

Peter W Laird

List of Publications by Year in Descending Order

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Version: 2024-04-26

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	How epigenomics broke the mold: an interview with Peter W Laird.. <i>Epigenomics</i> , 2022 , 14, 303-308	4.4	
219	The Exceptional Responders Initiative: Feasibility of a National Cancer Institute Pilot Study. <i>Journal of the National Cancer Institute</i> , 2021 , 113, 27-37	9.7	9
218	Molecular Features of Cancers Exhibiting Exceptional Responses to Treatment. <i>Cancer Cell</i> , 2021 , 39, 38-53.e7	24.3	18
217	Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707	10.6	7
216	Analytical protocol to identify local ancestry-associated molecular features in cancer. <i>STAR Protocols</i> , 2021 , 2, 100766	1.4	0
215	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	3.3	4
214	Comprehensive Analysis of Genetic Ancestry and Its Molecular Correlates in Cancer. <i>Cancer Cell</i> , 2020 , 37, 639-654.e6	24.3	56
213	Systematic Assessment of Tumor Purity and Its Clinical Implications. <i>JCO Precision Oncology</i> , 2020 , 4,	3.6	7
212	In vivo Application of the REMOTE-control System for the Manipulation of Endogenous Gene Expression. <i>Journal of Visualized Experiments</i> , 2019 ,	1.6	1
211	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	12.1	68
210	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsRData. <i>Cell Systems</i> , 2019 , 9, 24-34.e10	10.6	64
209	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. <i>Cancer Prevention Research</i> , 2019 , 12, 781-790	3.2	3
208	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11	56.2	1072
207	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
206	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	56.2	888
205	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018 , 173, 386-399.e12	56.2	133
204	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166

203	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15	56.2	560
202	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10	56.2	1124
201	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4	10.6	188
200	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3	10.6	235
199	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6	10.6	146
198	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	10.6	147
197	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5	10.6	295
196	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7	10.6	366
195	The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14	32.3	1754
194	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 172-180.e3	10.6	66
193	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3	26.6	56
192	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6	10.6	405
191	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018 , 23, 255-269.e4	10.6	112
190	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018 , 23, 270-281.e3	10.6	121
189	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	10.6	90
188	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
187	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7	10.6	320
186	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	10.6	159

185	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	24.3	275
184	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3	24.3	377
183	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
182	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
181	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018 , 50, 591-602	36.3	133
180	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6	24.3	327
179	SeSAME: reducing artifactual detection of DNA methylation by Infinium BeadChips in genomic deletions. <i>Nucleic Acids Research</i> , 2018 , 46, e123	20.1	94
178	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10	10.6	200
177	Abstract 3302: The molecular landscape of oncogenic signaling pathways in The Cancer Genome Atlas 2018 ,		5
176	MethyLight and Digital MethyLight. <i>Methods in Molecular Biology</i> , 2018 , 1708, 497-513	1.4	7
175	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
174	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018 , 362,	33.3	392
173	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018 , 25, 1304-1317.e5	10.6	152
172	Comparison of Breast Cancer Molecular Features and Survival by African and European Ancestry in The Cancer Genome Atlas. <i>JAMA Oncology</i> , 2017 , 3, 1654-1662	13.4	146
171	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
170	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
169	Transcriptional heterogeneity in the lactase gene within cell-type is linked to the epigenome. <i>Scientific Reports</i> , 2017 , 7, 41843	4.9	6
168	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794	10.6	247

167	Combination Epigenetic Therapy in Advanced Breast Cancer with 5-Azacididine and Entinostat: A Phase II National Cancer Institute/Stand Up to Cancer Study. <i>Clinical Cancer Research</i> , 2017 , 23, 2691-2701	12.9	84
166	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25	25.2	961
165	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	20.1	5
164	Combination epigenetic therapy in metastatic colorectal cancer (mCRC) with subcutaneous 5-azacididine and entinostat: a phase 2 consortium/stand up 2 cancer study. <i>Oncotarget</i> , 2017 , 8, 35326-35338	3.3	52
163	Comprehensive characterization, annotation and innovative use of Infinium DNA methylation BeadChip probes. <i>Nucleic Acids Research</i> , 2017 , 45, e22	20.1	254
162	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017 , 49, 1476-1486	36.3	255
161	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-201.e13	13.9	96
160	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
159	Association of high microvessel lumen 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	3.3	18
158	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas. <i>Journal of Clinical Oncology</i> , 2017 , 35, 4500-4500	2.2	4
157	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016 , 34, 726-37	44.5	204
156	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	6.3	6
155	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63	56.2	1140
154	Promoter Methylation Analysis Reveals That KCNA5 Ion Channel Silencing Supports Ewing Sarcoma Cell Proliferation. <i>Molecular Cancer Research</i> , 2016 , 14, 26-34	6.6	20
153	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45	59.2	753
152	Clinicopathologic Risk Factor Distributions for MLH1 Promoter Region Methylation in CIMP-Positive Tumors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016 , 25, 68-75	4	16
151	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	2.2	1
150	All Things in Moderation: Prevention of Intestinal Adenomas by DNA Hypomethylation. <i>Cancer Prevention Research</i> , 2016 , 9, 509-11	3.2	

149	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	7.8	25
148	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	5.8	40
147	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	4.3	9
146	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98	59.2	1828
145	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19	56.2	1055
144	Association between molecular subtypes of colorectal cancer and patient survival. <i>Gastroenterology</i> , 2015 , 148, 77-87.e2	13.3	273
143	Inferring regulatory element landscapes and transcription factor networks from cancer methylomes. <i>Genome Biology</i> , 2015 , 16, 105	18.3	123
142	Tumor Budding in Colorectal Carcinoma: Confirmation of Prognostic Significance and Histologic Cutoff in a Population-based Cohort. <i>American Journal of Surgical Pathology</i> , 2015 , 39, 1340-6	6.7	72
141	Whole-genome and multisector exome sequencing of primary and post-treatment glioblastoma reveals patterns of tumor evolution. <i>Genome Research</i> , 2015 , 25, 316-27	9.7	240
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	4	59
139	Abstract S2-04: Comprehensive molecular characterization of invasive lobular breast tumors 2015 ,		7
138	Abstract 2969: Progress in The Cancer Genome Atlas bladder cancer project 2015 ,		2
137	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
136	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
135	Multiscale representation of genomic signals. <i>Nature Methods</i> , 2014 , 11, 689-94	21.6	21
134	Non-specific filtering of beta-distributed data. <i>BMC Bioinformatics</i> , 2014 , 15, 199	3.6	11
133	Comprehensive molecular profiling of urothelial bladder cancer at the DNA, RNA, and protein levels: A TCGA project.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 4509-4509	2.2	1
132	Molecular subtypes of colorectal cancer in relation to disease survival.. <i>Journal of Clinical Oncology</i> , 2014 , 32, 451-451	2.2	

131	Inferring tumour purity and stromal and immune cell admixture from expression data. <i>Nature Communications</i> , 2013 , 4, 2612	17.4	2572
130	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.e9-15 ⁴	16	4
129	The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77	56.2	2900
128	The landscape of microsatellite instability in colorectal and endometrial cancer genomes. <i>Cell</i> , 2013 , 155, 858-68	56.2	247
127	Pan-cancer patterns of somatic copy number alteration. <i>Nature Genetics</i> , 2013 , 45, 1134-40	36.3	1198
126	Associations between colorectal cancer molecular markers and pathways with clinicopathologic features in older women. <i>Gastroenterology</i> , 2013 , 145, 348-56.e1-2	13.3	45
125	Interplay between the cancer genome and epigenome. <i>Cell</i> , 2013 , 153, 38-55	56.2	588
124	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73	50.4	2800
123	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2013 , 368, 2059-74	59.2	3137
122	Gene dysregulation by histone variant H2A.Z in bladder cancer. <i>Epigenetics and Chromatin</i> , 2013 , 6, 34	5.8	61
121	An epidemiologic and genomic investigation into the obesity paradox in renal cell carcinoma. <i>Journal of the National Cancer Institute</i> , 2013 , 105, 1862-70	9.7	161
120	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013 , 41, e90	20.1	393
119	Epigenetic analysis leads to identification of HNF1B as a subtype-specific susceptibility gene for ovarian cancer. <i>Nature Communications</i> , 2013 , 4, 1628	17.4	124
118	Alterations of immune response of Non-Small Cell Lung Cancer with Azacytidine. <i>Oncotarget</i> , 2013 , 4, 2067-79	3.3	285
117	Bis-SNP: combined DNA methylation and SNP calling for Bisulfite-seq data. <i>Genome Biology</i> , 2012 , 13, R61	18.3	179
116	In epigenetic therapy, less is more. <i>Cell Stem Cell</i> , 2012 , 10, 353-4	18	23
115	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012 , 61, 1299-305	19.2	34
114	Environmental epigenetics: prospects for studying epigenetic mediation of exposure-response relationships. <i>Human Genetics</i> , 2012 , 131, 1565-89	6.3	258

113	Absolute quantification of somatic DNA alterations in human cancer. <i>Nature Biotechnology</i> , 2012 , 30, 413-21	44.5	1229
112	Exploring the cancer methylome. <i>BMC Proceedings</i> , 2012 , 6,	2.3	78
111	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	2.8	27
110	A blueprint for an international cancer epigenome consortium. A report from the AACR Cancer Epigenome Task Force. <i>Cancer Research</i> , 2012 , 72, 6319-24	10.1	21
109	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012 , 22, 271-82	9.7	466
108	Discovery of multi-dimensional modules by integrative analysis of cancer genomic data. <i>Nucleic Acids Research</i> , 2012 , 40, 9379-91	20.1	225
107	Cancer risks for the relatives of colorectal cancer cases with a methylated MLH1 promoter region: data from the Colorectal Cancer Family Registry. <i>Cancer Prevention Research</i> , 2012 , 5, 328-35	3.2	9
106	Genome-scale discovery of DNA-methylation biomarkers for blood-based detection of colorectal cancer. <i>PLoS ONE</i> , 2012 , 7, e50266	3.7	88
105	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. <i>Nature Genetics</i> , 2011 , 44, 40-6	36.3	474
104	Alcohol intake and colorectal cancer risk by molecularly defined subtypes in a prospective study of older women. <i>Cancer Prevention Research</i> , 2011 , 4, 2035-43	3.2	16
103	Repeated assessment by high-throughput assay demonstrates that sperm DNA methylation levels are highly reproducible. <i>Fertility and Sterility</i> , 2011 , 96, 1325-30	4.8	6
102	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	3.7	10
101	Genome-scale screen for DNA methylation-based detection markers for ovarian cancer. <i>PLoS ONE</i> , 2011 , 6, e28141	3.7	45
100	Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011 , 12, 284	3.6	2
99	Frequency of deletions of EPCAM (TACSTD1) in MSH2-associated Lynch syndrome cases. <i>Journal of Molecular Diagnostics</i> , 2011 , 13, 93-9	5.1	71
98	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. <i>Nature Biotechnology</i> , 2011 , 29, 1132-44	44.5	406
97	Altered folate availability modifies the molecular environment of the human colorectum: implications for colorectal carcinogenesis. <i>Cancer Prevention Research</i> , 2011 , 4, 530-43	3.2	35
96	Reduction of pancreatic acinar cell tumor multiplicity in Dnmt1 hypomorphic mice. <i>Carcinogenesis</i> , 2011 , 32, 829-35	4.6	16

95	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer 2011 ,		4
94	Principles and challenges of genomewide DNA methylation analysis. <i>Nature Reviews Genetics</i> , 2010 , 11, 191-203	30.1	1226
93	DNA methylation profiles of ovarian epithelial carcinoma tumors and cell lines. <i>PLoS ONE</i> , 2010 , 5, e9359.	3.7	68
92	DNA methylation as a biomarker for cardiovascular disease risk. <i>PLoS ONE</i> , 2010 , 5, e9692	3.7	247
91	Epigenomics-based diagnostics. <i>Clinical Chemistry</i> , 2010 , 56, 1216-9	5.5	7
90	Cigarette smoking and colorectal cancer risk by molecularly defined subtypes. <i>Journal of the National Cancer Institute</i> , 2010 , 102, 1012-22	9.7	224
89	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, 8169-78	10.1	133
88	Epigenetic analysis of KSHV latent and lytic genomes. <i>PLoS Pathogens</i> , 2010 , 6, e1001013	7.6	175
87	Hormone therapy, DNA methylation and colon cancer. <i>Carcinogenesis</i> , 2010 , 31, 1060-7	4.6	28
86	Microcell-mediated chromosome transfer identifies EPB41L3 as a functional suppressor of epithelial ovarian cancers. <i>Neoplasia</i> , 2010 , 12, 579-89	6.4	32
85	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. <i>Genome Research</i> , 2010 , 20, 440-6	9.7	638
84	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. <i>Cancer Cell</i> , 2010 , 17, 510-22	24.3	1754
83	Vitamin C promotes widespread yet specific DNA demethylation of the epigenome in human embryonic stem cells. <i>Stem Cells</i> , 2010 , 28, 1848-55	5.8	131
82	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	3.7	32
81	DNA hypermethylation of ESR1 and PGR in breast cancer: pathologic and epidemiologic associations. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 3036-43	4	56
80	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. <i>Human Molecular Genetics</i> , 2009 , 18, 4808-17	5.6	206
79	The USC Epigenome Center. <i>Epigenomics</i> , 2009 , 1, 29-31	4.4	6
78	DNA Methylation in Colorectal Cancer: Multiple Facets of Tumorigenesis 2009 , 73-95		

77	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	7.5	73
76	Locking in on the human methylome. <i>Nature Biotechnology</i> , 2009 , 27, 341-2	44.5	18
75	MethylLight. <i>Methods in Molecular Biology</i> , 2009 , 507, 325-37	1.4	94
74	Analysis of the association between CIMP and BRAF in colorectal cancer by DNA methylation profiling. <i>PLoS ONE</i> , 2009 , 4, e8357	3.7	116
73	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. <i>Laboratory Investigation</i> , 2008 , 88, 161-70	5.9	139
72	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. <i>Molecular Cancer</i> , 2008 , 7, 62	42.1	91
71	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethylLight. <i>Nucleic Acids Research</i> , 2008 , 36, 4689-98	20.1	118
70	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> , 2008 , 266, 238-48	8.9	41
69	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> , 2008 , 17, 3208-15	4	171
68	Long-term epigenetic therapy with oral zebularine has minimal side effects and prevents intestinal tumors in mice. <i>Cancer Prevention Research</i> , 2008 , 1, 233-40	3.2	76
67	Ovarian cancer early detection claims are biased. <i>Clinical Cancer Research</i> , 2008 , 14, 7574; author reply 7577-9	12.9	30
66	Kaiso contributes to DNA methylation-dependent silencing of tumor suppressor genes in colon cancer cell lines. <i>Cancer Research</i> , 2008 , 68, 7258-63	10.1	83
65	DNA methylation profile of 28 potential marker loci in malignant mesothelioma. <i>Lung Cancer</i> , 2007 , 58, 220-30	5.9	59
64	Identification of a panel of sensitive and specific DNA methylation markers for lung adenocarcinoma. <i>Molecular Cancer</i> , 2007 , 6, 70	42.1	85
63	Role of methionine adenosyltransferase 2A and S-adenosylmethionine in mitogen-induced growth of human colon cancer cells. <i>Gastroenterology</i> , 2007 , 133, 207-18	13.3	72
62	The role of DNA methylation in the development and progression of lung adenocarcinoma. <i>Disease Markers</i> , 2007 , 23, 5-30	3.2	70
61	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, 2701-8	4.1	32
60	Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , 2007 , 39, 157-8	36.3	909

59	Promoter hypermethylation of tumor suppressor genes in urine from patients with cervical neoplasia. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2007 , 16, 1178-84	4	38
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	3.7	330
57	Widespread epigenetic abnormalities suggest a broad DNA methylation erasure defect in abnormal human sperm. <i>PLoS ONE</i> , 2007 , 2, e1289	3.7	215
56	Cluster analysis for DNA methylation profiles having a detection threshold. <i>BMC Bioinformatics</i> , 2006 , 7, 361	3.6	7
55	Modeling exposures for DNA methylation profiles. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2006 , 15, 567-72	4	5
54	Smad3 deficiency promotes tumorigenesis in the distal colon of ApcMin/+ mice. <i>Cancer Research</i> , 2006 , 66, 8430-8	10.1	78
53	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, 209-17	5.1	336
52	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	10.1	153
51	Rapid and quantitative method of allele-specific DNA methylation analysis. <i>BioTechniques</i> , 2006 , 41, 734-25	4.5	39
50	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, 1175-83	6.7	77
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