Daniel J Weisenberger

List of Publications by Citations

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137	77,161	78	151
papers	citations	h-index	g-index
151	94,349	18	9.22
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
137	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
136	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, **2008**, 455, 1061-8	50.4	5669
135	Comprehensive molecular characterization of human colon and rectal cancer. *Nature*, **2012**, 487, 330-7	50.4	5640
134	Integrated genomic analyses of ovarian carcinoma. *Nature*, **2011**, 474, 609-15	50.4	5210
133	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
132	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
131	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
130	The somatic genomic landscape of glioblastoma. *Cell*, **2013**, 155, 462-77	56.2	2900
129	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
128	Comprehensive molecular characterization of clear cell renal cell carcinoma. *Nature*, **2013**, 499, 43-9	50.4	2184
127	Comprehensive molecular characterization of urothelial bladder carcinoma. *Nature*, **2014**, 507, 315-22	50.4	1963
126	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. *New England Journal of Medicine*, **2015**, 372, 2481-98	59.2	1828
125	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
124	Identification of a CpG island methylator phenotype that defines a distinct subgroup of glioma. *Cancer Cell*, **2010**, 17, 510-22	24.3	1754
123	The Molecular Taxonomy of Primary Prostate Cancer. *Cell*, **2015**, 163, 1011-25	56.2	1713
122	Integrated genomic characterization of papillary thyroid carcinoma. *Cell*, **2014**, 159, 676-90	56.2	1660
121	CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. *Nature Genetics*, **2006**, 38, 787-93	36.3	1514

120	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell*, **2017**, 169, 1327-1341.e23	56.2	1125
119	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
118	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
117	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. *Cell*, **2017**, 171, 540-556.e25	56.2	961
116	Epigenetic stem cell signature in cancer. *Nature Genetics*, **2007**, 39, 157-8	36.3	909
115	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, **2017**, 32, 185-203.e13	24.3	896
114	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
113	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *New England Journal of Medicine*, **2016**, 374, 135-45	59.2	753
112	Age-dependent DNA methylation of genes that are suppressed in stem cells is a hallmark of cancer. *Genome Research*, **2010**, 20, 440-6	9.7	638
111	Analysis of repetitive element DNA methylation by MethyLight. *Nucleic Acids Research*, **2005**, 33, 6823-36	20.1	588
110	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
109	The somatic genomic landscape of chromophobe renal cell carcinoma. *Cancer Cell*, **2014**, 26, 319-330	24.3	521
108	Regions of focal DNA hypermethylation and long-range hypomethylation in colorectal cancer coincide with nuclear lamina-associated domains. *Nature Genetics*, **2011**, 44, 40-6	36.3	474
107	Genome-scale analysis of aberrant DNA methylation in colorectal cancer. *Genome Research*, **2012**, 22, 271-82	9.7	466
106	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
105	Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. *Nature Biotechnology*, **2011**, 29, 1132-44	44.5	406
104	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
103	Low-level processing of Illumina Infinium DNA Methylation BeadArrays. *Nucleic Acids Research*, **2013**, 41, e90	20.1	393

102	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
101	Distinct localization of histone H3 acetylation and H3-K4 methylation to the transcription start sites in the human genome. *Proceedings of the National Academy of Sciences of the United States of America*, **2004**, 101, 7357-62	11.5	374
100	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
99	Precision and performance characteristics of bisulfite conversion and real-time PCR (MethyLight) for quantitative DNA methylation analysis. *Journal of Molecular Diagnostics*, **2006**, 8, 209-17	5.1	336
98	DNA methylation in the human cerebral cortex is dynamically regulated throughout the life span and involves differentiated neurons. *PLoS ONE*, **2007**, 2, e895	3.7	330
97	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
96	Alterations of immune response of Non-Small Cell Lung Cancer with Azacytidine. *Oncotarget*, **2013**, 4, 2067-79	3.3	285
95	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	24.3	275
94	CpG island methylator phenotype (CIMP) of colorectal cancer is best characterised by quantitative DNA methylation analysis and prospective cohort studies. *Gut*, **2006**, 55, 1000-6	19.2	274
93	Histone H3-lysine 9 methylation is associated with aberrant gene silencing in cancer cells and is rapidly reversed by 5-aza-2Ʉdeoxycytidine. *Cancer Research*, **2002**, 62, 6456-61	10.1	274
92	Association between molecular subtypes of colorectal cancer and patient survival. *Gastroenterology*, **2015**, 148, 77-87.e2	13.3	273
91	The relationship of DNA methylation with age, gender and genotype in twins and healthy controls. *PLoS ONE*, **2009**, 4, e6767	3.7	262
90	Preferential response of cancer cells to zebularine. *Cancer Cell*, **2004**, 6, 151-8	24.3	255
89	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
88	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
87	Cigarette smoking and colorectal cancer risk by molecularly defined subtypes. *Journal of the National Cancer Institute*, **2010**, 102, 1012-22	9.7	224
86	Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. *Human Molecular Genetics*, **2009**, 18, 4808-17	5.6	206
85	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. *Nature Biotechnology*, **2016**, 34, 726-37	44.5	204

84	Integrated Molecular Characterization of Testicular Germ Cell Tumors. *Cell Reports*, **2018**, 23, 3392-3406	10.6	200
83	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188
82	Detection of methylated apoptosis-associated genes in urine sediments of bladder cancer patients. *Clinical Cancer Research*, **2004**, 10, 7457-65	12.9	186
81	Continuous zebularine treatment effectively sustains demethylation in human bladder cancer cells. *Molecular and Cellular Biology*, **2004**, 24, 1270-8	4.8	183
80	Molecular characterization of MSI-H colorectal cancer by MLHI promoter methylation, immunohistochemistry, and mismatch repair germline mutation screening. *Cancer Epidemiology Biomarkers and Prevention*, **2008**, 17, 3208-15	4	171
79	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
78	Footprinting of mammalian promoters: use of a CpG DNA methyltransferase revealing nucleosome positions at a single molecule level. *Nucleic Acids Research*, **2005**, 33, e176	20.1	158
77	DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. *Laboratory Investigation*, **2008**, 88, 161-70	5.9	139
76	DNA methylation loss in late-replicating domains is linked to mitotic cell division. *Nature Genetics*, **2018**, 50, 591-602	36.3	133
75	Unique DNA methylation patterns distinguish noninvasive and invasive urothelial cancers and establish an epigenetic field defect in premalignant tissue. *Cancer Research*, **2010**, 70, 8169-78	10.1	133
74	Characterizing DNA methylation alterations from The Cancer Genome Atlas. *Journal of Clinical Investigation*, **2014**, 124, 17-23	15.9	128
73	DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. *Nucleic Acids Research*, **2008**, 36, 4689-98	20.1	118
72	Quantitative analysis of associations between DNA hypermethylation, hypomethylation, and DNMT RNA levels in ovarian tumors. *Oncogene*, **2006**, 25, 2636-45	9.2	118
71	Analysis of the association between CIMP and BRAF in colorectal cancer by DNA methylation profiling. *PLoS ONE*, **2009**, 4, e8357	3.7	116
70	Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. *Molecular Cancer Research*, **2004**, 2, 62-72	6.6	108
69	The genomic landscape of tuberous sclerosis complex. *Nature Communications*, **2017**, 8, 15816	17.4	104
68	Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. *European Journal of Cancer*, **2005**, 41, 2769-78	7.5	101
67	MethyLight. *Methods in Molecular Biology*, **2009**, 507, 325-37	1.4	94

66	Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. *Molecular Cancer*, **2008**, 7, 62	42.1	91
65	The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. *Genes*, **2019**, 10,	4.2	89
64	Genome-scale discovery of DNA-methylation biomarkers for blood-based detection of colorectal cancer. *PLoS ONE*, **2012**, 7, e50266	3.7	88
63	Combination Epigenetic Therapy in Advanced Breast Cancer with 5-Azacitidine and Entinostat: A Phase II National Cancer Institute/Stand Up to Cancer Study. *Clinical Cancer Research*, **2017**, 23, 2691-2701	12.9	84
62	DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. *Leukemia*, **2008**, 22, 1035-43	10.7	78
61	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	7.5	73
60	Tumor Budding in Colorectal Carcinoma: Confirmation of Prognostic Significance and Histologic Cutoff in a Population-based Cohort. *American Journal of Surgical Pathology*, **2015**, 39, 1340-6	6.7	72
59	Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. *Molecular Cancer Research*, **2004**, 2, 62-72	6.6	72
58	Frequency of deletions of EPCAM (TACSTD1) in MSH2-associated Lynch syndrome cases. *Journal of Molecular Diagnostics*, **2011**, 13, 93-9	5.1	71
57	DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. *Epigenetics*, **2017**, 12, 416-432	5.7	66
56	Cell division is required for de novo methylation of CpG islands in bladder cancer cells. *Cancer Research*, **2002**, 62, 2378-84	10.1	63
55	Association of the colorectal CpG island methylator phenotype with molecular features, risk factors, and family history. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 512-519	4	59
54	Cytosine methylation in a CpG sequence leads to enhanced reactivity with Benzo[a]pyrene diol epoxide that correlates with a conformational change. *Journal of Biological Chemistry*, **1999**, 274, 23948-55	5.4	56
53	DNA methylation in the malignant transformation of meningiomas. *PLoS ONE*, **2013**, 8, e54114	3.7	53
52	Combination epigenetic therapy in metastatic colorectal cancer (mCRC) with subcutaneous 5-azacitidine and entinostat: a phase 2 consortium/stand up 2 cancer study. *Oncotarget*, **2017**, 8, 35326-35338	3.3	52
51	cis-Expression QTL analysis of established colorectal cancer risk variants in colon tumors and adjacent normal tissue. *PLoS ONE*, **2012**, 7, e30477	3.7	52
50	LINE-1 methylation in plasma DNA as a biomarker of activity of DNA methylation inhibitors in patients with solid tumors. *Epigenetics*, **2009**, 4, 176-84	5.7	50
49	Integrated analysis of genome-wide copy number alterations and gene expression in microsatellite stable, CpG island methylator phenotype-negative colon cancer. *Genes Chromosomes and Cancer*, **2013**, 52, 450-66	5	46

48	Associations between colorectal cancer molecular markers and pathways with clinicopathologic features in older women. *Gastroenterology*, **2013**, 145, 348-56.e1-2	13.3	45
47	Identification and characterization of alternatively spliced variants of DNA methyltransferase 3a in mammalian cells. *Gene*, **2002**, 298, 91-9	3.8	45
46	Insights into the Pathogenesis of Anaplastic Large-Cell Lymphoma through Genome-wide DNA Methylation Profiling. *Cell Reports*, **2016**, 17, 596-608	10.6	37
45	Genetic and Epigenetic Alterations in Bladder Cancer. *International Neurourology Journal*, **2016**, 20, S84-94	2.6	36
44	Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. *Gut*, **2012**, 61, 1299-305	19.2	34
43	Identifying aggressive prostate cancer foci using a DNA methylation classifier. *Genome Biology*, **2017**, 18, 3	18.3	31
42	Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGI-110) in Hepatocellular Carcinoma. *Hepatology*, **2018**, 68, 1412-1428	11.2	28
41	Associations between intake of folate and related micronutrients with molecularly defined colorectal cancer risks in the Iowa Women's Health Study. *Nutrition and Cancer*, **2012**, 64, 899-910	2.8	27
40	A pilot genome-scale profiling of DNA methylation in sporadic pituitary macroadenomas: association with tumor invasion and histopathological subtype. *PLoS ONE*, **2014**, 9, e96178	3.7	23
39	Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. *Theranostics*, **2018**, 8, 4520-4534	12.1	23
38	Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. *Cancer Research*, **2016**, 76, 1954-64	10.1	21
37	Promoter Methylation Analysis Reveals That KCNA5 Ion Channel Silencing Supports Ewing Sarcoma Cell Proliferation. *Molecular Cancer Research*, **2016**, 14, 26-34	6.6	20
36	Locking in on the human methylome. *Nature Biotechnology*, **2009**, 27, 341-2	44.5	18
35	Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. *Neurosurgical Focus*, **2013**, 35, E3	4.2	17
34	Clinicopathologic Risk Factor Distributions for MLH1 Promoter Region Methylation in CIMP-Positive Tumors. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 68-75	4	16
33	Alcohol intake and colorectal cancer risk by molecularly defined subtypes in a prospective study of older women. *Cancer Prevention Research*, **2011**, 4, 2035-43	3.2	16
32	Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. *PLoS ONE*, **2017**, 12, e0175112	3.7	16
31	3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. *BMC Pharmacology & Toxicology*, **2013**, 14, 11	2.6	15

30	Gene-specific methylation and subsequent risk of colorectal adenomas among participants of the polyp prevention trial. *Cancer Epidemiology Biomarkers and Prevention*, **2005**, 14, 1219-23	4	15
29	Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. *Oncotarget*, **2017**, 8, 5439-5448	3.3	13
28	Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. *Communications Biology*, **2021**, 4, 769	6.7	12
27	Epigenetic subgroups of esophageal and gastric adenocarcinoma with differential GATA5 DNA methylation associated with clinical and lifestyle factors. *PLoS ONE*, **2011**, 6, e25985	3.7	10
26	Glutamyl hydrolase modulation significantly influences global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. *Genes and Nutrition*, **2015**, 10, 444	4.3	9
25	Cancer risks for the relatives of colorectal cancer cases with a methylated MLH1 promoter region: data from the Colorectal Cancer Family Registry. *Cancer Prevention Research*, **2012**, 5, 328-35	3.2	9
24	Racial Disparities in Epigenetic Aging of the Right vs Left Colon. *Journal of the National Cancer Institute*, **2020**,	9.7	9
23	Aberrant DNA methylation of miRNAs in Fuchs endothelial corneal dystrophy. *Scientific Reports*, **2019**, 9, 16385	4.9	7
22	MethyLight and Digital MethyLight. *Methods in Molecular Biology*, **2018**, 1708, 497-513	1.4	7
21	Promoter methylation of ITF2, but not APC, is associated with microsatellite instability in two populations of colorectal cancer patients. *BMC Cancer*, **2016**, 16, 113	4.8	6
20	Effects of folylpolyglutamate synthase modulation on global and gene-specific DNA methylation and gene expression in human colon and breast cancer cells. *Journal of Nutritional Biochemistry*, **2016**, 29, 27-35	6.3	6
19	Cell death and survival pathways in Alzheimer's disease: an integrative hypothesis testing approach utilizing -omic data sets. *Neurobiology of Aging*, **2020**, 95, 15-25	5.6	5
18	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.e9-15	1.6	4
17	Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer **2011**,		4
16	Immunogenic cell death pathway polymorphisms for predicting oxaliplatin efficacy in metastatic colorectal cancer **2020**, 8,		4
15	A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. *Frontiers in Oncology*, **2021**, 11, 614927	5.3	4
14	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. *European Journal of Cancer*, **2019**, 111, 138-147	7.5	3
13	Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues.. *Nature Biotechnology*, **2022**,	44.5	3

12	Differences in Genome-wide DNA Methylation Profiles in Breast Milk by Race and Lactation Duration. *Cancer Prevention Research*, **2019**, 12, 781-790	3.2	3
11	Modeling measurement error in tumor characterization studies. *BMC Bioinformatics*, **2011**, 12, 284	3.6	2
10	DNA Demethylating Agents **2004**, 151-167		2
9	Albumin levels predict prognosis in advanced renal cell carcinoma treated with tyrosine kinase inhibitors: a systematic review and meta-analysis. *Urologic Oncology: Seminars and Original Investigations*, **2022**, 40, 12.e13-12.e22	2.8	1
8	Networks and Consortia for Epigenetic Drug Discovery **2016**, 143-166		1
7	Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. *Genome Medicine*, **2021**, 13, 130	14.4	1
6	AMPK variant, a candidate of novel predictor for chemotherapy in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC and FIRE3. *International Journal of Cancer*, **2019**, 145, 2082-2090	7.5	0
5	A Clinically Distinct and “Atypical” Subgroup of Head and Neck Cancers Positive for a CpG Island Methylator Phenotype. *EBioMedicine*, **2017**, 17, 22-23	8.8	
4	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	2.2	
3	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	2.2	
2	Whole-genome bisulfite sequencing of a complex karyotype AML and identification of regulatory aberrations distinct from normal karyotype AML.. *Journal of Clinical Oncology*, **2014**, 32, 11075-11075	2.2	
1	Molecular subtypes of colorectal cancer in relation to disease survival.. *Journal of Clinical Oncology*, **2014**, 32, 451-451	2.2	