

# Clare Stirzaker

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

6,973  
citations

81900

39  
h-index

138484

58  
g-index

66  
all docs

66  
docs citations

66  
times ranked

11185  
citing authors

#	ARTICLE	IF	CITATIONS
1	Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208.	8.8	912
2	Transcriptional Gene Silencing Promotes DNA Hypermethylation through a Sequential Change in Chromatin Modifications in Cancer Cells. <i>Cancer Research</i> , 2004, 64, 3871-3877.	0.9	374
3	Methyl-CpG-binding domain proteins: readers of the epigenome. <i>Epigenomics</i> , 2015, 7, 1051-1073.	2.1	367
4	Epigenetic remodeling in colorectal cancer results in coordinate gene suppression across an entire chromosome band. <i>Nature Genetics</i> , 2006, 38, 540-549.	21.4	355
5	Detection and measurement of PCR bias in quantitative methylation analysis of bisulphite-treated DNA. <i>Nucleic Acids Research</i> , 1997, 25, 4422-4426.	14.5	353
6	DNA methylation: Bisulphite modification and analysis. <i>Nature Protocols</i> , 2006, 1, 2353-2364.	12.0	326
7	Three-dimensional disorganization of the cancer genome occurs coincident with long-range genetic and epigenetic alterations. <i>Genome Research</i> , 2016, 26, 719-731.	5.5	312
8	Identification and resolution of artifacts in bisulfite sequencing. <i>Methods</i> , 2002, 27, 101-107.	3.8	271
9	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	17.5	270
10	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> , 2011, 6, 34-44.	2.7	189
11	Regional Activation of the Cancer Genome by Long-Range Epigenetic Remodeling. <i>Cancer Cell</i> , 2013, 23, 9-22.	16.8	185
12	Mining cancer methylomes: prospects and challenges. <i>Trends in Genetics</i> , 2014, 30, 75-84.	6.7	180
13	Consolidation of the cancer genome into domains of repressive chromatin by long-range epigenetic silencing (LRES) reduces transcriptional plasticity. <i>Nature Cell Biology</i> , 2010, 12, 235-246.	10.3	178
14	Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells. <i>Oncogene</i> , 2002, 21, 1048-1061.	5.9	175
15	The DNA methylation landscape in cancer. <i>Essays in Biochemistry</i> , 2019, 63, 797-811.	4.7	169
16	Bisulfite sequencing of chromatin immunoprecipitated DNA (BisChIP-seq) directly informs methylation status of histone-modified DNA. <i>Genome Research</i> , 2012, 22, 1120-1127.	5.5	163
17	Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015, 6, 5899.	12.8	162
18	Acetylation of H2A.Z is a key epigenetic modification associated with gene deregulation and epigenetic remodeling in cancer. <i>Genome Research</i> , 2012, 22, 307-321.	5.5	155

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19	Evaluation of affinity-based genome-wide DNA methylation data: Effects of CpG density, amplification bias, and copy number variation. <i>Genome Research</i> , 2010, 20, 1719-1729.	5.5	111
20	DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. <i>Nature Communications</i> , 2015, 6, 7758.	12.8	105
21	Epigenetic reprogramming at estrogen-receptor binding sites alters 3D chromatin landscape in endocrine-resistant breast cancer. <i>Nature Communications</i> , 2020, 11, 320.	12.8	103
22	Epigenetic-induced repression of microRNA-205 is associated with MED1 activation and a poorer prognosis in localized prostate cancer. <i>Oncogene</i> , 2013, 32, 2891-2899.	5.9	85
23	The signal peptide of the rotavirus glycoprotein VP7 is essential for its retention in the ER as an integral membrane protein. <i>Cell</i> , 1989, 56, 741-747.	28.9	80
24	Concordant Epigenetic Silencing of Transforming Growth Factor- $\beta$ Signaling Pathway Genes Occurs Early in Breast Carcinogenesis. <i>Cancer Research</i> , 2007, 67, 11517-11527.	0.9	76
25	Loss of Special AT-Rich Binding Protein 1 Expression is a Marker of Poor Survival in Lung Cancer. <i>Journal of Thoracic Oncology</i> , 2011, 6, 1179-1189.	1.1	76
26	Enduring epigenetic landmarks define the cancer microenvironment. <i>Genome Research</i> , 2018, 28, 625-638.	5.5	74
27	Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. <i>Nature Communications</i> , 2020, 11, 54.	12.8	72
28	Replication timing and epigenome remodelling are associated with the nature of chromosomal rearrangements in cancer. <i>Nature Communications</i> , 2019, 10, 416.	12.8	71
29	<code>Repitools</code> : an R package for the analysis of enrichment-based epigenomic data. <i>Bioinformatics</i> , 2010, 26, 1662-1663.	4.1	68
30	Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. <i>Epigenetics and Chromatin</i> , 2017, 10, 16.	3.9	68
31	Acetylated histone variant H2A.Z is involved in the activation of neo-enhancers in prostate cancer. <i>Nature Communications</i> , 2017, 8, 1346.	12.8	68
32	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> , 2009, 18, 3098-3109.	2.9	65
33	Epigenetic Inactivation of a Cluster of Genes Flanking <i>MLH1</i> in Microsatellite-Unstable Colorectal Cancer. <i>Cancer Research</i> , 2007, 67, 9107-9116.	0.9	63
34	DNA Hypermethylation Encroachment at CpG Island Borders in Cancer Is Predisposed by H3K4 Monomethylation Patterns. <i>Cancer Cell</i> , 2019, 35, 297-314.e8.	16.8	62
35	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> , 2017, 36, 1328-1338.	5.9	59
36	DNA methylation profile of triple negative breast cancer-specific genes comparing lymph node positive patients to lymph node negative patients. <i>Scientific Reports</i> , 2016, 6, 33435.	3.3	56

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37	A bioengineered microenvironment to quantitatively measure the tumorigenic properties of cancer-associated fibroblasts in human prostate cancer. <i>Biomaterials</i> , 2013, 34, 4777-4785.	11.4	53
38	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> , 2011, 20, 148-159.	2.5	51
39	Cytosines Adjacent to Methylated CpG Sites Can Be Partially Resistant to Conversion in Genomic Bisulfite Sequencing Leading to Methylation Artifacts. <i>Analytical Biochemistry</i> , 1998, 264, 129-132.	2.4	40
40	DNA methylation is required to maintain both DNA replication timing precision and 3D genome organization integrity. <i>Cell Reports</i> , 2021, 36, 109722.	6.4	39
41	BayMeth: improved DNA methylation quantification for affinity capture sequencing data using a flexible Bayesian approach. <i>Genome Biology</i> , 2014, 15, R35.	9.6	29
42	Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496.	5.5	28
43	Multiplex bisulfite PCR resequencing of clinical FFPE DNA. <i>Clinical Epigenetics</i> , 2015, 7, 28.	4.1	26
44	Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , 2015, 7, 52.	4.1	26
45	Genome-wide DNA methylation profiling in triple-negative breast cancer reveals epigenetic signatures with important clinical value. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1038424.	0.7	24
46	Methylome and transcriptome maps of human visceral and subcutaneous adipocytes reveal key epigenetic differences at developmental genes. <i>Scientific Reports</i> , 2019, 9, 9511.	3.3	24
47	Integrated epigenomic analysis stratifies chromatin remodellers into distinct functional groups. <i>Epigenetics and Chromatin</i> , 2019, 12, 12.	3.9	23
48	Sequences in rotavirus glycoprotein VP7 that mediate delayed translocation and retention of the protein in the endoplasmic reticulum.. <i>Journal of Cell Biology</i> , 1990, 111, 1343-1350.	5.2	22
49	Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. <i>Bioinformatics</i> , 2019, 35, 560-570.	4.1	17
50	Alterations in the methylome of the stromal tumour microenvironment signal the presence and severity of prostate cancer. <i>Clinical Epigenetics</i> , 2020, 12, 48.	4.1	17
51	Advances in Prognostic Methylation Biomarkers for Prostate Cancer. <i>Cancers</i> , 2020, 12, 2993.	3.7	16
52	Comprehensive evaluation of targeted multiplex bisulphite PCR sequencing for validation of DNA methylation biomarker panels. <i>Clinical Epigenetics</i> , 2020, 12, 90.	4.1	16
53	Epigenetic Therapies and Biomarkers in Breast Cancer. <i>Cancers</i> , 2022, 14, 474.	3.7	16
54	Identification of DNA methylation biomarkers with potential to predict response to neoadjuvant chemotherapy in triple-negative breast cancer. <i>Clinical Epigenetics</i> , 2021, 13, 226.	4.1	13

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55	Ubiquitin chromatin remodelling after DNA damage is associated with the expression of key cancer genes and pathways. Cellular and Molecular Life Sciences, 2021, 78, 1011-1027.	5.4	10
56	Bisulphite Sequencing of Chromatin Immunoprecipitated DNA (BisChIP-seq). Methods in Molecular Biology, 2018, 1708, 285-302.	0.9	5
57	Cancer Methylation Biomarkers in Circulating Cell-Free DNA. , 2019, , 217-245.		3
58	Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells. , 0, .		1
59	MethPanel: a parallel pipeline and interactive analysis tool for multiplex bisulphite PCR sequencing to assess DNA methylation biomarker panels for disease detection. Bioinformatics, 2021, 37, 2198-2200.	4.1	1
60	Evaluation and measurement of epigenetic modifications in population-based studies. , 2021, , 17-39.		0