

Peter W Laird

List of Publications by Year in descending order

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241
papers

94,391
citations

1296

112
h-index

2072

211
g-index

251
all docs

251
docs citations

251
times ranked

98870
citing authors

#	ARTICLE	IF	CITATIONS
1	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	5.8	5,788
2	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
3	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
4	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	13.5	3,979
5	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
6	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	13.9	2,582
7	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
8	Cancer-epigenetics comes of age. Nature Genetics, 1999, 21, 163-167.	9.4	2,125
9	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
10	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522.	7.7	2,078
11	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	13.5	1,794
12	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	1,742
13	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
14	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. Nature Genetics, 2006, 38, 787-793.	9.4	1,715
15	Absolute quantification of somatic DNA alterations in human cancer. Nature Biotechnology, 2012, 30, 413-421.	9.4	1,710
16	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	13.5	1,695
17	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
18	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	9.4	1,616

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19	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	13.5	1,485
20	Principles and challenges of genome-wide DNA methylation analysis. <i>Nature Reviews Genetics</i> , 2010, 11, 191-203.	7.7	1,432
21	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
22	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
23	The power and the promise of DNA methylation markers. <i>Nature Reviews Cancer</i> , 2003, 3, 253-266.	12.8	1,414
24	Simplified mammalian DNA isolation procedure. <i>Nucleic Acids Research</i> , 1991, 19, 4293-4293.	6.5	1,355
25	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	1,242
26	MethylLight: a high-throughput assay to measure DNA methylation. <i>Nucleic Acids Research</i> , 2000, 28, 32e-0.	6.5	1,216
27	COBRA: a sensitive and quantitative DNA methylation assay. <i>Nucleic Acids Research</i> , 1997, 25, 2532-2534.	6.5	1,090
28	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
29	Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , 2007, 39, 157-158.	9.4	1,023
30	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
31	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
32	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
33	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
34	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
35	Interplay between the Cancer Genome and Epigenome. <i>Cell</i> , 2013, 153, 38-55.	13.5	733
36	Suppression of intestinal neoplasia by DNA hypomethylation. <i>Cell</i> , 1995, 81, 197-205.	13.5	694

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37	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	2.9	683
38	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
39	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.	6.5	647
40	Analysis of repetitive element DNA methylation by MethyLight. <i>Nucleic Acids Research</i> , 2005, 33, 6823-6836.	6.5	636
41	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	7.7	623
42	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
43	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , 2012, 44, 40-46.	9.4	588
44	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	2.4	527
45	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
46	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , 2011, 29, 1132-1144.	9.4	509
47	Cooperativity between DNA Methyltransferases in the Maintenance Methylation of Repetitive Elements. <i>Molecular and Cellular Biology</i> , 2002, 22, 480-491.	1.1	508
48	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
49	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017, 45, gkw967.	6.5	466
50	THE ROLE OF DNA METHYLATION IN CANCER GENETICS AND EPIGENETICS. <i>Annual Review of Genetics</i> , 1996, 30, 441-464.	3.2	455
51	Survival and Development of Neonatal Rat Cardiomyocytes Transplanted into Adult Myocardium. <i>Journal of Molecular and Cellular Cardiology</i> , 2002, 34, 107-116.	0.9	455
52	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.	9.4	427
53	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
54	Cancer epigenetics. <i>Human Molecular Genetics</i> , 2005, 14, R65-R76.	1.4	409

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55	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
56	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> , 2018, 33, 706-720.e9.	7.7	400
57	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
58	DNA Methylation in the Human Cerebral Cortex Is Dynamically Regulated throughout the Life Span and Involves Differentiated Neurons. <i>PLoS ONE</i> , 2007, 2, e895.	1.1	375
59	Precision and Performance Characteristics of Bisulfite Conversion and Real-Time PCR (MethyLight) for Quantitative DNA Methylation Analysis. <i>Journal of Molecular Diagnostics</i> , 2006, 8, 209-217.	1.2	361
60	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015, 25, 316-327.	2.4	343
61	Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. <i>Gastroenterology</i> , 2015, 148, 77-87.e2.	0.6	342
62	Alterations of immune response of non-small cell lung cancer with Azacytidine. <i>Oncotarget</i> , 2013, 4, 2067-2079.	0.8	336
63	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	2.9	333
64	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
65	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
66	The Landscape of Microsatellite Instability in Colorectal and Endometrial Cancer Genomes. <i>Cell</i> , 2013, 155, 858-868.	13.5	311
67	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309
68	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012, 40, 9379-9391.	6.5	305
69	Association of Breast Cancer DNA Methylation Profiles with Hormone Receptor Status and Response to Tamoxifen. <i>Cancer Research</i> , 2004, 64, 3807-3813.	0.4	304
70	Environmental epigenetics: prospects for studying epigenetic mediation of exposure–response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.	1.8	294
71	DNA Methylation as a Biomarker for Cardiovascular Disease Risk. <i>PLoS ONE</i> , 2010, 5, e9692.	1.1	289
72	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018, 6, 282-300.e2.	2.9	284

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73	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
74	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270
75	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
76	Cigarette Smoking and Colorectal Cancer Risk by Molecularly Defined Subtypes. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1012-1022.	3.0	261
77	DNA Methylation: An Alternative Pathway to Cancer. <i>Annals of Surgery</i> , 2001, 234, 10-20.	2.1	260
78	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018, 50, 591-602.	9.4	258
79	Widespread Epigenetic Abnormalities Suggest a Broad DNA Methylation Erasure Defect in Abnormal Human Sperm. <i>PLoS ONE</i> , 2007, 2, e1289.	1.1	254
80	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	2.9	245
81	Rebuilding a Damaged Heart. <i>Circulation</i> , 2002, 105, 1720-1726.	1.6	239
82	An Epidemiologic and Genomic Investigation Into the Obesity Paradox in Renal Cell Carcinoma. <i>Journal of the National Cancer Institute</i> , 2013, 105, 1862-1870.	3.0	231
83	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. <i>Human Molecular Genetics</i> , 2009, 18, 4808-4817.	1.4	230
84	Bis-SNP: Combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , 2012, 13, R61.	13.9	230
85	Epigenetic Analysis of KSHV Latent and Lytic Genomes. <i>PLoS Pathogens</i> , 2010, 6, e1001013.	2.1	229
86	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
87	DNA Hypomethylation and Ovarian Cancer Biology. <i>Cancer Research</i> , 2004, 64, 4472-4480.	0.4	221
88	SeSAME: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , 2018, 46, e123.	6.5	213
89	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017, 3, 1654.	3.4	208
90	Molecular Characterization of MSI-H Colorectal Cancer by <i>MLH1</i> Promoter Methylation, Immunohistochemistry, and Mismatch Repair Germline Mutation Screening. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2008, 17, 3208-3215.	1.1	207

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91	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
92	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
93	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105.	13.9	178
94	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	2.9	177
95	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> , 2006, 66, 29-33.	0.4	166
96	Hypomethylation and hypermethylation of DNA in Wilms tumors. <i>Oncogene</i> , 2002, 21, 6694-6702.	2.6	165
97	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. <i>Laboratory Investigation</i> , 2008, 88, 161-170.	1.7	156
98	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells A. <i>Stem Cells</i> , 2010, 28, 1848-1855.	1.4	156
99	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	7.7	151
100	Unique DNA Methylation Patterns Distinguish Noninvasive and Invasive Urothelial Cancers and Establish an Epigenetic Field Defect in Premalignant Tissue. <i>Cancer Research</i> , 2010, 70, 8169-8178.	0.4	148
101	Non-invasive diagnosis of early-stage lung cancer using high-throughput targeted DNA methylation sequencing of circulating tumor DNA (ctDNA). <i>Theranostics</i> , 2019, 9, 2056-2070.	4.6	147
102	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	5.8	144
103	Complete genetic suppression of polyp formation and reduction of CpG-island hypermethylation in Apc(Min/+) Dnmt1-hypomorphic Mice. <i>Cancer Research</i> , 2002, 62, 1296-9.	0.4	141
104	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. <i>Cell Reports</i> , 2018, 23, 637-651.	2.9	137
105	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β 2 Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
106	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. <i>Nucleic Acids Research</i> , 2008, 36, 4689-4698.	6.5	133
107	Analysis of the Association between CIMP and BRAFV600E in Colorectal Cancer by DNA Methylation Profiling. <i>PLoS ONE</i> , 2009, 4, e8357.	1.1	133
108	DNA Methylation Analysis by MethyLight Technology. <i>Methods</i> , 2001, 25, 456-462.	1.9	121

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109	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	2.9	119
110	Thymidylate synthase: a novel genetic determinant of plasma homocysteine and folate levels. <i>Human Genetics</i> , 2002, 111, 299-302.	1.8	115
111	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. <i>Molecular Cancer</i> , 2008, 7, 62.	7.9	114
112	Mature mRNAs of <i>Trypanosoma brucei</i> possess a 5' cap acquired by discontinuous RNA synthesis. <i>Nucleic Acids Research</i> , 1985, 13, 4253-4266.	6.5	106
113	MethylLight. <i>Methods in Molecular Biology</i> , 2009, 507, 325-337.	0.4	106
114	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> , 2017, 23, 2691-2701.	3.2	106
115	Identification of a panel of sensitive and specific DNA methylation markers for lung adenocarcinoma. <i>Molecular Cancer</i> , 2007, 6, 70.	7.9	105
116	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	2.9	103
117	Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. <i>PLoS ONE</i> , 2012, 7, e50266.	1.1	103
118	A comparison of cluster analysis methods using DNA methylation data. <i>Bioinformatics</i> , 2004, 20, 1896-1904.	1.8	102
119	Kaiso Contributes to DNA Methylation-Dependent Silencing of Tumor Suppressor Genes in Colon Cancer Cell Lines. <i>Cancer Research</i> , 2008, 68, 7258-7263.	0.4	101
120	Trans splicing in trypanosomes – archaism or adaptation?. <i>Trends in Genetics</i> , 1989, 5, 204-208.	2.9	100
121	Distinct methylation profiles of glioma subtypes. <i>International Journal of Cancer</i> , 2003, 106, 52-59.	2.3	100
122	Sensitive Detection of DNA Methylation. <i>Annals of the New York Academy of Sciences</i> , 2003, 983, 120-130.	1.8	100
123	DNA Methyltransferase Deficiency Modifies Cancer Susceptibility in Mice Lacking DNA Mismatch Repair. <i>Molecular and Cellular Biology</i> , 2002, 22, 2906-2917.	1.1	95
124	Tumor Budding in Colorectal Carcinoma. <i>American Journal of Surgical Pathology</i> , 2015, 39, 1340-1346.	2.1	95
125	Long-term Epigenetic Therapy with Oral Zebularine Has Minimal Side Effects and Prevents Intestinal Tumors in Mice. <i>Cancer Prevention Research</i> , 2008, 1, 233-240.	0.7	93
126	Smad3 Deficiency Promotes Tumorigenesis in the Distal Colon of <i>ApcMin/+</i> Mice. <i>Cancer Research</i> , 2006, 66, 8430-8438.	0.4	86

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127	Role of Methionine Adenosyltransferase 2A and S-adenosylmethionine in Mitogen-Induced Growth of Human Colon Cancer Cells. <i>Gastroenterology</i> , 2007, 133, 207-218.	0.6	86
128	The Mutagenic Potential of Duodeno-esophageal Reflux. <i>Annals of Surgery</i> , 2005, 241, 63-68.	2.1	85
129	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> , 2006, 30, 1175-1183.	2.1	85
130	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
131	Transcription of the intergenic regions of the tubulin gene cluster of <i>Trypanosoma brucei</i> : evidence for a polyclstronic transcription unit in a eukaryote. <i>Nucleic Acids Research</i> , 1987, 15, 7357-7368.	6.5	81
132	Distinct DNA methylation profiles in malignant mesothelioma, lung adenocarcinoma, and non-tumor lung. <i>Lung Cancer</i> , 2005, 47, 193-204.	0.9	81
133	Dnmt1 deficiency leads to enhanced microsatellite instability in mouse embryonic stem cells. <i>Nucleic Acids Research</i> , 2004, 32, 5742-5749.	6.5	80
134	The Role of DNA Methylation in the Development and Progression of Lung Adenocarcinoma. <i>Disease Markers</i> , 2007, 23, 5-30.	0.6	80
135	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> , 2009, 124, 1999-2005.	2.3	80
136	DNA Methylation Profiles of Ovarian Epithelial Carcinoma Tumors and Cell Lines. <i>PLoS ONE</i> , 2010, 5, e9359.	1.1	80
137	Frequency of Deletions of EPCAM (TACSTD1) in MSH2-Associated Lynch Syndrome Cases. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 93-99.	1.2	79
138	Sex differential in methylation patterns of selected genes in Singapore Chinese. <i>Human Genetics</i> , 2005, 117, 402-403.	1.8	78
139	Gene dysregulation by histone variant H2A.Z in bladder cancer. <i>Epigenetics and Chromatin</i> , 2013, 6, 34.	1.8	74
140	Association of the Colorectal CpG Island Methylator Phenotype with Molecular Features, Risk Factors, and Family History. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 512-519.	1.1	71
141	Oncogenic mechanisms mediated by DNA methylation. <i>Trends in Molecular Medicine</i> , 1997, 3, 223-229.	2.6	67
142	Reduced Rates of Gene Loss, Gene Silencing, and Gene Mutation in Dnmt1 -Deficient Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2001, 21, 7587-7600.	1.1	66
143	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> , 2017, 8, 35326-35338.	0.8	66
144	Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. <i>PLoS ONE</i> , 2011, 6, e28141.	1.1	65

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145	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	7.7	65
146	DNA methylation profile of 28 potential marker loci in malignant mesothelioma. <i>Lung Cancer</i> , 2007, 58, 220-230.	0.9	61
147	DNA Hypermethylation of <i>ESR1</i> and <i>PGR</i> in Breast Cancer: Pathologic and Epidemiologic Associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009, 18, 3036-3043.	1.1	60
148	Combined Bisulfite Restriction Analysis (COBRA). , 2002, 200, 071-085.		59
149	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> , 2016, 9, 50.	1.8	53
150	Associations Between Colorectal Cancer Molecular Markers and Pathways With Clinicopathologic Features in Older Women. <i>Gastroenterology</i> , 2013, 145, 348-356.e2.	0.6	49
151	2-Deoxy-N4-[2-(4-nitrophenyl)ethoxycarbonyl]-5-azacytidine: A novel inhibitor of DNA methyltransferase that requires activation by human carboxylesterase 1. <i>Cancer Letters</i> , 2008, 266, 238-248.	3.2	45
152	Promoter Hypermethylation of Tumor Suppressor Genes in Urine from Patients with Cervical Neoplasia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007, 16, 1178-1184.	1.1	44
153	Mild Depletion of Dietary Folate Combined with Other B Vitamins Alters Multiple Components of the Wnt Pathway in Mouse Colon. <i>Journal of Nutrition</i> , 2007, 137, 2701-2708.	1.3	42
154	Rapid and quantitative method of allele-specific DNA methylation analysis. <i>BioTechniques</i> , 2006, 41, 734-739.	0.8	41
155	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. <i>Cancer Prevention Research</i> , 2011, 4, 530-543.	0.7	41
156	A <i>pgk::hprt</i> fusion as a selectable marker for targeting of genes in mouse embryonic stem cells: disruption of the T-cell receptor β -chain-encoding gene. <i>Gene</i> , 1991, 105, 263-267.	1.0	39
157	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. <i>Neoplasia</i> , 2010, 12, 579-IN18.	2.3	38
158	Ovarian Cancer Early Detection Claims Are Biased. <i>Clinical Cancer Research</i> , 2008, 14, 7574.1-7574.	3.2	37
159	Hierarchical clustering of lung cancer cell lines using DNA methylation markers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2002, 11, 291-7.	1.1	37
160	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. <i>Cell Genomics</i> , 2022, 2, 100144.	3.0	37
161	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012, 61, 1299-1305.	6.1	36
162	Specific Variants in the MLH1 Gene Region May Drive DNA Methylation, Loss of Protein Expression, and MSI-H Colorectal Cancer. <i>PLoS ONE</i> , 2010, 5, e13314.	1.1	35

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