

# Peter W Laird

## List of Publications by Year in descending order

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241  
papers

94,391  
citations

1099

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1799

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251  
all docs

251  
docs citations

251  
times ranked

91356  
citing authors

#	ARTICLE	IF	CITATIONS
1	How epigenomics broke the mold: an interview with Peter WÃ Laird. Epigenomics, 2022, 14, 303-308.	2.1	2
2	DNA methylation dynamics and dysregulation delineated by high-throughput profiling in the mouse. Cell Genomics, 2022, 2, 100144.	6.5	37
3	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. Journal of the National Cancer Institute, 2021, 113, 27-37.	6.3	17
4	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. Cancer Cell, 2021, 39, 38-53.e7.	16.8	65
5	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
6	Analytical protocol to identify local ancestry-associated molecular features in cancer. STAR Protocols, 2021, 2, 100766.	1.2	2
7	Systematic Assessment of Tumor Purity and Its Clinical Implications. JCO Precision Oncology, 2020, 4, 995-1005.	3.0	23
8	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. Cancer Cell, 2020, 37, 639-654.e6.	16.8	151
9	Abstract GS3-08: Multiplatform analysis of matched primary and metastatic breast tumors from the AURORA US Network. , 2020, , .		1
10	Phase I trial of TRC102 (methoxyamine HCl) in combination with temozolomide in patients with relapsed solid tumors and lymphomas. Oncotarget, 2020, 11, 3959-3971.	1.8	8
11	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commonsâ€™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
12	In vivo Application of the REMOTE-control System for the Manipulation of Endogenous Gene Expression. Journal of Visualized Experiments, 2019, , .	0.3	2
13	Non-invasive diagnosis of early-stage lung cancer using high-throughput targeted DNA methylation sequencing of circulating tumor DNA (ctDNA). Theranostics, 2019, 9, 2056-2070.	10.0	147
14	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. Cancer Prevention Research, 2019, 12, 781-790.	1.5	5
15	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
16	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
17	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
18	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	28.9	228

#	ARTICLE	IF	CITATIONS
19	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
20	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	28.9	1,417
21	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	28.9	2,111
22	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	333
23	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
24	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018, 23, 194-212.e6.	6.4	245
25	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	205
26	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	6.4	523
27	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	683
28	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	14.3	3,706
29	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 172-180.e3.	6.4	119
30	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	6.4	83
31	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	6.4	801
32	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	6.4	204
33	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
34	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.	6.4	137
35	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	16.8	270
36	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	6.2	605

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37	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.	6.2	284
38	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.	16.8	400
39	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	16.8	750
40	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	16.8	396
41	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	16.8	478
42	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018, 50, 591-602.	21.4	258
43	MethylLight and Digital MethyLight. <i>Methods in Molecular Biology</i> , 2018, 1708, 497-513.	0.9	11
44	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	6.2	134
45	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
46	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	6.4	329
47	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018, 34, 211-224.e6.	16.8	623
48	SeSAME: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , 2018, 46, e123.	14.5	213
49	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	6.4	324
50	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas. , 2018, , .		9
51	Abstract LB-373: Comprehensive analysis of cancer stemness. , 2018, , .		1
52	Abstract 5312: The effect of Dnmt1 overexpression on intestinal tumorigenesis. , 2018, , .		0
53	Abstract 5327: DNA methylation loss in late-replicating domains is linked to mitotic cell division. , 2018, , .		1
54	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017, 45, gkw967.	14.5	466

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55	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.	7.1	208
56	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	28.9	1,794
57	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	16.8	309
58	Transcriptional heterogeneity in the lactase gene within cell-type is linked to the epigenome. <i>Scientific Reports</i> , 2017, 7, 41843.	3.3	9
59	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	6.4	416
60	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.	7.0	106
61	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	28.9	1,742
62	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.	14.5	10
63	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.	21.4	427
64	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	16.8	1,428
65	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	28.9	738
66	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.	1.8	24
67	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.	1.8	66
68	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas. <i>Journal of Clinical Oncology</i> , 2017, 35, 4500-4500.	1.6	4
69	Abstract 5381: A highly sensitive method for noninvasive cancer profiling through targeted methylation sequencing of circulating cell-free DNA. , 2017, , .		0
70	Abstract LB-004: Molecular hallmarks of cancer: Stemness. , 2017, , .		0
71	All Things in Moderation: Prevention of Intestinal Adenomas by DNA Hypomethylation. <i>Cancer Prevention Research</i> , 2016, 9, 509-511.	1.5	0
72	DNA defects, epigenetics, and gene expression in cancer-adjacent breast: a study from The Cancer Genome Atlas. <i>Npj Breast Cancer</i> , 2016, 2, 16007.	5.2	33

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73	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.	3.9	53
74	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	17.5	270
75	Effects of folylpolyglutamate 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.	4.2	7
76	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016, 164, 550-563.	28.9	1,695
77	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.	3.4	22
78	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	27.0	1,040
79	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.	2.5	21
80	Comprehensive characterization of 412 muscle invasive urothelial carcinomas: Final analysis of The Cancer Genome Atlas (TCGA) project.. <i>Journal of Clinical Oncology</i> , 2016, 34, 405-405.	1.6	1
81	Abstract 128: Comprehensive molecular characterization of 412 muscle-invasive urothelial bladder carcinomas: final analysis of The Cancer Genome Atlas (TCGA) project. , 2016, , .		0
82	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015, 16, 105.	9.6	178
83	Tumor Budding in Colorectal Carcinoma. <i>American Journal of Surgical Pathology</i> , 2015, 39, 1340-1346.	3.7	95
84	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.	5.5	343
85	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.	2.5	71
86	$\beta$ -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, 444.	2.5	10
87	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	27.0	2,582
88	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015, 163, 506-519.	28.9	1,485
89	Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. <i>Gastroenterology</i> , 2015, 148, 77-87.e2.	1.3	342
90	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors. , 2015, , .		10

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91	Abstract 3288: The KCNA5 promoter is hypermethylated in Ewing sarcoma and silencing contributes to cell proliferation. , 2015, , .		0
92	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project. , 2015, , .		2
93	Non-specific filtering of beta-distributed data. BMC Bioinformatics, 2014, 15, 199.	2.6	15
94	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
95	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
96	Multiscale representation of genomic signals. Nature Methods, 2014, 11, 689-694.	19.0	31
97	Comprehensive molecular profiling of urothelial bladder cancer at the DNA, RNA, and protein levels: A TCGA project.. Journal of Clinical Oncology, 2014, 32, 4509-4509.	1.6	1
98	Molecular subtypes of colorectal cancer in relation to disease survival.. Journal of Clinical Oncology, 2014, 32, 451-451.	1.6	0
99	Abstract 984: Alteration of the p53 pathway is associated with subclonal tumor progression in glioblastoma. , 2014, , .		0
100	Abstract 987: Comprehensive characterization of urothelial bladder cancer: a TCGA Project update. , 2014, , .		0
101	Inferring tumour purity and stromal and immune cell admixture from expression data. Nature Communications, 2013, 4, 2612.	12.8	5,788
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. Urology, 2013, 82, 253.e9-253.e15.	1.0	4
103	The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477.	28.9	3,979
104	The Landscape of Microsatellite Instability in Colorectal and Endometrial Cancer Genomes. Cell, 2013, 155, 858-868.	28.9	311
105	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	21.4	1,616
106	Associations Between Colorectal Cancer Molecular Markers and Pathways With Clinicopathologic Features in Older Women. Gastroenterology, 2013, 145, 348-356.e2.	1.3	49
107	Interplay between the Cancer Genome and Epigenome. Cell, 2013, 153, 38-55.	28.9	733
108	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075

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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.	27.0	4,139
110	Clinical applications of DNA methylation biomarkers in colorectal cancer. <i>Epigenomics</i> , 2013, 5, 105-108.	2.1	28
111	Gene dysregulation by histone variant H2A.Z in bladder cancer. <i>Epigenetics and Chromatin</i> , 2013, 6, 34.	3.9	74
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.	6.3	231
113	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.	14.5	647
114	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013, 4, 1628.	12.8	144
115	Alterations of immune response of non-small cell lung cancer with Azacytidine. <i>Oncotarget</i> , 2013, 4, 2067-2079.	1.8	336
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.	2.0	33
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.	0.9	22
120	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	5.5	527
121	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012, 40, 9379-9391.	14.5	305
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.	1.5	12
123	Bis-SNP: Combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , 2012, 13, R61.	9.6	230
124	In Epigenetic Therapy, Less Is More. <i>Cell Stem Cell</i> , 2012, 10, 353-354.	11.1	29
125	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012, 61, 1299-1305.	12.1	36
126	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012, 131, 1565-1589.	3.8	294



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127	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012, 30, 413-421.	17.5	1,710
128	Exploring the cancer methylome. <i>BMC Proceedings</i> , 2012, 6, .	1.6	0
129	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.	21.4	588
130	Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. <i>PLoS ONE</i> , 2012, 7, e50266.	2.5	103
131	Abstract 5518: Clinicopathologic associations with colorectal cancer molecular pathways in a cohort study of older women. , 2012, , .		0
132	Abstract 4492: Colorectal cancer survival by molecular subtypes in a population-based cohort of older women. , 2012, , .		0
133	Frequency of Deletions of EPCAM (TACSTD1) in MSH2-Associated Lynch Syndrome Cases. <i>Journal of Molecular Diagnostics</i> , 2011, 13, 93-99.	2.8	79
134	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , 2011, 29, 1132-1144.	17.5	509
135	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.	1.5	17
136	Repeated assessment by high-throughput assay demonstrates that sperm DNA methylation levels are highly reproducible. <i>Fertility and Sterility</i> , 2011, 96, 1325-1330.	1.0	7
137	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
138	Genome-Scale Screen for DNA Methylation-Based Detection Markers for Ovarian Cancer. <i>PLoS ONE</i> , 2011, 6, e28141.	2.5	65
139	Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011, 12, 284.	2.6	3
140	Altered Folate Availability Modifies the Molecular Environment of the Human Colorectum: Implications for Colorectal Carcinogenesis. <i>Cancer Prevention Research</i> , 2011, 4, 530-543.	1.5	41
141	Reduction of pancreatic acinar cell tumor multiplicity in Dnmt1 hypomorphic mice. <i>Carcinogenesis</i> , 2011, 32, 829-835.	2.8	19
142	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer. , 2011, , .		5
143	Abstract 1620: Effects of $\text{I}^3$ -glutamyl hydrolase and folylpolyglutamyl synthase modulation on gene-specific promoter CpG island methylation. , 2011, , .		0
144	Abstract SY15-01: Modeling the initiation of Ewing sarcoma in human neural crest stem cells. , 2011, , .		0

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145	Abstract LB-233: Modeling Ewing sarcoma initiation in human neural crest stem cells. , 2011, , .		0
146	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	16.8	2,078
147	Vitamin C Promotes Widespread Yet Specific DNA Demethylation of the Epigenome in Human Embryonic Stem Cells. <i>Stem Cells</i> , 2010, 28, 1848-1855.	3.2	156
148	Principles and challenges of genome-wide DNA methylation analysis. <i>Nature Reviews Genetics</i> , 2010, 11, 191-203.	16.3	1,432
149	DNA Methylation Profiles of Ovarian Epithelial Carcinoma Tumors and Cell Lines. <i>PLoS ONE</i> , 2010, 5, e9359.	2.5	80
150	DNA Methylation as a Biomarker for Cardiovascular Disease Risk. <i>PLoS ONE</i> , 2010, 5, e9692.	2.5	289
151	Epigenomics-Based Diagnostics. <i>Clinical Chemistry</i> , 2010, 56, 1216-1219.	3.2	8
152	Cigarette Smoking and Colorectal Cancer Risk by Molecularly Defined Subtypes. <i>Journal of the National Cancer Institute</i> , 2010, 102, 1012-1022.	6.3	261
153	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.	0.9	148
154	Epigenetic Analysis of KSHV Latent and Lytic Genomes. <i>PLoS Pathogens</i> , 2010, 6, e1001013.	4.7	229
155	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010, 31, 1060-1067.	2.8	30
156	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.	1.3	0
157	Microcell-Mediated Chromosome Transfer Identifies EPB41L3 as a Functional Suppressor of Epithelial Ovarian Cancers. <i>Neoplasia</i> , 2010, 12, 579-IN18.	5.3	38
158	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.	5.5	740
159	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	35
160	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.	2.5	60
161	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.	2.9	230
162	Institutional Profile: The USC Epigenome Center. <i>Epigenomics</i> , 2009, 1, 29-31.	2.1	7

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163	DNA Methylation in Colorectal Cancer: Multiple Facets of Tumorigenesis. , 2009, , 73-95.		0
164	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. International Journal of Cancer, 2009, 124, 1999-2005.	5.1	80
165	Locking in on the human methylome. Nature Biotechnology, 2009, 27, 341-342.	17.5	19
166	MethylLight. Methods in Molecular Biology, 2009, 507, 325-337.	0.9	106
167	S1950 Folate Intake and Colorectal Cancer Risks By CIMP and BRAF-Mutation Status Among Older Women. Gastroenterology, 2009, 136, A-299-A-300.	1.3	0
168	Analysis of the Association between CIMP and BRAFV600E in Colorectal Cancer by DNA Methylation Profiling. PLoS ONE, 2009, 4, e8357.	2.5	133
169	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. Laboratory Investigation, 2008, 88, 161-170.	3.7	156
170	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. Molecular Cancer, 2008, 7, 62.	19.2	114
171	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethylLight. Nucleic Acids Research, 2008, 36, 4689-4698.	14.5	133
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