

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 | Epigenetic Therapies and Biomarkers in Breast Cancer. <i>Cancers</i> , 2022, 14, 474. | 3.7 | 16 |
| 2 | Ubiquitin chromatin remodelling after DNA damage is associated with the expression of key cancer genes and pathways. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1011-1027. | 5.4 | 10 |
| 3 | Evaluation and measurement of epigenetic modifications in population-based studies. , 2021, , 17-39. | | 0 |
| 4 | 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 |
| 5 | MethPanel: a parallel pipeline and interactive analysis tool for multiplex bisulphite PCR sequencing to assess DNA methylation biomarker panels for disease detection. <i>Bioinformatics</i> , 2021, 37, 2198-2200. | 4.1 | 1 |
| 6 | 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 |
| 7 | Constitutively bound CTCF sites maintain 3D chromatin architecture and long-range epigenetically regulated domains. <i>Nature Communications</i> , 2020, 11, 54. | 12.8 | 72 |
| 8 | Advances in Prognostic Methylation Biomarkers for Prostate Cancer. <i>Cancers</i> , 2020, 12, 2993. | 3.7 | 16 |
| 9 | 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 |
| 10 | 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 |
| 11 | 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 |
| 12 | Evaluation of cross-platform and interlaboratory concordance via consensus modelling of genomic measurements. <i>Bioinformatics</i> , 2019, 35, 560-570. | 4.1 | 17 |
| 13 | 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 |
| 14 | 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 |
| 15 | Integrated epigenomic analysis stratifies chromatin remodellers into distinct functional groups. <i>Epigenetics and Chromatin</i> , 2019, 12, 12. | 3.9 | 23 |
| 16 | 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 |
| 17 | The DNA methylation landscape in cancer. <i>Essays in Biochemistry</i> , 2019, 63, 797-811. | 4.7 | 169 |
| 18 | Cancer Methylation Biomarkers in Circulating Cell-Free DNA. , 2019, , 217-245. | | 3 |

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|----|---|------|-----------|
| 19 | Enduring epigenetic landmarks define the cancer microenvironment. <i>Genome Research</i> , 2018, 28, 625-638. | 5.5 | 74 |
| 20 | Bisulphite Sequencing of Chromatin Immunoprecipitated DNA (BisChIP-seq). <i>Methods in Molecular Biology</i> , 2018, 1708, 285-302. | 0.9 | 5 |
| 21 | Comprehensive evaluation of genome-wide 5-hydroxymethylcytosine profiling approaches in human DNA. <i>Epigenetics and Chromatin</i> , 2017, 10, 16. | 3.9 | 68 |
| 22 | 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 |
| 23 | 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 |
| 24 | 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 |
| 25 | Critical evaluation of the Illumina MethylationEPIC BeadChip microarray for whole-genome DNA methylation profiling. <i>Genome Biology</i> , 2016, 17, 208. | 8.8 | 912 |
| 26 | 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 |
| 27 | Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737. | 17.5 | 270 |
| 28 | 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 |
| 29 | Methylome sequencing in triple-negative breast cancer reveals distinct methylation clusters with prognostic value. <i>Nature Communications</i> , 2015, 6, 5899. | 12.8 | 162 |
| 30 | DNA methylation of oestrogen-regulated enhancers defines endocrine sensitivity in breast cancer. <i>Nature Communications</i> , 2015, 6, 7758. | 12.8 | 105 |
| 31 | Multiplex bisulfite PCR resequencing of clinical FFPE DNA. <i>Clinical Epigenetics</i> , 2015, 7, 28. | 4.1 | 26 |
| 32 | Coordinated epigenetic remodelling of transcriptional networks occurs during early breast carcinogenesis. <i>Clinical Epigenetics</i> , 2015, 7, 52. | 4.1 | 26 |
| 33 | Methyl-CpG-binding domain proteins: readers of the epigenome. <i>Epigenomics</i> , 2015, 7, 1051-1073. | 2.1 | 367 |
| 34 | 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 |
| 35 | Mining cancer methylomes: prospects and challenges. <i>Trends in Genetics</i> , 2014, 30, 75-84. | 6.7 | 180 |
| 36 | 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 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 37 | Regional Activation of the Cancer Genome by Long-Range Epigenetic Remodeling. <i>Cancer Cell</i> , 2013, 23, 9-22. | 16.8 | 185 |
| 38 | 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 |
| 39 | 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 |
| 40 | Copy-number-aware differential analysis of quantitative DNA sequencing data. <i>Genome Research</i> , 2012, 22, 2489-2496. | 5.5 | 28 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | 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 |
| 46 | Repitools: an R package for the analysis of enrichment-based epigenomic data. <i>Bioinformatics</i> , 2010, 26, 1662-1663. | 4.1 | 68 |
| 47 | 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 |
| 48 | 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 |
| 49 | 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 |
| 50 | Concordant Epigenetic Silencing of Transforming Growth Factor- β Signaling Pathway Genes Occurs Early in Breast Carcinogenesis. <i>Cancer Research</i> , 2007, 67, 11517-11527. | 0.9 | 76 |
| 51 | 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 |
| 52 | DNA methylation: Bisulphite modification and analysis. <i>Nature Protocols</i> , 2006, 1, 2353-2364. | 12.0 | 326 |
| 53 | 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 |
| 54 | Identification and resolution of artifacts in bisulfite sequencing. <i>Methods</i> , 2002, 27, 101-107. | 3.8 | 271 |

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|----|--|------|-----------|
| 55 | Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells. <i>Oncogene</i> , 2002, 21, 1048-1061. | 5.9 | 175 |
| 56 | 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 |
| 57 | 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 |
| 58 | 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 |
| 59 | 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 |
| 60 | Hypermethylation trigger of the glutathione-S-transferase gene (GSTP1) in prostate cancer cells. , 0, . | | 1 |