

Daniel J Weisenberger

List of Publications by Year in descending order

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Version: 2024-02-01

147
papers

105,388
citations

6254

80
h-index

12272

133
g-index

151
all docs

151
docs citations

151
times ranked

104366
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70. | 27.8 | 10,282 |
| 2 | Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337. | 27.8 | 7,168 |
| 3 | Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068. | 27.8 | 6,879 |
| 4 | Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615. | 27.8 | 6,541 |
| 5 | Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209. | 27.8 | 5,055 |
| 6 | Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550. | 27.8 | 4,572 |
| 7 | Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074. | 27.0 | 4,139 |
| 8 | Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73. | 27.8 | 4,075 |
| 9 | The Somatic Genomic Landscape of Glioblastoma. Cell, 2013, 155, 462-477. | 28.9 | 3,979 |
| 10 | Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49. | 27.8 | 2,839 |
| 11 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498. | 27.0 | 2,582 |
| 12 | Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696. | 28.9 | 2,562 |
| 13 | Comprehensive molecular characterization of urothelial bladder carcinoma. Nature, 2014, 507, 315-322. | 27.8 | 2,496 |
| 14 | The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025. | 28.9 | 2,435 |
| 15 | Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690. | 28.9 | 2,318 |
| 16 | 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 |
| 17 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10. | 28.9 | 2,111 |
| 18 | Identification of a CpG Island Methylator Phenotype that Defines a Distinct Subgroup of Glioma. Cancer Cell, 2010, 17, 510-522. | 16.8 | 2,078 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23. | 28.9 | 1,794 |
| 20 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25. | 28.9 | 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. | 28.9 | 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. | 21.4 | 1,715 |
| 23 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13. | 16.8 | 1,428 |
| 24 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018, 173, 338-354.e15. | 28.9 | 1,417 |
| 25 | Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016, 374, 135-145. | 27.0 | 1,040 |
| 26 | Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , 2007, 39, 157-158. | 21.4 | 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. | 6.4 | 801 |
| 28 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3. | 16.8 | 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. | 5.5 | 740 |
| 30 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28. | 28.9 | 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. | 6.4 | 683 |
| 32 | The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330. | 16.8 | 665 |
| 33 | Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013, 41, e90-e90. | 14.5 | 647 |
| 34 | Analysis of repetitive element DNA methylation by MethyLight. <i>Nucleic Acids Research</i> , 2005, 33, 6823-6836. | 14.5 | 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. | 21.4 | 588 |
| 36 | Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012, 22, 271-282. | 5.5 | 527 |

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|----|--|------|-----------|
| 37 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5. | 6.4 | 523 |
| 38 | Screening ethnically diverse human embryonic stem cells identifies a chromosome 20 minimal amplicon conferring growth advantage. Nature Biotechnology, 2011, 29, 1132-1144. | 17.5 | 509 |
| 39 | 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, 7357-7362. | 7.1 | 435 |
| 40 | Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794. | 6.4 | 416 |
| 41 | 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. | 16.8 | 400 |
| 42 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8. | 16.8 | 396 |
| 43 | DNA Methylation in the Human Cerebral Cortex Is Dynamically Regulated throughout the Life Span and Involves Differentiated Neurons. PLoS ONE, 2007, 2, e895. | 2.5 | 375 |
| 44 | Precision and Performance Characteristics of Bisulfite Conversion and Real-Time PCR (MethyLight) for Quantitative DNA Methylation Analysis. Journal of Molecular Diagnostics, 2006, 8, 209-217. | 2.8 | 361 |
| 45 | Association Between Molecular Subtypes of Colorectal Cancer and Patient Survival. Gastroenterology, 2015, 148, 77-87.e2. | 1.3 | 342 |
| 46 | Alterations of immune response of non-small cell lung cancer with Azacytidine. Oncotarget, 2013, 4, 2067-2079. | 1.8 | 336 |
| 47 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4. | 6.4 | 333 |
| 48 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406. | 6.4 | 324 |
| 49 | The Relationship of DNA Methylation with Age, Gender and Genotype in Twins and Healthy Controls. PLoS ONE, 2009, 4, e6767. | 2.5 | 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. Cancer Research, 2002, 62, 6456-61. | 0.9 | 310 |
| 51 | CpG island methylator phenotype (CIMP) of colorectal cancer is best characterised by quantitative DNA methylation analysis and prospective cohort studies. Gut, 2006, 55, 1000-1006. | 12.1 | 308 |
| 52 | Preferential response of cancer cells to zebularine. Cancer Cell, 2004, 6, 151-158. | 16.8 | 282 |
| 53 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10. | 28.9 | 272 |
| 54 | Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737. | 17.5 | 270 |

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|----|---|------|-----------|
| 55 | Cigarette Smoking and Colorectal Cancer Risk by Molecularly Defined Subtypes. Journal of the National Cancer Institute, 2010, 102, 1012-1022. | 6.3 | 261 |
| 56 | DNA methylation loss in late-replicating domains is linked to mitotic cell division. Nature Genetics, 2018, 50, 591-602. | 21.4 | 258 |
| 57 | Epigenetic profiling of somatic tissues from human autopsy specimens identifies tissue- and individual-specific DNA methylation patterns. Human Molecular Genetics, 2009, 18, 4808-4817. | 2.9 | 230 |
| 58 | Molecular Characterization of MSI-H Colorectal Cancer by <i>MLH1</i> Promoter Methylation, Immunohistochemistry, and Mismatch Repair Germline Mutation Screening. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 3208-3215. | 2.5 | 207 |
| 59 | Continuous Zebularine Treatment Effectively Sustains Demethylation in Human Bladder Cancer Cells. Molecular and Cellular Biology, 2004, 24, 1270-1278. | 2.3 | 205 |
| 60 | Detection of Methylated Apoptosis-Associated Genes in Urine Sediments of Bladder Cancer Patients. Clinical Cancer Research, 2004, 10, 7457-7465. | 7.0 | 202 |
| 61 | Footprinting of mammalian promoters: use of a CpG DNA methyltransferase revealing nucleosome positions at a single molecule level. Nucleic Acids Research, 2005, 33, e176-e176. | 14.5 | 185 |
| 62 | Characterizing DNA methylation alterations from The Cancer Genome Atlas. Journal of Clinical Investigation, 2014, 124, 17-23. | 8.2 | 162 |
| 63 | DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. Laboratory Investigation, 2008, 88, 161-170. | 3.7 | 156 |
| 64 | The genomic landscape of tuberous sclerosis complex. Nature Communications, 2017, 8, 15816. | 12.8 | 154 |
| 65 | Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. Molecular Cancer Research, 2004, 2, 62-72. | 3.4 | 151 |
| 66 | Unique DNA Methylation Patterns Distinguish Noninvasive and Invasive Urothelial Cancers and Establish an Epigenetic Field Defect in Premalignant Tissue. Cancer Research, 2010, 70, 8169-8178. | 0.9 | 148 |
| 67 | The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. Genes, 2019, 10, 172. | 2.4 | 134 |
| 68 | DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. Nucleic Acids Research, 2008, 36, 4689-4698. | 14.5 | 133 |
| 69 | Analysis of the Association between CIMP and BRAFV600E in Colorectal Cancer by DNA Methylation Profiling. PLoS ONE, 2009, 4, e8357. | 2.5 | 133 |
| 70 | Quantitative analysis of associations between DNA hypermethylation, hypomethylation, and DNMT RNA levels in ovarian tumors. Oncogene, 2006, 25, 2636-2645. | 5.9 | 129 |
| 71 | Identification of a panel of sensitive and specific DNA methylation markers for squamous cell lung cancer. Molecular Cancer, 2008, 7, 62. | 19.2 | 114 |
| 72 | Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. European Journal of Cancer, 2005, 41, 2769-2778. | 2.8 | 109 |

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|----|--|-----|-----------|
| 73 | MethylLight. Methods in Molecular Biology, 2009, 507, 325-337. | 0.9 | 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. Clinical Cancer Research, 2017, 23, 2691-2701. | 7.0 | 106 |
| 75 | Genome-Scale Discovery of DNA-Methylation Biomarkers for Blood-Based Detection of Colorectal Cancer. PLoS ONE, 2012, 7, e50266. | 2.5 | 103 |
| 76 | DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. Epigenetics, 2017, 12, 416-432. | 2.7 | 98 |
| 77 | Tumor Budding in Colorectal Carcinoma. American Journal of Surgical Pathology, 2015, 39, 1340-1346. | 3.7 | 95 |
| 78 | DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. Leukemia, 2008, 22, 1035-1043. | 7.2 | 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. International Journal of Cancer, 2009, 124, 1999-2005. | 5.1 | 80 |
| 80 | Frequency of Deletions of EPCAM (TACSTD1) in MSH2-Associated Lynch Syndrome Cases. Journal of Molecular Diagnostics, 2011, 13, 93-99. | 2.8 | 79 |
| 81 | Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. Molecular Cancer Research, 2004, 2, 62-72. | 3.4 | 74 |
| 82 | Cell division is required for de novo methylation of CpG islands in bladder cancer cells. Cancer Research, 2002, 62, 2378-84. | 0.9 | 72 |
| 83 | 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. | 2.5 | 71 |
| 84 | DNA Methylation in the Malignant Transformation of Meningiomas. PLoS ONE, 2013, 8, e54114. | 2.5 | 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. Oncotarget, 2017, 8, 35326-35338. | 1.8 | 66 |
| 86 | Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. Communications Biology, 2021, 4, 769. | 4.4 | 65 |
| 87 | 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, 23948-23955. | 3.4 | 61 |
| 88 | cis-Expression QTL Analysis of Established Colorectal Cancer Risk Variants in Colon Tumors and Adjacent Normal Tissue. PLoS ONE, 2012, 7, e30477. | 2.5 | 55 |
| 89 | Insights into the Pathogenesis of Anaplastic Large-Cell Lymphoma through Genome-wide DNA Methylation Profiling. Cell Reports, 2016, 17, 596-608. | 6.4 | 55 |
| 90 | LINE-1 methylation in plasma DNA as a biomarker of activity of DNA methylation inhibitors in patients with solid tumors. Epigenetics, 2009, 4, 176-184. | 2.7 | 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. | 2.2 | 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. | 2.8 | 51 |
| 93 | Associations Between Colorectal Cancer Molecular Markers and Pathways With Clinicopathologic Features in Older Women. <i>Gastroenterology</i> , 2013, 145, 348-356.e2. | 1.3 | 49 |
| 94 | Genetic and Epigenetic Alterations in Bladder Cancer. <i>International Neurourology Journal</i> , 2016, 20, S84-94. | 1.2 | 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. | 7.3 | 48 |
| 96 | Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017, 18, 3. | 8.8 | 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. | 10.0 | 40 |
| 98 | Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012, 61, 1299-1305. | 12.1 | 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. | 2.5 | 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. | 2.0 | 33 |
| 101 | Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. <i>Neurosurgical Focus</i> , 2013, 35, E3. | 2.3 | 28 |
| 102 | Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016, 76, 1954-1964. | 0.9 | 28 |
| 103 | Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. <i>PLoS ONE</i> , 2017, 12, e0175112. | 2.5 | 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. | 3.1 | 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. | 6.3 | 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. | 3.4 | 22 |
| 108 | Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues. <i>Nature Biotechnology</i> , 2022, 40, 720-730. | 17.5 | 22 |

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|-----|---|------|-----------|
| 109 | 3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. BMC Pharmacology & Toxicology, 2013, 14, 11. | 2.4 | 21 |
| 110 | Clinicopathologic Risk Factor Distributions for <i>MLH1</i> Promoter Region Methylation in CIMP-Positive Tumors. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 68-75. | 2.5 | 21 |
| 111 | Locking in on the human methylome. Nature Biotechnology, 2009, 27, 341-342. | 17.5 | 19 |
| 112 | Gene-Specific Methylation and Subsequent Risk of Colorectal Adenomas among Participants of the Polyp Prevention Trial. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1219-1223. | 2.5 | 17 |
| 113 | Alcohol Intake and Colorectal Cancer Risk by Molecularly Defined Subtypes in a Prospective Study of Older Women. Cancer Prevention Research, 2011, 4, 2035-2043. | 1.5 | 17 |
| 114 | Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. Oncotarget, 2017, 8, 5439-5448. | 1.8 | 17 |
| 115 | Aberrant DNA methylation of miRNAs in Fuchs endothelial corneal dystrophy. Scientific Reports, 2019, 9, 16385. | 3.3 | 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. Cancer Prevention Research, 2012, 5, 328-335. | 1.5 | 12 |
| 117 | Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. Genome Medicine, 2021, 13, 130. | 8.2 | 12 |
| 118 | MethylLight and Digital MethyLight. Methods in Molecular Biology, 2018, 1708, 497-513. | 0.9 | 11 |
| 119 | Epigenetic Subgroups of Esophageal and Gastric Adenocarcinoma with Differential GATA5 DNA Methylation Associated with Clinical and Lifestyle Factors. PLoS ONE, 2011, 6, e25985. | 2.5 | 10 |
| 120 | Î³-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. | 2.5 | 10 |
| 121 | Promoter methylation of ITF2, but not APC, is associated with microsatellite instability in two populations of colorectal cancer patients. BMC Cancer, 2016, 16, 113. | 2.6 | 7 |
| 122 | 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. | 4.2 | 7 |
| 123 | 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. | 1.6 | 6 |
| 124 | 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 |
| 125 | A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. Frontiers in Oncology, 2021, 11, 614927. | 2.8 | 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. | 1.0 | 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. | 2.8 | 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. | 5.1 | 4 |
| 130 | Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011, 12, 284. | 2.6 | 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. | 0.4 | 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. | 4.6 | 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. | 6.1 | 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. | 1.6 | 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. | 1.6 | 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. | 1.6 | 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. | 1.6 | 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. | 0.9 | 0 |