

# Peter W Laird

## List of Publications by Citations

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220  
papers

65,036  
citations

105  
h-index

251  
g-index

251  
ext. papers

82,113  
ext. citations

15.7  
avg, IF

7.35  
L-index

#	Paper	IF	Citations
220	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , <b>2013</b> , 368, 2059-74	59.2	3137
219	The somatic genomic landscape of glioblastoma. <i>Cell</i> , <b>2013</b> , 155, 462-77	56.2	2900
218	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , <b>2013</b> , 497, 67-73	50.4	2800
217	Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> , <b>2013</b> , 4, 2612	17.4	2572
216	Cancer epigenetics comes of age. <i>Nature Genetics</i> , <b>1999</b> , 21, 163-7	36.3	1927
215	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , <b>2015</b> , 372, 2481-98	59.2	1828
214	The Immune Landscape of Cancer. <i>Immunity</i> , <b>2018</b> , 48, 812-830.e14	32.3	1754
213	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. <i>Cancer Cell</i> , <b>2010</b> , 17, 510-22	24.3	1754
212	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. <i>Nature Genetics</i> , <b>2006</b> , 38, 787-93	36.3	1514
211	The power and the promise of DNA methylation markers. <i>Nature Reviews Cancer</i> , <b>2003</b> , 3, 253-66	31.3	1260
210	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 413-21	44.5	1229
209	Principles and challenges of genomewide DNA methylation analysis. <i>Nature Reviews Genetics</i> , <b>2010</b> , 11, 191-203	30.1	1226
208	Simplified mammalian DNA isolation procedure. <i>Nucleic Acids Research</i> , <b>1991</b> , 19, 4293	20.1	1202
207	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , <b>2013</b> , 45, 1134-40	36.3	1198
206	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , <b>2016</b> , 164, 550-63	56.2	1140
205	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , <b>2017</b> , 169, 1327-1341.e23	56.2	1125
204	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , <b>2018</b> , 173, 321-337.e10	56.2	1124

203	MethyLight: a high-throughput assay to measure DNA methylation. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, E32	20.1	1083
202	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , <b>2018</b> , 173, 400-416.e11	56.2	1072
201	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , <b>2015</b> , 163, 506-19	56.2	1055
200	COBRA: a sensitive and quantitative DNA methylation assay. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 2532-4	20.1	1020
199	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , <b>2017</b> , 171, 540-556.e25	56.2	961
198	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , <b>2014</b> , 158, 929-944	56.2	935
197	Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , <b>2007</b> , 39, 157-8	36.3	909
196	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , <b>2017</b> , 32, 185-203.e13	56.2	13896
195	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , <b>2018</b> , 173, 291-304.e6	56.2	888
194	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , <b>2018</b> , 173, 371-385.e18	56.2	854
193	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 135-45	59.2	753
192	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , <b>2010</b> , 20, 440-6	9.7	638
191	Suppression of intestinal neoplasia by DNA hypomethylation. <i>Cell</i> , <b>1995</b> , 81, 197-205	56.2	636
190	Interplay between the cancer genome and epigenome. <i>Cell</i> , <b>2013</b> , 153, 38-55	56.2	588
189	Analysis of repetitive element DNA methylation by MethyLight. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, 6823-36	20.1	588
188	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , <b>2018</b> , 173, 338-354.e15	56.2	560
187	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , <b>2014</b> , 26, 319-330	24.3	521
186	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , <b>2011</b> , 44, 40-6	36.3	474

185	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , <b>2012</b> , 22, 271-82	9.7	466
184	Cooperativity between DNA methyltransferases in the maintenance methylation of repetitive elements. <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 480-91	4.8	452
183	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , <b>2017</b> , 171, 950-965.e28	56.2	451
182	The role of DNA methylation in cancer genetic and epigenetics. <i>Annual Review of Genetics</i> , <b>1996</b> , 30, 441-645	14.5	419
181	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 1132-44	44.5	406
180	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 239-254.e6	10.6	405
179	Survival and development of neonatal rat cardiomyocytes transplanted into adult myocardium. <i>Journal of Molecular and Cellular Cardiology</i> , <b>2002</b> , 34, 107-16	5.8	403
178	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, e90	20.1	393
177	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , <b>2018</b> , 362,	33.3	392
176	Cancer epigenetics. <i>Human Molecular Genetics</i> , <b>2005</b> , 14 Spec No 1, R65-76	5.6	384
175	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , <b>2018</b> , 33, 676-689.e3	24.3	377
174	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , <b>2018</b> , 23, 181-193.e7	10.6	366
173	Precision and performance characteristics of bisulfite conversion and real-time PCR (MethyLight) for quantitative DNA methylation analysis. <i>Journal of Molecular Diagnostics</i> , <b>2006</b> , 8, 209-17	5.1	336
172	DNA methylation in the human cerebral cortex is dynamically regulated throughout the life span and involves differentiated neurons. <i>PLoS ONE</i> , <b>2007</b> , 2, e895	3.7	330
171	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , <b>2018</b> , 34, 211-224.e6	24.3	327
170	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , <b>2018</b> , 6, 271-281.e7	10.6	320
169	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , <b>2018</b> , 23, 313-326.e5	10.6	295
168	Alterations of immune response of Non-Small Cell Lung Cancer with Azacytidine. <i>Oncotarget</i> , <b>2013</b> , 4, 2067-79	3.3	285

167	Association of breast cancer DNA methylation profiles with hormone receptor status and response to tamoxifen. <i>Cancer Research</i> , <b>2004</b> , 64, 3807-13	10.1	284
166	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , <b>2018</b> , 33, 690-705.e9	24.3	277
165	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , <b>2018</b> , 33, 706-720.e9	24.3	275
164	Association between molecular subtypes of colorectal cancer and patient survival. <i>Gastroenterology</i> , <b>2015</b> , 148, 77-87.e2	13.3	273
163	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , <b>2012</b> , 131, 1565-89	6.3	258
162	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , <b>2017</b> , 49, 1476-1486	36.3	255
161	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, e22	20.1	254
160	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , <b>2017</b> , 18, 2780-2794	10.6	247
159	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. <i>Cell</i> , <b>2013</b> , 155, 858-68	56.2	247
158	DNA methylation as a biomarker for cardiovascular disease risk. <i>PLoS ONE</i> , <b>2010</b> , 5, e9692	3.7	247
157	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , <b>2015</b> , 25, 316-27	9.7	240
156	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 227-238.e3	10.6	235
155	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , <b>2018</b> , 33, 721-735.e8	24.3	228
154	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 9379-91	20.1	225
153	Cigarette smoking and colorectal cancer risk by molecularly defined subtypes. <i>Journal of the National Cancer Institute</i> , <b>2010</b> , 102, 1012-22	9.7	224
152	Widespread epigenetic abnormalities suggest a broad DNA methylation erasure defect in abnormal human sperm. <i>PLoS ONE</i> , <b>2007</b> , 2, e1289	3.7	215
151	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , <b>2017</b> , 31, 411-423	24.3	210
150	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 4808-17	5.6	206

149	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
148	Rebuilding a damaged heart: long-term survival of transplanted neonatal rat cardiomyocytes after myocardial infarction and effect on cardiac function. <i>Circulation</i> , <b>2002</b> , 105, 1720-6	16.7	204
147	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , <b>2018</b> , 23, 3392-3406	10.6	200
146	DNA hypomethylation and ovarian cancer biology. <i>Cancer Research</i> , <b>2004</b> , 64, 4472-80	10.1	193
145	DNA methylation: an alternative pathway to cancer. <i>Annals of Surgery</i> , <b>2001</b> , 234, 10-20	7.8	191
144	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 282-296.e4	10.6	188
143	Bis-SNP: combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , <b>2012</b> , 13, R61	18.3	179
142	Epigenetic analysis of KSHV latent and lytic genomes. <i>PLoS Pathogens</i> , <b>2010</b> , 6, e1001013	7.6	175
141	Molecular characterization of MSI-H colorectal cancer by MLHI promoter methylation, immunohistochemistry, and mismatch repair germline mutation screening. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2008</b> , 17, 3208-15	4	171
140	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , <b>2018</b> , 173, 305-320.e10	56.2	166
139	An epidemiologic and genomic investigation into the obesity paradox in renal cell carcinoma. <i>Journal of the National Cancer Institute</i> , <b>2013</b> , 105, 1862-70	9.7	161
138	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , <b>2018</b> , 6, 282-300.e2	10.6	159
137	Hypomethylation and hypermethylation of DNA in Wilms tumors. <i>Oncogene</i> , <b>2002</b> , 21, 6694-702	9.2	154
136	Breast cancer DNA methylation profiles in cancer cells and tumor stroma: association with HER-2/neu status in primary breast cancer. <i>Cancer Research</i> , <b>2006</b> , 66, 29-33	10.1	153
135	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , <b>2018</b> , 25, 1304-1317.e5	10.6	152
134	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , <b>2018</b> , 33, 244-258.e10	24.3	150
133	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , <b>2018</b> , 23, 297-312.e12	10.6	147
132	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , <b>2017</b> , 3, 1654-1662	13.4	146

131	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , <b>2018</b> , 23, 194-212.e6	10.6	146
130	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. <i>Laboratory Investigation</i> , <b>2008</b> , 88, 161-70	5.9	139
129	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , <b>2018</b> , 173, 386-399.e12	10.2	133
128	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , <b>2018</b> , 50, 591-602	36.3	133
127	Unique DNA methylation patterns distinguish noninvasive and invasive urothelial cancers and establish an epigenetic field defect in premalignant tissue. <i>Cancer Research</i> , <b>2010</b> , 70, 8169-78	10.1	133
126	Vitamin C promotes widespread yet specific DNA demethylation of the epigenome in human embryonic stem cells. <i>Stem Cells</i> , <b>2010</b> , 28, 1848-55	5.8	131
125	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , <b>2013</b> , 4, 1628	17.4	124
124	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , <b>2015</b> , 16, 105	18.3	123
123	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , <b>2018</b> , 23, 270-281.e3	10.6	121
122	Complete genetic suppression of polyp formation and reduction of CpG-island hypermethylation in Apc(Min/+) Dnmt1-hypomorphic Mice. <i>Cancer Research</i> , <b>2002</b> , 62, 1296-9	10.1	120
121	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, 4689-98	20.1	118
120	Analysis of the association between CIMP and BRAF in colorectal cancer by DNA methylation profiling. <i>PLoS ONE</i> , <b>2009</b> , 4, e8357	3.7	116
119	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , <b>2018</b> , 23, 255-269.e4	10.6	112
118	Thymidylate synthase: a novel genetic determinant of plasma homocysteine and folate levels. <i>Human Genetics</i> , <b>2002</b> , 111, 299-302	6.3	108
117	DNA methylation analysis by MethyLight technology. <i>Methods</i> , <b>2001</b> , 25, 456-62	4.6	103
116	Mature mRNAs of <i>Trypanosoma brucei</i> possess a 5Rcap acquired by discontinuous RNA synthesis. <i>Nucleic Acids Research</i> , <b>1985</b> , 13, 4253-66	20.1	102
115	Trans splicing in trypanosomes--archaism or adaptation?. <i>Trends in Genetics</i> , <b>1989</b> , 5, 204-8	8.5	97
114	SeSAMe: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, e123	20.1	94

113	MethylLight. <i>Methods in Molecular Biology</i> , <b>2009</b> , 507, 325-37	1.4	94
112	Sensitive detection of DNA methylation. <i>Annals of the New York Academy of Sciences</i> , <b>2003</b> , 983, 120-30	6.5	94
111	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. <i>Molecular Cancer</i> , <b>2008</b> , 7, 62	42.1	91
110	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. <i>Cell Reports</i> , <b>2018</b> , 23, 637-651	10.6	90
109	DNA methyltransferase deficiency modifies cancer susceptibility in mice lacking DNA mismatch repair. <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 2906-17	4.8	90
108	Genome-scale discovery of DNA-methylation biomarkers for blood-based detection of colorectal cancer. <i>PLoS ONE</i> , <b>2012</b> , 7, e50266	3.7	88
107	Distinct methylation profiles of glioma subtypes. <i>International Journal of Cancer</i> , <b>2003</b> , 106, 52-9	7.5	86
106	Identification of a panel of sensitive and specific DNA methylation markers for lung adenocarcinoma. <i>Molecular Cancer</i> , <b>2007</b> , 6, 70	42.1	85
105	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , <b>2018</b> , 7, 422-437.e7	10.6	85
104	Combination Epigenetic Therapy in Advanced Breast Cancer with 5-Azacitidine and Entinostat: A Phase II National Cancer Institute/Stand Up to Cancer Study. <i>Clinical Cancer Research</i> , <b>2017</b> , 23, 2691-2701	12.9	84
103	Kaiso contributes to DNA methylation-dependent silencing of tumor suppressor genes in colon cancer cell lines. <i>Cancer Research</i> , <b>2008</b> , 68, 7258-63	10.1	83
102	Transcription of the intergenic regions of the tubulin gene cluster of <i>Trypanosoma brucei</i> : evidence for a polycistronic transcription unit in a eukaryote. <i>Nucleic Acids Research</i> , <b>1987</b> , 15, 7357-68	20.1	80
101	Exploring the cancer methylome. <i>BMC Proceedings</i> , <b>2012</b> , 6,	2.3	78
100	Smad3 deficiency promotes tumorigenesis in the distal colon of ApcMin/+ mice. <i>Cancer Research</i> , <b>2006</b> , 66, 8430-8	10.1	78
99	Correlation of pathologic features with CpG island methylator phenotype (CIMP) by quantitative DNA methylation analysis in colorectal carcinoma. <i>American Journal of Surgical Pathology</i> , <b>2006</b> , 30, 1175-83	6.7	77
98	Long-term epigenetic therapy with oral zebularine has minimal side effects and prevents intestinal tumors in mice. <i>Cancer Prevention Research</i> , <b>2008</b> , 1, 233-40	3.2	76
97	A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , <b>2004</b> , 20, 1896-904	4.2	76
96	The mutagenic potential of duodenoesophageal reflux. <i>Annals of Surgery</i> , <b>2005</b> , 241, 63-8	7.8	74



95	The methylenetetrahydrofolate reductase C677T mutation induces cell-specific changes in genomic DNA methylation and uracil misincorporation: a possible molecular basis for the site-specific cancer risk modification. <i>International Journal of Cancer</i> , <b>2009</b> , 124, 1999-2005	7.5	73
94	Tumor Budding in Colorectal Carcinoma: Confirmation of Prognostic Significance and Histologic Cutoff in a Population-based Cohort. <i>American Journal of Surgical Pathology</i> , <b>2015</b> , 39, 1340-6	6.7	72
93	Role of methionine adenosyltransferase 2A and S-adenosylmethionine in mitogen-induced growth of human colon cancer cells. <i>Gastroenterology</i> , <b>2007</b> , 133, 207-18	13.3	72
92	Frequency of deletions of EPCAM (TACSTD1) in MSH2-associated Lynch syndrome cases. <i>Journal of Molecular Diagnostics</i> , <b>2011</b> , 13, 93-9	5.1	71
91	Distinct DNA methylation profiles in malignant mesothelioma, lung adenocarcinoma, and non-tumor lung. <i>Lung Cancer</i> , <b>2005</b> , 47, 193-204	5.9	71
90	The role of DNA methylation in the development and progression of lung adenocarcinoma. <i>Disease Markers</i> , <b>2007</b> , 23, 5-30	3.2	70
89	Dnmt1 deficiency leads to enhanced microsatellite instability in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 5742-9	20.1	69
88	Non-invasive diagnosis of early-stage lung cancer using high-throughput targeted DNA methylation sequencing of circulating tumor DNA (ctDNA). <i>Theranostics</i> , <b>2019</b> , 9, 2056-2070	12.1	68
87	DNA methylation profiles of ovarian epithelial carcinoma tumors and cell lines. <i>PLoS ONE</i> , <b>2010</b> , 5, e9359	3.7	68
86	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , <b>2018</b> , 23, 172-180.e3	10.6	66
85	Sex differential in methylation patterns of selected genes in Singapore Chinese. <i>Human Genetics</i> , <b>2005</b> , 117, 402-3	6.3	66
84	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsRData. <i>Cell Systems</i> , <b>2019</b> , 9, 24-34.e10	10.6	64
83	Gene dysregulation by histone variant H2A.Z in bladder cancer. <i>Epigenetics and Chromatin</i> , <b>2013</b> , 6, 34	5.8	61
82	Association of the colorectal CpG island methylator phenotype with molecular features, risk factors, and family history. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 512-519	4	59
81	DNA methylation profile of 28 potential marker loci in malignant mesothelioma. <i>Lung Cancer</i> , <b>2007</b> , 58, 220-30	5.9	59
80	Reduced rates of gene loss, gene silencing, and gene mutation in Dnmt1-deficient embryonic stem cells. <i>Molecular and Cellular Biology</i> , <b>2001</b> , 21, 7587-600	4.8	59
79	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , <b>2018</b> , 23, 213-226.e3	26.63	56
78	DNA hypermethylation of ESR1 and PGR in breast cancer: pathologic and epidemiologic associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2009</b> , 18, 3036-43	4	56

77	Oncogenic mechanisms mediated by DNA methylation. <i>Trends in Molecular Medicine</i> , <b>1997</b> , 3, 223-9		56
76	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , <b>2020</b> , 37, 639-654.e6	24.3	56
75	Combination epigenetic therapy in metastatic colorectal cancer (mCRC) with subcutaneous 5-azacitidine and entinostat: a phase 2 consortium/stand up 2 cancer study. <i>Oncotarget</i> , <b>2017</b> , 8, 35326-35338	3.3	52
74	Combined bisulfite restriction analysis (COBRA). <i>Methods in Molecular Biology</i> , <b>2002</b> , 200, 71-85	1.4	49
73	Associations between colorectal cancer molecular markers and pathways with clinicopathologic features in older women. <i>Gastroenterology</i> , <b>2013</b> , 145, 348-56.e1-2	13.3	45
72	Genome-scale screen for DNA methylation-based detection markers for ovarian cancer. <i>PLoS ONE</i> , <b>2011</b> , 6, e28141	3.7	45
71	2RDeoxy-N4-[2-(4-nitrophenyl)ethoxycarbonyl]-5-azacytidine: a novel inhibitor of DNA methyltransferase that requires activation by human carboxylesterase 1. <i>Cancer Letters</i> , <b>2008</b> , 266, 238-48	9.9	41
70	Identification of activated enhancers and linked transcription factors in breast, prostate, and kidney tumors by tracing enhancer networks using epigenetic traits. <i>Epigenetics and Chromatin</i> , <b>2016</b> , 9, 50	5.8	40
69	Rapid and quantitative method of allele-specific DNA methylation analysis. <i>BioTechniques</i> , <b>2006</b> , 41, 734-25	2.5	39
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