

# Peter W Laird

## List of Publications by Year in descending order

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237  
papers

89,670  
citations

870

111  
h-index

1099

220  
g-index

296  
all docs

296  
docs citations

296  
times ranked

103681  
citing authors

#	ARTICLE	IF	CITATIONS
1	BISCUIT: an efficient, standards-compliant tool suite for simultaneous genetic and epigenetic inference in bulk and single-cell studies. <i>Nucleic Acids Research</i> , 2024, 52, e32-e32.	16.2	5
2	Single-cell chromatin accessibility reveals malignant regulatory programs in primary human cancers. <i>Science</i> , 2024, 385, .	38.2	1
3	DAB2IP Is a Bifunctional Tumor Suppressor That Regulates Wild-Type RAS and Inflammatory Cascades in KRAS Mutant Colon Cancer. <i>Cancer Research</i> , 2023, 83, 1800-1814.	0.6	3
4	How Epigenomics Broke the Mold: An Interview with Peter W Laird. <i>Epigenomics</i> , 2022, 14, 303-308.	2.3	2
5	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. <i>Cell Genomics</i> , 2022, 2, 100144.	7.1	44
6	High-Resolution Profiling of Lung Adenocarcinoma Identifies Expression Subtypes with Specific Biomarkers and Clinically Relevant Vulnerabilities. <i>Cancer Research</i> , 2022, 82, 3917-3931.	0.6	16
7	Cell division drives DNA methylation loss in late-replicating domains in primary human cells. <i>Nature Communications</i> , 2022, 13, .	14.1	28
8	Multiomics in primary and metastatic breast tumors from the AURORA US network finds microenvironment and epigenetic drivers of metastasis. <i>Nature Cancer</i> , 2022, , .	13.9	17
9	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. <i>Journal of the National Cancer Institute</i> , 2021, 113, 27-37.	5.1	21
10	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021, 39, 38-53.e7.	33.4	66
11	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	6.4	16
12	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021, 2, 100766.	1.1	4
13	Systematic Assessment of Tumor Purity and Its Clinical Implications. <i>JCO Precision Oncology</i> , 2020, , 995-1005.	2.1	26
14	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020, 37, 639-654.e6.	33.4	177
15	Abstract GS3-08: Multiplatform analysis of matched primary and metastatic breast tumors from the AURORA US Network. <i>Cancer Research</i> , 2020, 80, GS3-08-GS3-08.	0.6	1
16	Phase I trial of TRC102 (methoxyamine HCl) in combination with temozolomide in patients with relapsed solid tumors and lymphomas. <i>Oncotarget</i> , 2020, 11, 3959-3971.	1.7	11
17	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.0	102
18	In vivo Application of the REMOTE-control System for the Manipulation of Endogenous Gene Expression. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	1

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19	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.	11.4	182
20	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. <i>Cancer Prevention Research</i> , 2019, 12, 781-790.	1.1	4
21	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	35.1	2,212
22	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	35.1	1,486
23	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018, 173, 291-304.e6.	35.1	1,566
24	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	35.1	202
25	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	35.1	256
26	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	35.1	1,407
27	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	35.1	2,023
28	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018, 23, 282-296.e4.	6.4	303
29	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	401
30	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	6.4	233
31	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.	6.4	186
32	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	534
33	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018, 23, 181-193.e7.	6.4	668
34	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	22.7	3,724
35	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	106
36	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	6.4	78

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37	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	752
38	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	6.4	209
39	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	179
40	A Distinct DNA Methylation Shift in a Subset of Glioma CpG Island Methylator Phenotypes during Tumor Recurrence. Cell Reports, 2018, 23, 637-651.	6.4	130
41	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	33.4	278
42	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.0	518
43	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.0	273
44	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	33.4	365
45	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	33.4	669
46	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	33.4	386
47	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	33.4	424
48	DNA methylation loss in late-replicating domains is linked to mitotic cell division. Nature Genetics, 2018, 50, 591-602.	16.3	223
49	MethylLight and Digital MethyLight. Methods in Molecular Biology, 2018, , 497-513.	0.0	14
50	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.0	138
51	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	38.2	705
52	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	6.4	323
53	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	33.4	586
54	SeSAME: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. Nucleic Acids Research, 2018, , .	16.2	174

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55	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	331
56	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. <i>Cancer Research</i> , 2018, 78, 3302-3302.	0.6	11
57	Abstract 5312: The effect of Dnmt1 overexpression on intestinal tumorigenesis. , 2018, , .		0
58	Abstract 5327: DNA methylation loss in late-replicating domains is linked to mitotic cell division. , 2018, , .		0
59	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017, , gkw967.	16.2	359
60	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.	13.6	206
61	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	35.1	1,756
62	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	33.4	322
63	Transcriptional heterogeneity in the lactase gene within cell-type is linked to the epigenome. <i>Scientific Reports</i> , 2017, 7, .	3.7	9
64	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	440
65	Combination Epigenetic Therapy in Advanced Breast Cancer with 5-Azacytidine and Eentinostat: A Phase II National Cancer Institute/Stand Up to Cancer Study. <i>Clinical Cancer Research</i> , 2017, 23, 2691-2701.	6.4	119
66	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	35.1	1,678
67	The REMOTE-control system: a system for reversible and tunable control of endogenous gene expression in mice. <i>Nucleic Acids Research</i> , 2017, 45, 12256-12269.	16.2	9
68	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.	16.3	378
69	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	33.4	1,371
70	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	35.1	760
71	Association of high microvessel density and low PTEN with poor outcome in stage 3 neuroblastoma: rationale for using first in class dual PI3K/BRD4 inhibitor, SF1126. <i>Oncotarget</i> , 2017, 8, 52193-52210.	1.7	23
72	Combination epigenetic therapy in metastatic colorectal cancer (mCRC) with subcutaneous 5-azacytidine and entinostat: a phase 2 consortium/stand up 2 cancer study. <i>Oncotarget</i> , 2017, 8, 35326-35338.	1.7	68

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73	Abstract 5381: A highly sensitive method for noninvasive cancer profiling through targeted methylation sequencing of circulating cell-free DNA. , 2017, , .		0
74	All Things in Moderation: Prevention of Intestinal Adenomas by DNA Hypomethylation. <i>Cancer Prevention Research</i> , 2016, 9, 509-511.	1.1	0
75	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. <i>Npj Breast Cancer</i> , 2016, 2, .	6.8	28
76	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, .	3.3	46
77	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	18.1	255
78	Effects of folypolyglutamate synthase modulation on global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. <i>Journal of Nutritional Biochemistry</i> , 2016, 29, 27-35.	4.9	6
79	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	35.1	1,567
80	Promoter Methylation Analysis Reveals That <i>KCNA5</i> Ion Channel Silencing Supports Ewing Sarcoma Cell Proliferation. <i>Molecular Cancer Research</i> , 2016, 14, 26-34.	2.9	23
81	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	25.5	1,017
82	Clinicopathologic Risk Factor Distributions for <i>MLH1</i> Promoter Region Methylation in CIMP-Positive Tumors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 68-75.	0.9	24
83	Abstract 128: Comprehensive molecular characterization of 412 muscle-invasive urothelial bladder carcinomas: final analysis of The Cancer Genome Atlas (TCGA) project. , 2016, , .		0
84	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, .	14.0	142
85	Tumor Budding in Colorectal Carcinoma. <i>American Journal of Surgical Pathology</i> , 2015, 39, 1340-1346.	3.9	99
86	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.	4.6	322
87	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.	0.9	73
88	Î³-Glutamyl hydrolase modulation significantly influences global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. <i>Genes and Nutrition</i> , 2015, 10, .	4.5	10
89	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	25.5	2,437
90	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	35.1	1,399

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91	Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. <i>Gastroenterology</i> , 2015, 148, 77-87.e2.	1.0	338
92	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors. , 2015, , .		10
93	Abstract 3288: The KCNA5 promoter is hypermethylated in Ewing sarcoma and silencing contributes to cell proliferation. , 2015, , .		0
94	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project. <i>Cancer Research</i> , 2015, 75, 2969-2969.	0.6	2
95	Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014, 15, .	3.3	15
96	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	33.4	632
97	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	35.1	1,127
98	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014, 11, 689-694.	14.5	24
99	Abstract 984: Alteration of the p53 pathway is associated with subclonal tumor progression in glioblastoma. <i>Cancer Research</i> , 2014, 74, 984-984.	0.6	0
100	Abstract 987: Comprehensive characterization of urothelial bladder cancer: a TCGA Project update. <i>Cancer Research</i> , 2014, 74, 987-987.	0.6	0
101	Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> , 2013, 4, .	14.1	5,865
102	Alterations in Deoxyribonucleic Acid (DNA) Methylation Patterns of Calca, Timp3, Mmp2, and Igf2r Are Associated With Chronic Cystitis in a Cyclophosphamide-induced Mouse Model. <i>Urology</i> , 2013, 82, 253.e9-253.e15.	1.5	3
103	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	35.1	3,785
104	The Landscape of Microsatellite Instability in Colorectal and Endometrial Cancer Genomes. <i>Cell</i> , 2013, 155, 858-868.	35.1	289
105	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013, 45, 1134-1140.	16.3	1,398
106	Associations Between Colorectal Cancer Molecular Markers and Pathways With Clinicopathologic Features in Older Women. <i>Gastroenterology</i> , 2013, 145, 348-356.e2.	1.0	46
107	Interplay between the Cancer Genome and Epigenome. <i>Cell</i> , 2013, 153, 38-55.	35.1	722
108	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	40.1	4,141

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109	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	25.5	3,959
110	Clinical Applications of DNA Methylation Biomarkers in Colorectal Cancer. <i>Epigenomics</i> , 2013, 5, 105-108.	2.3	28
111	Gene dysregulation by histone variant H2A.Z in bladder cancer. <i>Epigenetics and Chromatin</i> , 2013, 6, .	3.3	73
112	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.	5.1	235
113	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.	16.2	583
114	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, .	14.1	135
115	Alterations of immune response of non-small cell lung cancer with Azacytidine. <i>Oncotarget</i> , 2013, 4, 2067-2079.	1.7	321
116	Abstract PL02-01: Cancer genetic and epigenetic interactions.. , 2013, , .		0
117	Abstract B130: The intratumoral heterogeneity of glioblastoma suggests a pivotal role for clonal evolution.. , 2013, , .		0
118	Associations Between Intake of Folate and Related Micronutrients with Molecularly Defined Colorectal Cancer Risks in the Iowa Women's Health Study. <i>Nutrition and Cancer</i> , 2012, 64, 899-910.	2.5	34
119	A Blueprint for an International Cancer Epigenome Consortium. A Report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012, 72, 6319-6324.	0.6	22
120	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	4.6	510
121	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012, 40, 9379-9391.	16.2	283
122	Cancer Risks for the Relatives of Colorectal Cancer Cases with a Methylated <i>MLH1</i> Promoter Region: Data from the Colorectal Cancer Family Registry. <i>Cancer Prevention Research</i> , 2012, 5, 328-335.	1.1	12
123	Bis-SNP: Combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , 2012, 13, .	8.4	201
124	In Epigenetic Therapy, Less Is More. <i>Cell Stem Cell</i> , 2012, 10, 353-354.	17.2	25
125	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012, 61, 1299-1305.	14.8	38
126	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.	3.1	262

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127	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	18.1	1,508
128	Exploring the cancer methylome. <i>BMC Proceedings</i> , 2012, 6, .	2.4	0
129	Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. <i>PLoS ONE</i> , 2012, 7, e50266.	2.5	95
130	Abstract 5518: Clinicopathologic associations with colorectal cancer molecular pathways in a cohort study of older women. , 2012, , .		0
131	Abstract 4492: Colorectal cancer survival by molecular subtypes in a population-based cohort of older women. , 2012, , .		0
132	Frequency of Deletions of EPCAM (TACSTD1) in MSH2-Associated Lynch Syndrome Cases. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 93-99.	2.9	80
133	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , 2011, 29, 1132-1144.	18.1	456
134	Alcohol Intake and Colorectal Cancer Risk by Molecularly Defined Subtypes in a Prospective Study of Older Women. <i>Cancer Prevention Research</i> , 2011, 4, 2035-2043.	1.1	18
135	Repeated assessment by high-throughput assay demonstrates that sperm DNA methylation levels are highly reproducible. <i>Fertility and Sterility</i> , 2011, 96, 1325-1330.	1.2	6
136	Epigenetic Subgroups of Esophageal and Gastric Adenocarcinoma with Differential GATA5 DNA Methylation Associated with Clinical and Lifestyle Factors. <i>PLoS ONE</i> , 2011, 6, e25985.	2.5	10
137	Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. <i>PLoS ONE</i> , 2011, 6, e28141.	2.5	50
138	Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011, 12, .	3.3	2
139	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. <i>Cancer Prevention Research</i> , 2011, 4, 530-543.	1.1	40
140	Reduction of pancreatic acinar cell tumor multiplicity in Dnmt1 hypomorphic mice. <i>Carcinogenesis</i> , 2011, 32, 829-835.	2.9	18
141	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , 2011, 44, 40-46.	16.3	522
142	Abstract 1620: Effects of $\beta$ -glutamyl hydrolase and folylpolyglutamyl synthase modulation on gene-specific promoter CpG island methylation. , 2011, , .		0
143	Abstract SY15-01: Modeling the initiation of Ewing sarcoma in human neural crest stem cells. , 2011, , .		0
144	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	33.4	1,978

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145	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1848-1855.	3.3	145
146	Principles and challenges of genome-wide DNA methylation analysis. <i>Nature Reviews Genetics</i> , 2010, 11, 191-203.	19.1	1,257
147	DNA Methylation Profiles of Ovarian Epithelial Carcinoma Tumors and Cell Lines. <i>PLoS ONE</i> , 2010, 5, e9359.	2.5	69
148	DNA Methylation as a Biomarker for Cardiovascular Disease Risk. <i>PLoS ONE</i> , 2010, 5, e9692.	2.5	279
149	Epigenomics-Based Diagnostics. <i>Clinical Chemistry</i> , 2010, 56, 1216-1219.	1.1	6
150	Cigarette Smoking and Colorectal Cancer Risk by Molecularly Defined Subtypes. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1012-1022.	5.1	252
151	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.	0.6	148
152	Epigenetic Analysis of KSHV Latent and Lytic Genomes. <i>PLoS Pathogens</i> , 2010, 6, e1001013.	4.5	205
153	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010, 31, 1060-1067.	2.9	25
154	146 Diabetes Mellitus (DM) and Colorectal Cancer (CRC) Risk by Molecularly-Defined Subtypes in a Prospective Study of Older Women. <i>Gastroenterology</i> , 2010, 138, S-28.	1.0	0
155	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. <i>Neoplasia</i> , 2010, 12, 579-IN18.	7.2	41
156	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.	4.6	703
157	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.	2.5	36
158	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.	0.9	55
159	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.	3.1	215
160	Institutional Profile: The USC Epigenome Center. <i>Epigenomics</i> , 2009, 1, 29-31.	2.3	9
161	DNA Methylation in Colorectal Cancer: Multiple Facets of Tumorigenesis. , 2009, , 73-95.		0
162	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.	4.5	69

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163	Locking in on the human methylome. <i>Nature Biotechnology</i> , 2009, 27, 341-342.	18.1	19
164	MethylLight. <i>Methods in Molecular Biology</i> , 2009, , 325-337.	0.0	95
165	S1950 Folate Intake and Colorectal Cancer Risks By CIMP and BRAF-Mutation Status Among Older Women. <i>Gastroenterology</i> , 2009, 136, A-299-A-300.	1.0	0
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