

Daniel J Weisenberger

List of Publications by Year in descending order

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147
papers

105,388
citations

7251

80
h-index

14012

133
g-index

151
all docs

151
docs citations

151
times ranked

112574
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
2	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
3	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008, 455, 1061-1068.	13.7	6,879
4	Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011, 474, 609-615.	13.7	6,541
5	Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014, 513, 202-209.	13.7	5,055
6	Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014, 511, 543-550.	13.7	4,572
7	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	13.9	4,139
8	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
9	The Somatic Genomic Landscape of Glioblastoma. <i>Cell</i> , 2013, 155, 462-477.	13.5	3,979
10	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	2,839
11	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015, 372, 2481-2498.	13.9	2,582
12	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	13.5	2,562
13	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
14	The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015, 163, 1011-1025.	13.5	2,435
15	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. <i>Cell</i> , 2014, 159, 676-690.	13.5	2,318
16	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
17	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
18	Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. <i>Cancer Cell</i> , 2010, 17, 510-522.	7.7	2,078

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19	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
20	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
21	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.	13.5	1,718
22	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. <i>Nature Genetics</i> , 2006, 38, 787-793.	9.4	1,715
23	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
24	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15.	13.5	1,417
25	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145.	13.9	1,040
26	Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , 2007, 39, 157-158.	9.4	1,023
27	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
28	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
29	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
30	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
31	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
32	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
33	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90.	6.5	647
34	Analysis of repetitive element DNA methylation by MethyLight. <i>Nucleic Acids Research</i> , 2005, 33, 6823-6836.	6.5	636
35	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
36	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282.	2.4	527

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37	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018, 23, 313-326.e5.	2.9	523
38	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
39	Distinct localization of histone H3 acetylation and H3-K4 methylation to the transcription start sites in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7357-7362.	3.3	435
40	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017, 18, 2780-2794.	2.9	416
41	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
42	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
43	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
44	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
45	Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. <i>Gastroenterology</i> , 2015, 148, 77-87.e2.	0.6	342
46	Alterations of immune response of non-small cell lung cancer with Azacytidine. <i>Oncotarget</i> , 2013, 4, 2067-2079.	0.8	336
47	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
48	Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018, 23, 3392-3406.	2.9	324
49	The Relationship of DNA Methylation with Age, Gender and Genotype in Twins and Healthy Controls. <i>PLoS ONE</i> , 2009, 4, e6767.	1.1	311
50	Histone H3-lysine 9 methylation is associated with aberrant gene silencing in cancer cells and is rapidly reversed by 5-aza-2'-deoxycytidine. <i>Cancer Research</i> , 2002, 62, 6456-61.	0.4	310
51	CpG island methylator phenotype (CIMP) of colorectal cancer is best characterised by quantitative DNA methylation analysis and prospective cohort studies. <i>Gut</i> , 2006, 55, 1000-1006.	6.1	308
52	Preferential response of cancer cells to zebularine. <i>Cancer Cell</i> , 2004, 6, 151-158.	7.7	282
53	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
54	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737.	9.4	270

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55	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
56	DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018, 50, 591-602.	9.4	258
57	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
58	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
59	Continuous Zebularine Treatment Effectively Sustains Demethylation in Human Bladder Cancer Cells. <i>Molecular and Cellular Biology</i> , 2004, 24, 1270-1278.	1.1	205
60	Detection of Methylated Apoptosis-Associated Genes in Urine Sediments of Bladder Cancer Patients. <i>Clinical Cancer Research</i> , 2004, 10, 7457-7465.	3.2	202
61	Footprinting of mammalian promoters: use of a CpG DNA methyltransferase revealing nucleosome positions at a single molecule level. <i>Nucleic Acids Research</i> , 2005, 33, e176-e176.	6.5	185
62	Characterizing DNA methylation alterations from The Cancer Genome Atlas. <i>Journal of Clinical Investigation</i> , 2014, 124, 17-23.	3.9	162
63	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. <i>Laboratory Investigation</i> , 2008, 88, 161-170.	1.7	156
64	The genomic landscape of tuberous sclerosis complex. <i>Nature Communications</i> , 2017, 8, 15816.	5.8	154
65	Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. <i>Molecular Cancer Research</i> , 2004, 2, 62-72.	1.5	151
66	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
67	The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. <i>Genes</i> , 2019, 10, 172.	1.0	134
68	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. <i>Nucleic Acids Research</i> , 2008, 36, 4689-4698.	6.5	133
69	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
70	Quantitative analysis of associations between DNA hypermethylation, hypomethylation, and DNMT RNA levels in ovarian tumors. <i>Oncogene</i> , 2006, 25, 2636-2645.	2.6	129
71	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
72	Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. <i>European Journal of Cancer</i> , 2005, 41, 2769-2778.	1.3	109

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73	MethylLight. <i>Methods in Molecular Biology</i> , 2009, 507, 325-337.	0.4	106
74	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
75	Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. <i>PLoS ONE</i> , 2012, 7, e50266.	1.1	103
76	DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. <i>Epigenetics</i> , 2017, 12, 416-432.	1.3	98
77	Tumor Budding in Colorectal Carcinoma. <i>American Journal of Surgical Pathology</i> , 2015, 39, 1340-1346.	2.1	95
78	DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. <i>Leukemia</i> , 2008, 22, 1035-1043.	3.3	83
79	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
80	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
81	Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. <i>Molecular Cancer Research</i> , 2004, 2, 62-72.	1.5	74
82	Cell division is required for de novo methylation of CpG islands in bladder cancer cells. <i>Cancer Research</i> , 2002, 62, 2378-84.	0.4	72
83	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
84	DNA Methylation in the Malignant Transformation of Meningiomas. <i>PLoS ONE</i> , 2013, 8, e54114.	1.1	67
85	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
86	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. <i>Communications Biology</i> , 2021, 4, 769.	2.0	65
87	Cytosine Methylation in a CpG Sequence Leads to Enhanced Reactivity with Benzo[a]pyrene Diol Epoxide That Correlates with a Conformational Change. <i>Journal of Biological Chemistry</i> , 1999, 274, 23948-23955.	1.6	61
88	cis-Expression QTL Analysis of Established Colorectal Cancer Risk Variants in Colon Tumors and Adjacent Normal Tissue. <i>PLoS ONE</i> , 2012, 7, e30477.	1.1	55
89	Insights into the Pathogenesis of Anaplastic Large-Cell Lymphoma through Genome-wide DNA Methylation Profiling. <i>Cell Reports</i> , 2016, 17, 596-608.	2.9	55
90	LINE-1 methylation in plasma DNA as a biomarker of activity of DNA methylation inhibitors in patients with solid tumors. <i>Epigenetics</i> , 2009, 4, 176-184.	1.3	53

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91	Identification and characterization of alternatively spliced variants of DNA methyltransferase 3a in mammalian cells. <i>Gene</i> , 2002, 298, 91-99.	1.0	51
92	Integrated analysis of genome-wide copy number alterations and gene expression in microsatellite stable, CpG island methylator phenotype-negative colon cancer. <i>Genes Chromosomes and Cancer</i> , 2013, 52, 450-466.	1.5	51
93	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
94	Genetic and Epigenetic Alterations in Bladder Cancer. <i>International Neurourology Journal</i> , 2016, 20, S84-94.	0.5	49
95	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGI-110) in Hepatocellular Carcinoma. <i>Hepatology</i> , 2018, 68, 1412-1428.	3.6	48
96	Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3.	3.8	43
97	Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. <i>Theranostics</i> , 2018, 8, 4520-4534.	4.6	40
98	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012, 61, 1299-1305.	6.1	36
99	A Pilot Genome-Scale Profiling of DNA Methylation in Sporadic Pituitary Macroadenomas: Association with Tumor Invasion and Histopathological Subtype. <i>PLoS ONE</i> , 2014, 9, e96178.	1.1	36
100	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.	0.9	33
101	Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. <i>Neurosurgical Focus</i> , 2013, 35, E3.	1.0	28
102	Identification of DNA Methylation-independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016, 76, 1954-1964.	0.4	28
103	Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. <i>PLoS ONE</i> , 2017, 12, e0175112.	1.1	26
104	Immunogenic cell death pathway polymorphisms for predicting oxaliplatin efficacy in metastatic colorectal cancer. , 2020, 8, e001714.		23
105	Cell death and survival pathways in Alzheimer's disease: an integrative hypothesis testing approach utilizing -omic data sets. <i>Neurobiology of Aging</i> , 2020, 95, 15-25.	1.5	23
106	Racial Disparities in Epigenetic Aging of the Right vs Left Colon. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1779-1782.	3.0	23
107	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.	1.5	22
108	Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues. <i>Nature Biotechnology</i> , 2022, 40, 720-730.	9.4	22

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109	3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. <i>BMC Pharmacology & Toxicology</i> , 2013, 14, 11.	1.0	21
110	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.	1.1	21
111	Locking in on the human methylome. <i>Nature Biotechnology</i> , 2009, 27, 341-342.	9.4	19
112	Gene-Specific Methylation and Subsequent Risk of Colorectal Adenomas among Participants of the Polyp Prevention Trial. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2005, 14, 1219-1223.	1.1	17
113	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.	0.7	17
114	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017, 8, 5439-5448.	0.8	17
115	Aberrant DNA methylation of miRNAs in Fuchs endothelial corneal dystrophy. <i>Scientific Reports</i> , 2019, 9, 16385.	1.6	16
116	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.	0.7	12
117	Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. <i>Genome Medicine</i> , 2021, 13, 130.	3.6	12
118	MethylLight and Digital MethylLight. <i>Methods in Molecular Biology</i> , 2018, 1708, 497-513.	0.4	11
119	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.	1.1	10
120	β -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.	1.2	10
121	Promoter methylation of ITF2, but not APC, is associated with microsatellite instability in two populations of colorectal cancer patients. <i>BMC Cancer</i> , 2016, 16, 113.	1.1	7
122	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.	1.9	7
123	Albumin levels predict prognosis in advanced renal cell carcinoma treated with tyrosine kinase inhibitors: a systematic review and meta-analysis. <i>Urologic Oncology: Seminars and Original Investigations</i> , 2022, 40, 12.e13-12.e22.	0.8	6
124	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. <i>Cancer Prevention Research</i> , 2019, 12, 781-790.	0.7	5
125	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 614927.	1.3	5
126	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer. , 2011, , .		5

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127	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.	0.5	4
128	Impact of polymorphisms within genes involved in regulating DNA methylation in patients with metastatic colorectal cancer enrolled in three independent, randomised, open-label clinical trials: a meta-analysis from TRIBE, MAVERICC and FIRE-3. <i>European Journal of Cancer</i> , 2019, 111, 138-147.	1.3	4
129	AMPK variant, a candidate of novel predictor for chemotherapy in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC and FIRE3. <i>International Journal of Cancer</i> , 2019, 145, 2082-2090.	2.3	4
130	Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011, 12, 284.	1.2	3
131	DNA Demethylating Agents. , 2004, , 151-167.		2
132	Networks and Consortia for Epigenetic Drug Discovery. , 2016, , 143-166.		1
133	Tea and Chocolate Consumption and Colorectal Cancer Risk by Molecularly Defined Subtypes in a Prospective Cohort Study of Older Women: Presidential Poster. <i>American Journal of Gastroenterology</i> , 2013, 108, S635-S636.	0.2	1
134	Abstract 5327: DNA methylation loss in late-replicating domains is linked to mitotic cell division. , 2018, , .		1
135	Genes regulated by DNA methylation are involved in distinct phenotypes during melanoma progression and are prognostic factors for patients. <i>Molecular Oncology</i> , 2022, 16, 1913-1930.	2.1	1
136	A Clinically Distinct and "Atypical"™ Subgroup of Head and Neck Cancers Positive for a CpG Island Methylator Phenotype. <i>EBioMedicine</i> , 2017, 17, 22-23.	2.7	0
137	Abstract 155: A comparison of DNA methylation in identical twins discordant for Hodgkin lymphoma. , 2010, , .		0
138	Abstract 1620: Effects of β -glutamyl hydrolase and folylpolyglutamyl synthase modulation on gene-specific promoter CpG island methylation. , 2011, , .		0
139	Abstract 5518: Clinicopathologic associations with colorectal cancer molecular pathways in a cohort study of older women. , 2012, , .		0
140	Abstract 4492: Colorectal cancer survival by molecular subtypes in a population-based cohort of older women. , 2012, , .		0
141	Molecular subtypes of colorectal cancer in relation to disease survival.. <i>Journal of Clinical Oncology</i> , 2014, 32, 451-451.	0.8	0
142	Whole-genome bisulfite sequencing of a complex karyotype AML and identification of regulatory aberrations distinct from normal karyotype AML.. <i>Journal of Clinical Oncology</i> , 2014, 32, 11075-11075.	0.8	0
143	Abstract 3288: The KCNA5 promoter is hypermethylated in Ewing sarcoma and silencing contributes to cell proliferation. , 2015, , .		0
144	Abstract 779: Integrative analysis reveals therapeutic targets to the DNA methyltransferase inhibitor SGI-110 in hepatocellular carcinoma. , 2018, , .		0

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145	Th17 cell pathway-related genetic variants in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC, and FIRE-3.. Journal of Clinical Oncology, 2019, 37, 594-594.	0.8	0
146	Genetic variants in RNA binding protein (RBP) to predict outcome in metastatic colorectal cancer (mCRC): Data from FIRE-3, TRIBE, and MAVERICC trials.. Journal of Clinical Oncology, 2019, 37, 3545-3545.	0.8	0
147	Abstract 3736: SETD2 aberrancy enhanced the synergetic anti-tumor effects of DNA hypomethylating agents and PARP inhibitors in aggressive clear cell renal cell carcinoma. Cancer Research, 2022, 82, 3736-3736.	0.4	0