

Andrew E Teschendorff

List of Publications by Year in descending order

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Version: 2024-02-01

149
papers

20,044
citations

11608

70
h-index

12233

133
g-index

166
all docs

166
docs citations

166
times ranked

29839
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential oestrogen receptor binding is associated with clinical outcome in breast cancer. <i>Nature</i> , 2012, 481, 389-393.	13.7	1,655
2	A beta-mixture quantile normalization method for correcting probe design bias in Illumina Infinium 450 k DNA methylation data. <i>Bioinformatics</i> , 2013, 29, 189-196.	1.8	1,295
3	Mutational evolution in a lobular breast tumour profiled at single nucleotide resolution. <i>Nature</i> , 2009, 461, 809-813.	13.7	984
4	MicroRNA expression profiling of human breast cancer identifies new markers of tumor subtype. <i>Genome Biology</i> , 2007, 8, R214.	13.9	828
5	ChAMP: 450k Chip Analysis Methylation Pipeline. <i>Bioinformatics</i> , 2014, 30, 428-430.	1.8	757
6	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010, 20, 440-446.	2.4	740
7	ChAMP: updated methylation analysis pipeline for Illumina BeadChips. <i>Bioinformatics</i> , 2017, 33, 3982-3984.	1.8	572
8	DNA methylation aging clocks: challenges and recommendations. <i>Genome Biology</i> , 2019, 20, 249.	3.8	552
9	An immune response gene expression module identifies a good prognosis subtype in estrogen receptor negative breast cancer. <i>Genome Biology</i> , 2007, 8, R157.	13.9	433
10	Menopause accelerates biological aging. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9327-9332.	3.3	363
11	Tumor origin detection with tissue-specific miRNA and DNA methylation markers. <i>Bioinformatics</i> , 2018, 34, 398-406.	1.8	308
12	A comparison of reference-based algorithms for correcting cell-type heterogeneity in Epigenome-Wide Association Studies. <i>BMC Bioinformatics</i> , 2017, 18, 105.	1.2	297
13	dbDEMC 2.0: updated database of differentially expressed miRNAs in human cancers. <i>Nucleic Acids Research</i> , 2017, 45, D812-D818.	6.5	296
14	An Epigenetic Signature in Peripheral Blood Predicts Active Ovarian Cancer. <i>PLoS ONE</i> , 2009, 4, e8274.	1.1	291
15	High-resolution aCGH and expression profiling identifies a novel genomic subtype of ER negative breast cancer. <i>Genome Biology</i> , 2007, 8, R215.	13.9	275
16	Genome-wide DNA methylation analysis for diabetic nephropathy in type 1 diabetes mellitus. <i>BMC Medical Genomics</i> , 2010, 3, 33.	0.7	261
17	Age-associated epigenetic drift: implications, and a case of epigenetic thrift?. <i>Human Molecular Genetics</i> , 2013, 22, R7-R15.	1.4	261
18	Phenotypic and functional characterisation of the luminal cell hierarchy of the mammary gland. <i>Breast Cancer Research</i> , 2012, 14, R134.	2.2	260

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19	Allele-Specific Up-Regulation of FGFR2 Increases Susceptibility to Breast Cancer. <i>PLoS Biology</i> , 2008, 6, e108.	2.6	254
20	Independent surrogate variable analysis to deconvolve confounding factors in large-scale microarray profiling studies. <i>Bioinformatics</i> , 2011, 27, 1496-1505.	1.8	232
21	Single-cell entropy for accurate estimation of differentiation potency from a cell's transcriptome. <i>Nature Communications</i> , 2017, 8, 15599.	5.8	230
22	Statistical and integrative system-level analysis of DNA methylation data. <i>Nature Reviews Genetics</i> , 2018, 19, 129-147.	7.7	228
23	Integrated Genetic and Epigenetic Analysis Identifies Haplotype-Specific Methylation in the FTO Type 2 Diabetes and Obesity Susceptibility Locus. <i>PLoS ONE</i> , 2010, 5, e14040.	1.1	215
24	Differential expression of selected histone modifier genes in human solid cancers. <i>BMC Genomics</i> , 2006, 7, 90.	1.2	209
25	Correlation of an epigenetic mitotic clock with cancer risk. <i>Genome Biology</i> , 2016, 17, 205.	3.8	197
26	DNA methylation outliers in normal breast tissue identify field defects that are enriched in cancer. <i>Nature Communications</i> , 2016, 7, 10478.	5.8	195
27	An evaluation of analysis pipelines for DNA methylation profiling using the Illumina HumanMethylation450 BeadChip platform. <i>Epigenetics</i> , 2013, 8, 333-346.	1.3	192
28	Correlation of Smoking-Associated DNA Methylation Changes in Buccal Cells With DNA Methylation Changes in Epithelial Cancer. <i>JAMA Oncology</i> , 2015, 1, 476.	3.4	177
29	Identification of differentially methylated cell types in epigenome-wide association studies. <i>Nature Methods</i> , 2018, 15, 1059-1066.	9.0	166
30	Epigenetic variability in cells of normal cytology is associated with the risk of future morphological transformation. <i>Genome Medicine</i> , 2012, 4, 24.	3.6	162
31	Differential network entropy reveals cancer system hallmarks. <i>Scientific Reports</i> , 2012, 2, 802.	1.6	154
32	Meta-analysis of IDH-mutant cancers identifies EBF1 as an interaction partner for TET2. <i>Nature Communications</i> , 2013, 4, 2166.	5.8	152
33	Variational Bayesian Matrix Factorization for Bounded Support Data. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2015, 37, 876-889.	9.7	151
34	A systems-level integrative framework for genome-wide DNA methylation and gene expression data identifies differential gene expression modules under epigenetic control. <i>Bioinformatics</i> , 2014, 30, 2360-2366.	1.8	148
35	A 1.5-Mb minimal amplicon at 8p11 in breast cancer identifies new candidate oncogenes. <i>Oncogene</i> , 2005, 24, 5235-5245.	2.6	146
36	Improved prognostic classification of breast cancer defined by antagonistic activation patterns of immune response pathway modules. <i>BMC Cancer</i> , 2010, 10, 604.	1.1	144

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37	Increased DNA methylation variability in type 1 diabetes across three immune effector cell types. <i>Nature Communications</i> , 2016, 7, 13555.	5.8	142
38	The lncRNA HOTAIR impacts on mesenchymal stem cells via triple helix formation. <i>Nucleic Acids Research</i> , 2016, 44, 10631-10643.	6.5	141
39	Genomic Architecture Characterizes Tumor Progression Paths and Fate in Breast Cancer Patients. <i>Science Translational Medicine</i> , 2010, 2, 38ra47.	5.8	138
40	HOTAIR and its surrogate DNA methylation signature indicate carboplatin resistance in ovarian cancer. <i>Genome Medicine</i> , 2015, 7, 108.	3.6	138
41	Role of DNA Methylation and Epigenetic Silencing of HAND2 in Endometrial Cancer Development. <i>PLoS Medicine</i> , 2013, 10, e1001551.	3.9	135
42	Genome-wide age-related changes in DNA methylation and gene expression in human PBMCs. <i>Age</i> , 2014, 36, 9648.	3.0	135
43	An Integrative Multi-scale Analysis of the Dynamic DNA Methylation Landscape in Aging. <i>PLoS Genetics</i> , 2015, 11, e1004996.	1.5	132
44	Cell-type deconvolution in epigenome-wide association studies: a review and recommendations. <i>Epigenomics</i> , 2017, 9, 757-768.	1.0	131
45	Cellular network entropy as the energy potential in Waddington's differentiation landscape. <i>Scientific Reports</i> , 2013, 3, 3039.	1.6	129
46	Epigenome-based cancer risk prediction: rationale, opportunities and challenges. <i>Nature Reviews Clinical Oncology</i> , 2018, 15, 292-309.	12.5	129
47	The potential of circulating tumor DNA methylation analysis for the early detection and management of ovarian cancer. <i>Genome Medicine</i> , 2017, 9, 116.	3.6	122
48	Differential variability improves the identification of cancer risk markers in DNA methylation studies profiling precursor cancer lesions. <i>Bioinformatics</i> , 2012, 28, 1487-1494.	1.8	119
49	Identification and functional validation of HPV-mediated hypermethylation in head and neck squamous cell carcinoma. <i>Genome Medicine</i> , 2013, 5, 15.	3.6	118
50	A functional methylome map of ulcerative colitis. <i>Genome Research</i> , 2012, 22, 2130-2137.	2.4	116
51	A novel cell-type deconvolution algorithm reveals substantial contamination by immune cells in saliva, buccal and cervix. <i>Epigenomics</i> , 2018, 10, 925-940.	1.0	116
52	A comprehensive analysis of prognostic signatures reveals the high predictive capacity of the Proliferation, Immune response and RNA splicing modules in breast cancer. <i>Breast Cancer Research</i> , 2008, 10, R93.	2.2	113
53	Using high-density DNA methylation arrays to profile copy number alterations. <i>Genome Biology</i> , 2014, 15, R30.	13.9	113
54	The Dynamics and Prognostic Potential of DNA Methylation Changes at Stem Cell Gene Loci in Women's Cancer. <i>PLoS Genetics</i> , 2012, 8, e1002517.	1.5	111

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55	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. PLoS Computational Biology, 2007, 3, e161.	1.5	108
56	eFORGE: A Tool for Identifying Cell Type-Specific Signal in Epigenomic Data. Cell Reports, 2016, 17, 2137-2150.	2.9	102
57	Psychosocial adversity and socioeconomic position during childhood and epigenetic age: analysis of two prospective cohort studies. Human Molecular Genetics, 2018, 27, 1301-1308.	1.4	102
58	Epigenetic drift, epigenetic clocks and cancer risk. Epigenomics, 2016, 8, 705-719.	1.0	101
59	Interferon- α treatment of cervical keratinocytes naturally infected with human papillomavirus 16 episomes promotes rapid reduction in episome numbers and emergence of latent integrants. Carcinogenesis, 2006, 27, 2341-2353.	1.3	100
60	TGF β ² induces the formation of tumour-initiating cells in claudinlow breast cancer. Nature Communications, 2012, 3, 1055.	5.8	95
61	A comparison of feature selection and classification methods in DNA methylation studies using the Illumina Infinium platform. BMC Bioinformatics, 2012, 13, 59.	1.2	95
62	Comparative methylome analysis of benign and malignant peripheral nerve sheath tumors. Genome Research, 2011, 21, 515-524.	2.4	94
63	Glioblastoma Stem Cells Respond to Differentiation Cues but Fail to Undergo Commitment and Terminal Cell-Cycle Arrest. Stem Cell Reports, 2015, 5, 829-842.	2.3	93
64	Genome-wide DNA methylation analysis of archival formalin-fixed paraffin-embedded tissue using the Illumina Infinium HumanMethylation27 BeadChip. Methods, 2010, 52, 248-254.	1.9	92
65	Increased entropy of signal transduction in the cancer metastasis phenotype. BMC Systems Biology, 2010, 4, 104.	3.0	91
66	An integrative network algorithm identifies age-associated differential methylation interactome hotspots targeting stem-cell differentiation pathways. Scientific Reports, 2013, 3, 1630.	1.6	88
67	A robust classifier of high predictive value to identify good prognosis patients in ER-negative breast cancer. Breast Cancer Research, 2008, 10, R73.	2.2	87
68	Making sense of the ageing methylome. Nature Reviews Genetics, 2022, 23, 585-605.	7.7	86
69	eFORGE v2.0: updated analysis of cell type-specific signal in epigenomic data. Bioinformatics, 2019, 35, 4767-4769.	1.8	84
70	Avoiding common pitfalls in machine learning omic data science. Nature Materials, 2019, 18, 422-427.	13.3	83
71	A consensus prognostic gene expression classifier for ER positive breast cancer. Genome Biology, 2006, 7, R101.	13.9	82
72	<i>BEX2</i> Is Overexpressed in a Subset of Primary Breast Cancers and Mediates Nerve Growth Factor/Nuclear Factor- κ B Inhibition of Apoptosis in Breast Cancer Cell Lines. Cancer Research, 2007, 67, 6725-6736.	0.4	81

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73	Genomic gain of 5p15 leads to over-expression of Misu (NSUN2) in breast cancer. <i>Cancer Letters</i> , 2010, 289, 71-80.	3.2	80
74	A variational Bayesian mixture modelling framework for cluster analysis of gene-expression data. <i>Bioinformatics</i> , 2005, 21, 3025-3033.	1.8	73
75	Fine scale mapping of the breast cancer 16q12 locus. <i>Human Molecular Genetics</i> , 2010, 19, 2507-2515.	1.4	68
76	Signalling entropy: A novel network-theoretical framework for systems analysis and interpretation of functional omic data. <i>Methods</i> , 2014, 67, 282-293.	1.9	67
77	Statistical mechanics meets single-cell biology. <i>Nature Reviews Genetics</i> , 2021, 22, 459-476.	7.7	65
78	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018, 142, 874-882.	2.3	64
79	ESR1 gene amplification in breast cancer: a common phenomenon?. <i>Nature Genetics</i> , 2008, 40, 806-807.	9.4	62
80	Intra-Tumour Signalling Entropy Determines Clinical Outcome in Breast and Lung Cancer. <i>PLoS Computational Biology</i> , 2015, 11, e1004115.	1.5	62
81	PACK: Profile Analysis using Clustering and Kurtosis to find molecular classifiers in cancer. <i>Bioinformatics</i> , 2006, 22, 2269-2275.	1.8	61
82	An integrative pan-cancer-wide analysis of epigenetic enzymes reveals universal patterns of epigenomic deregulation in cancer. <i>Genome Biology</i> , 2015, 16, 140.	3.8	60
83	Increased signaling entropy in cancer requires the scale-free property of proteininteraction networks. <i>Scientific Reports</i> , 2015, 5, 9646.	1.6	59
84	Correcting for cell-type heterogeneity in epigenome-wide association studies: revisiting previous analyses. <i>Nature Methods</i> , 2017, 14, 216-217.	9.0	59
85	EPISCOPE: cell type deconvolution of bulk tissue DNA methylomes from single-cell RNA-Seq data. <i>Genome Biology</i> , 2020, 21, 221.	3.8	58
86	A comparison of epigenetic mitotic-like clocks for cancer risk prediction. <i>Genome Medicine</i> , 2020, 12, 56.	3.6	56
87	A BRCA1-mutation associated DNA methylation signature in blood cells predicts sporadic breast cancer incidence and survival. <i>Genome Medicine</i> , 2014, 6, 47.	3.6	53
88	Appraising the causal relevance of DNA methylation for risk of lung cancer. <i>International Journal of Epidemiology</i> , 2019, 48, 1493-1504.	0.9	53
89	The Dynamics of DNA Methylation Covariation Patterns in Carcinogenesis. <i>PLoS Computational Biology</i> , 2014, 10, e1003709.	1.5	52
90	β 2 catenin is central to DUX4-driven network rewiring in facioscapulohumeral muscular dystrophy. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20140797.	1.5	52

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91	Epigenetic dysregulation and poorer prognosis in DAXX-deficient pancreatic neuroendocrine tumours. <i>Endocrine-Related Cancer</i> , 2015, 22, L13-L18.	1.6	50
92	Distinctive topology of age-associated epigenetic drift in the human interactome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 14138-14143.	3.3	49
93	Systems-epigenomics inference of transcription factor activity implicates aryl-hydrocarbon-receptor inactivation as a key event in lung cancer development. <i>Genome Biology</i> , 2017, 18, 236.	3.8	46
94	A pan-tissue DNA methylation atlas enables in silico decomposition of human tissue methylomes at cell-type resolution. <i>Nature Methods</i> , 2022, 19, 296-306.	9.0	46
95	Aberrant regulation of RANKL/OPG in women at high risk of developing breast cancer. <i>Oncotarget</i> , 2017, 8, 3811-3825.	0.8	45
96	Cell and tissue type independent age-associated DNA methylation changes are not rare but common. <i>Aging</i> , 2018, 10, 3541-3557.	1.4	42
97	Single-cell landscape in mammary epithelium reveals bipotent-like cells associated with breast cancer risk and outcome. <i>Communications Biology</i> , 2019, 2, 306.	2.0	41
98	Tissue-independent and tissue-specific patterns of DNA methylation alteration in cancer. <i>Epigenetics and Chromatin</i> , 2016, 9, 10.	1.8	40
99	EpiDISH web server: Epigenetic Dissection of Intra-Sample-Heterogeneity with online GUI. <i>Bioinformatics</i> , 2020, 36, 1950-1951.	1.8	40
100	Stochastic epigenetic outliers can define field defects in cancer. <i>BMC Bioinformatics</i> , 2016, 17, 178.	1.2	36
101	Are objective measures of physical capability related to accelerated epigenetic age? Findings from a British birth cohort. <i>BMJ Open</i> , 2017, 7, e016708.	0.8	36
102	Common germline polymorphisms in <i>COMT</i> , <i>CYP19A1</i> , <i>ESR1</i> , <i>PGR</i> , <i>SULT1E1</i> and <i>STS</i> and survival after a diagnosis of breast cancer. <i>International Journal of Cancer</i> , 2009, 125, 2687-2696.	2.3	34
103	DNA methylome analysis reveals distinct epigenetic patterns of ascending aortic dissection and bicuspid aortic valve. <i>Cardiovascular Research</i> , 2017, 113, 692-704.	1.8	33
104	Quantifying Waddington's epigenetic landscape: a comparison of single-cell potency measures. <i>Briefings in Bioinformatics</i> , 2018, , .	3.2	33
105	A cell-type deconvolution meta-analysis of whole blood EWAS reveals lineage-specific smoking-associated DNA methylation changes. <i>Nature Communications</i> , 2020, 11, 4779.	5.8	32
106	dbDEMC 3.0: Functional Exploration of Differentially Expressed miRNAs in Cancers of Human and Model Organisms. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 446-454.	3.0	32
107	Co-amplification of 8p12 and 11q13 in breast cancers is not the result of a single genomic event. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 427-439.	1.5	27
108	The breast cancer somatic 'muta-ome': tackling the complexity. <i>Breast Cancer Research</i> , 2009, 11, 301.	2.2	27

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109	DNA Methylation Patterns in Normal Tissue Correlate more Strongly with Breast Cancer Status than Copy-Number Variants. <i>EBioMedicine</i> , 2018, 31, 243-252.	2.7	27
110	DART: Denoising Algorithm based on Relevance network Topology improves molecular pathway activity inference. <i>BMC Bioinformatics</i> , 2011, 12, 403.	1.2	26
111	The multi-omic landscape of transcription factor inactivation in cancer. <i>Genome Medicine</i> , 2016, 8, 89.	3.6	26
112	Pan-cancer characterization of long non-coding RNA and DNA methylation mediated transcriptional dysregulation. <i>EBioMedicine</i> , 2021, 68, 103399.	2.7	25
113	The integrative epigenomic-transcriptomic landscape of ER positive breast cancer. <i>Clinical Epigenetics</i> , 2015, 7, 126.	1.8	24
114	Expression profiling of nuclear receptors in breast cancer identifies TLX as a mediator of growth and invasion in triple-negative breast cancer. <i>Oncotarget</i> , 2015, 6, 21685-21703.	0.8	24
115	Clinical outcomes, Kadish-INSICA staging and therapeutic targeting of somatostatin receptor 2 in olfactory neuroblastoma. <i>European Journal of Cancer</i> , 2022, 162, 221-236.	1.3	22
116	Tensorial blind source separation for improved analysis of multi-omic data. <i>Genome Biology</i> , 2018, 19, 76.	3.8	20
117	JAK2-Centered Interactome Hotspot Identified by an Integrative Network Algorithm in Acute Stanford Type A Aortic Dissection. <i>PLoS ONE</i> , 2014, 9, e89406.	1.1	19
118	Corruption of the Intra-Gene DNA Methylation Architecture Is a Hallmark of Cancer. <i>PLoS ONE</i> , 2013, 8, e68285.	1.1	19
119	Integrative analysis of 3604 GWAS reveals multiple novel cell type-specific regulatory associations. <i>Genome Biology</i> , 2022, 23, 13.	3.8	19
120	Epigenetic and genetic deregulation in cancer target distinct signaling pathway domains. <i>Nucleic Acids Research</i> , 2017, 45, 583-596.	6.5	18
121	Cell-type heterogeneity: Why we should adjust for it in epigenome and biomarker studies. <i>Clinical Epigenetics</i> , 2022, 14, 31.	1.8	18
122	Distribution of breakpoints on chromosome 18 in breast, colorectal, and pancreatic carcinoma cell lines. <i>Cancer Genetics and Cytogenetics</i> , 2006, 164, 97-109.	1.0	17
123	A VARIATIONAL BAYES BETA MIXTURE MODEL FOR FEATURE SELECTION IN DNA METHYLATION STUDIES. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350005.	0.3	17
124	ebGSEA: an improved Gene Set Enrichment Analysis method for Epigenome-Wide-Association Studies. <i>Bioinformatics</i> , 2019, 35, 3514-3516.	1.8	15
125	Improved detection of tumor suppressor events in single-cell RNA-Seq data. <i>Npj Genomic Medicine</i> , 2020, 5, 43.	1.7	15
126	Inference of age-associated transcription factor regulatory activity changes in single cells. <i>Nature Aging</i> , 2022, 2, 548-561.	5.3	15

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127	Epigenetics makes its mark on women-specific cancers—an opportunity to redefine oncological approaches?. <i>Gynecologic Oncology</i> , 2013, 128, 134-143.	0.6	13
128	Ultra-fast scalable estimation of single-cell differentiation potency from scRNA-Seq data. <i>Bioinformatics</i> , 2021, 37, 1528-1534.	1.8	13
129	Approximate entropy of network parameters. <i>Physical Review E</i> , 2012, 85, 046111.	0.8	12
130	Estimating Differentiation Potency of Single Cells Using Single-Cell Entropy (SCENT). <i>Methods in Molecular Biology</i> , 2019, 1935, 125-139.	0.4	12
131	A comparison of epithelial cell content of oral samples estimated using cytology and DNA methylation. <i>Epigenetics</i> , 2022, 17, 327-334.	1.3	11
132	Novel epigenetic network biomarkers for early detection of esophageal cancer. <i>Clinical Epigenetics</i> , 2022, 14, 23.	1.8	11
133	Accounting for differential variability in detecting differentially methylated regions. <i>Briefings in Bioinformatics</i> , 2019, 20, 47-57.	3.2	10
134	International Multicenter Study of Clinical Outcomes of Sinonasal Melanoma Shows Survival Benefit for Patients Treated with Immune Checkpoint Inhibitors and Potential Improvements to the Current TNM Staging System. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , 2023, 84, 307-319.	0.4	10
135	Detection of epigenetic field defects using a weighted epigenetic distance-based method. <i>Nucleic Acids Research</i> , 2019, 47, e6-e6.	6.5	9
136	Computational Identification of Preneoplastic Cells Displaying High Stemness and Risk of Cancer Progression. <i>Cancer Research</i> , 2022, 82, 2520-2537.	0.4	9
137	Epigenetic aging: insights from network biology. <i>Aging</i> , 2013, 5, 719-720.	1.4	8
138	Comparisons of Non-Gaussian Statistical Models in DNA Methylation Analysis. <i>International Journal of Molecular Sciences</i> , 2014, 15, 10835-10854.	1.8	6
139	Denoising perturbation signatures reveal an actionable AKT-signaling gene module underlying a poor clinical outcome in endocrine-treated ER+ breast cancer. <i>Genome Biology</i> , 2015, 16, 61.	3.8	5
140	Epigenetic clocks galore: a new improved clock predicts age-acceleration in Hutchinson Gilford Progeria Syndrome patients. <i>Aging</i> , 2018, 10, 1799-1800.	1.4	4
141	Comments on: Interpretation of genome-wide infinium methylation data from ligated DNA in formalin-fixed paraffin-embedded paired tumor and normal tissue. <i>BMC Research Notes</i> , 2012, 5, 631.	0.6	2
142	A Network Systems Approach to Identify Functional Epigenetic Drivers in Cancer. <i>Translational Bioinformatics</i> , 2013, , 131-152.	0.0	1
143	Prognostic gene network modules in breast cancer hold promise. <i>Breast Cancer Research</i> , 2010, 12, 317.	2.2	0
144	A General Strategy for Inter-sample Variability Assessment and Normalisation. <i>Translational Bioinformatics</i> , 2015, , 51-68.	0.0	0

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145	Systems Epigenomics and Applications to Ageing and Cancer. <i>Translational Bioinformatics</i> , 2015, , 161-185.	0.0	0
146	Elucidating the Altered Transcriptional Programs in Breast Cancer using Independent Component Analysis. <i>PLoS Computational Biology</i> , 2005, preprint, e161.	1.5	0
147	Supervised Normalization of Large-Scale Omic Datasets Using Blind Source Separation. <i>Signals and Communication Technology</i> , 2014, , 465-497.	0.4	0
148	Detection of Epigenetic Field Defects Using a Weighted Epigenetic Distance-Based Method. <i>Methods in Molecular Biology</i> , 2020, 2117, 109-131.	0.4	0
149	Multicenter Analysis of Clinical Outcomes of Sinonasal Mucosal Melanoma. <i>Journal of Neurological Surgery, Part B: Skull Base</i> , 2022, 83, .	0.4	0