>Vaccine</i> , <b>1988</b> , 6, 389-92	4.1	11
46	Comprehensive evaluation of targeted multiplex bisulphite PCR sequencing for validation of DNA methylation biomarker panels. <i>Clinical Epigenetics</i> , <b>2020</b> , 12, 90	7.7	10
45	Profiling the tyrosine phosphoproteome of different mouse mammary tumour models reveals distinct, model-specific signalling networks and conserved oncogenic pathways. <i>Breast Cancer Research</i> , <b>2014</b> , 16, 437	8.3	10
44	Transient exposure to miR-203 enhances the differentiation capacity of established pluripotent stem cells. <i>EMBO Journal</i> , <b>2020</b> , 39, e104324	13	10
43	Nucleotide-Level Profiling of m <sup>1</sup> C RNA Methylation. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1358, 269-84	1.4	9
42	Genome-wide nucleosome occupancy and DNA methylation profiling of four human cell lines. <i>Genomics Data</i> , <b>2015</b> , 3, 94-6		9
41	Human histone genes are interspersed with members of the Alu family and with other transcribed sequences. <i>Biochemical and Biophysical Research Communications</i> , <b>1982</b> , 104, 785-92	3.4	9
40	Hypermethylation of E-cadherin in leukemia. <i>Blood</i> , <b>2000</b> , 95, 3208-3213	2.2	9
39	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , <b>2019</b> , 9, 9511	4.9	8
38	GWAS of DNA methylation variation within imprinting control regions suggests parent-of-origin association. <i>Twin Research and Human Genetics</i> , <b>2013</b> , 16, 767-81	2.2	8
37	ELF5 modulates the estrogen receptor cistrome in breast cancer. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1008531	6	8
36	Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. <i>Bioinformatics</i> , <b>2019</b> , 35, 560-570	7.2	7
35	COBRA-Seq: Sensitive and Quantitative Methylome Profiling. <i>Genes</i> , <b>2015</b> , 6, 1140-63	4.2	7
34	Dynamics of bivalent chromatin domains upon drug induced reactivation and resilencing in cancer cells. <i>Epigenetics</i> , <b>2011</b> , 6, 1138-48	5.7	7

33	Advances in Prognostic Methylation Biomarkers for Prostate Cancer. <i>Cancers</i> , <b>2020</b> , 12,	6.6	7
32	BRG1 knockdown inhibits proliferation through multiple cellular pathways in prostate cancer. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 37	7.7	7
31	Bisulphite differential denaturation PCR for analysis of DNA methylation. <i>Epigenetics</i> , <b>2006</b> , 1, 94-100	5.7	6
30	Methylated glutathione s-transferase 1 (mGSTP1) as a potential plasma epigenetic marker of prognosis and response to chemotherapy in castrate-resistant prostate cancer (CRPC).. <i>Journal of Clinical Oncology</i> , <b>2014</b> , 32, 11-11	2.2	6
29	Benchmark study comparing liftover tools for genome conversion of epigenome sequencing data. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa054	3.7	5
28	Calling differentially methylated regions from whole genome bisulphite sequencing with DMRcate. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e109	20.1	4
27	Bisulphite Sequencing of Chromatin Immunoprecipitated DNA (BisChIP-seq). <i>Methods in Molecular Biology</i> , <b>2018</b> , 1708, 285-302	1.4	4
26	Bisulfite methylation analysis of tumor suppressor genes in prostate cancer from fresh and archival tissue samples. <i>Methods in Molecular Medicine</i> , <b>2003</b> , 81, 219-40		3
25	Epigenetic Therapies and Biomarkers in Breast Cancer.. <i>Cancers</i> , <b>2022</b> , 14,	6.6	3
24	The H2A.Z-nucleosome code in mammals: emerging functions. <i>Trends in Genetics</i> , <b>2021</b> ,	8.5	3
23	Widespread Aberrant Alternative Splicing despite Molecular Remission in Chronic Myeloid Leukaemia Patients. <i>Cancers</i> , <b>2020</b> , 12,	6.6	3
22	Epigenetic therapy suppresses endocrine-resistant breast tumour growth by re-wiring ER-mediated 3D chromatin interactions		3
21	Genome-scale methylation assessment did not identify prognostic biomarkers in oral tongue carcinomas. <i>Clinical Epigenetics</i> , <b>2016</b> , 8, 74	7.7	3
20	A Read/Write Mechanism Connects p300 Bromodomain Function to H2A.Z Acetylation. <i>IScience</i> , <b>2019</b> , 21, 773-788	6.1	3
19	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. <i>Cell Reports</i> , <b>2021</b> , 36, 109722	10.6	3
18	Identification of DNA methylation biomarkers with potential to predict response to neoadjuvant chemotherapy in triple-negative breast cancer.. <i>Clinical Epigenetics</i> , <b>2021</b> , 13, 226	7.7	2
17	Studying Mammalian DNA Methylation <b>2004</b> , 53-63		2
16	Mapping genomic and epigenomic evolution in cancer ecosystems. <i>Science</i> , <b>2021</b> , 373, 1474-1479	33.3	2

15	Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells		1
14	Multiple links between 5-methylcytosine content of mRNA and translation		1
13	MethPanel: a parallel pipeline and interactive analysis tool for multiplex bisulphite PCR sequencing to assess DNA methylation biomarker panels for disease detection		1
12	DNA methylation is required to maintain DNA replication timing precision and 3D genome integrity		1
11	Target-Specific Profiling of RNA mC Methylation Level Using Amplicon Sequencing. <i>Methods in Molecular Biology</i> , <b>2022</b> , 2404, 375-392	1.4	0
10	Early Insights into Cancer Epigenetics: Gene Promoter Hypermethylation Emerges as a Potential Biomarker for Cancer Detection.. <i>Cancer Research</i> , <b>2022</b> , 82, 1461-1463	10.1	0
9	We are what we Eat: How Nutritional Compounds Such as Isoflavones Shape Our Epigenome <b>2011</b> , 249-261		
8	High-resolution Epigenome Mapping Reveals Distinct and Divergent Roles for UHRF1 in the Maintenance of DNA Methylation. <i>FASEB Journal</i> , <b>2020</b> , 34, 1-1	0.9	
7	Post hoc analysis of a phase III study to test the association between circulating methylated glutathione s transferase (mGSTP1) DNA levels and response to docetaxel (DTX) in metastatic castration resistant prostate cancer (mCRPC).. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 5014-5014	2.2	
6	Circulating microRNAs associated with docetaxel-resistant castration resistant prostate cancer.. <i>Journal of Clinical Oncology</i> , <b>2014</b> , 32, 44-44	2.2	
5	GUIDE: a randomised non-comparative phase II trial of biomarker-driven intermittent docetaxel standard-of-care docetaxel in metastatic castration-resistant prostate cancer (clinical trial protocol).. <i>Therapeutic Advances in Medical Oncology</i> , <b>2022</b> , 14, 17588359221092486	5.4	
4	ELF5 modulates the estrogen receptor cistrome in breast cancer <b>2020</b> , 16, e1008531		
3	ELF5 modulates the estrogen receptor cistrome in breast cancer <b>2020</b> , 16, e1008531		
2	ELF5 modulates the estrogen receptor cistrome in breast cancer <b>2020</b> , 16, e1008531		
1	ELF5 modulates the estrogen receptor cistrome in breast cancer <b>2020</b> , 16, e1008531		