

Daniel J Weisenberger

List of Publications by Year in Descending Order

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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.

137
papers

77,161
citations

78
h-index

151
g-index

151
ext. papers

94,349
ext. citations

18
avg, IF

9.22
L-index

| # | Paper | IF | Citations |
|-----|--|------|-----------|
| 137 | Fluctuating methylation clocks for cell lineage tracing at high temporal resolution in human tissues.. <i>Nature Biotechnology</i> , 2022 , | 44.5 | 3 |
| 136 | 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 | 2.8 | 1 |
| 135 | Exploring the evidence for epigenetic regulation of environmental influences on child health across generations. <i>Communications Biology</i> , 2021 , 4, 769 | 6.7 | 12 |
| 134 | A Novel DNA Methylation Signature as an Independent Prognostic Factor in Muscle-Invasive Bladder Cancer. <i>Frontiers in Oncology</i> , 2021 , 11, 614927 | 5.3 | 4 |
| 133 | Characterizing DNA methylation signatures and their potential functional roles in Merkel cell carcinoma. <i>Genome Medicine</i> , 2021 , 13, 130 | 14.4 | 1 |
| 132 | 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 | 5.6 | 5 |
| 131 | Racial Disparities in Epigenetic Aging of the Right vs Left Colon. <i>Journal of the National Cancer Institute</i> , 2020 , | 9.7 | 9 |
| 130 | Immunogenic cell death pathway polymorphisms for predicting oxaliplatin efficacy in metastatic colorectal cancer 2020 , 8, | | 4 |
| 129 | The Roles of Human DNA Methyltransferases and Their Isoforms in Shaping the Epigenome. <i>Genes</i> , 2019 , 10, | 4.2 | 89 |
| 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 | 7.5 | 3 |
| 127 | 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 | 7.5 | 0 |
| 126 | Aberrant DNA methylation of miRNAs in Fuchs endothelial corneal dystrophy. <i>Scientific Reports</i> , 2019 , 9, 16385 | 4.9 | 7 |
| 125 | Th17 cell pathway-related genetic variants in metastatic colorectal cancer: A meta-analysis using TRIBE, MAVERICC, and FIRE-3.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 594-594 | 2.2 | |
| 124 | Genetic variants in RNA binding protein (RBP) to predict outcome in metastatic colorectal cancer (mCRC): Data from FIRE-3, TRIBE, and MAVERICC trials.. <i>Journal of Clinical Oncology</i> , 2019 , 37, 3545-3545 ^{2.2} | | |
| 123 | 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 |
| 122 | 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 |
| 121 | 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 |

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| 120 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10 | 56.2 | 166 |
| 119 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15 | 56.2 | 560 |
| 118 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10 | 56.2 | 1124 |
| 117 | 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 |
| 116 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5 | 10.6 | 295 |
| 115 | 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 |
| 114 | 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 |
| 113 | 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 |
| 112 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3 | 24.3 | 377 |
| 111 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8 | 24.3 | 228 |
| 110 | DNA methylation loss in late-replicating domains is linked to mitotic cell division. <i>Nature Genetics</i> , 2018 , 50, 591-602 | 36.3 | 133 |
| 109 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10 | 10.6 | 200 |
| 108 | MethyLight and Digital MethyLight. <i>Methods in Molecular Biology</i> , 2018 , 1708, 497-513 | 1.4 | 7 |
| 107 | Rewiring of cisplatin-resistant bladder cancer cells through epigenetic regulation of genes involved in amino acid metabolism. <i>Theranostics</i> , 2018 , 8, 4520-4534 | 12.1 | 23 |
| 106 | Integrative Epigenetic Analysis Reveals Therapeutic Targets to the DNA Methyltransferase Inhibitor Guadecitabine (SGI-110) in Hepatocellular Carcinoma. <i>Hepatology</i> , 2018 , 68, 1412-1428 | 11.2 | 28 |
| 105 | Identifying aggressive prostate cancer foci using a DNA methylation classifier. <i>Genome Biology</i> , 2017 , 18, 3 | 18.3 | 31 |
| 104 | Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23 | 56.2 | 1125 |
| 103 | A Clinically Distinct and Unusual Subgroup of Head and Neck Cancers Positive for a CpG Island Methylator Phenotype. <i>EBioMedicine</i> , 2017 , 17, 22-23 | 8.8 | |

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|-----|--|------|-----|
| 102 | DNA methylation aberrancies as a guide for surveillance and treatment of human cancers. <i>Epigenetics</i> , 2017 , 12, 416-432 | 5.7 | 66 |
| 101 | Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794 | 10.6 | 247 |
| 100 | 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 |
| 99 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25 | 35.2 | 961 |
| 98 | 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 | 3.3 | 52 |
| 97 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13 | 21.9 | 96 |
| 96 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28 | 56.2 | 451 |
| 95 | The genomic landscape of tuberous sclerosis complex. <i>Nature Communications</i> , 2017 , 8, 15816 | 17.4 | 104 |
| 94 | Comprehensive characterization of DNA methylation changes in Fuchs endothelial corneal dystrophy. <i>PLoS ONE</i> , 2017 , 12, e0175112 | 3.7 | 16 |
| 93 | Improving needle biopsy accuracy in small renal mass using tumor-specific DNA methylation markers. <i>Oncotarget</i> , 2017 , 8, 5439-5448 | 3.3 | 13 |
| 92 | Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016 , 34, 726-37 | 44.5 | 204 |
| 91 | 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 | 4.8 | 6 |
| 90 | Identification of DNA Methylation-Independent Epigenetic Events Underlying Clear Cell Renal Cell Carcinoma. <i>Cancer Research</i> , 2016 , 76, 1954-64 | 10.1 | 21 |
| 89 | 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 |
| 88 | 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 |
| 87 | Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45 | 59.2 | 753 |
| 86 | 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 |
| 85 | Genetic and Epigenetic Alterations in Bladder Cancer. <i>International Neurourology Journal</i> , 2016 , 20, S84-94 | 2.6 | 36 |

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| 84 | Networks and Consortia for Epigenetic Drug Discovery 2016 , 143-166 | | 1 |
| 83 | Insights into the Pathogenesis of Anaplastic Large-Cell Lymphoma through Genome-wide DNA Methylation Profiling. <i>Cell Reports</i> , 2016 , 17, 596-608 | 10.6 | 37 |
| 82 | EGlutamyl 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 |
| 81 | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96 | 56.2 | 1807 |
| 80 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98 | 59.2 | 1828 |
| 79 | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25 | 56.2 | 1713 |
| 78 | Association between molecular subtypes of colorectal cancer and patient survival. <i>Gastroenterology</i> , 2015 , 148, 77-87.e2 | 13.3 | 273 |
| 77 | 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 |
| 76 | 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 |
| 75 | Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22 | 50.4 | 1963 |
| 74 | Comprehensive molecular characterization of gastric adenocarcinoma. <i>Nature</i> , 2014 , 513, 202-9 | 50.4 | 3659 |
| 73 | The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330 | 24.3 | 521 |
| 72 | Comprehensive molecular profiling of lung adenocarcinoma. <i>Nature</i> , 2014 , 511, 543-50 | 50.4 | 3310 |
| 71 | Characterizing DNA methylation alterations from The Cancer Genome Atlas. <i>Journal of Clinical Investigation</i> , 2014 , 124, 17-23 | 15.9 | 128 |
| 70 | Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90 | 56.2 | 1660 |
| 69 | 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 | 3.7 | 23 |
| 68 | 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 | 2.2 | |
| 67 | Molecular subtypes of colorectal cancer in relation to disease survival. <i>Journal of Clinical Oncology</i> , 2014 , 32, 451-451 | 2.2 | |

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| 66 | 3-D DNA methylation phenotypes correlate with cytotoxicity levels in prostate and liver cancer cell models. <i>BMC Pharmacology & Toxicology</i> , 2013 , 14, 11 | 2.6 | 15 |
| 65 | 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 | 1.6 | 4 |
| 64 | The somatic genomic landscape of glioblastoma. <i>Cell</i> , 2013 , 155, 462-77 | 56.2 | 2900 |
| 63 | 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 |
| 62 | 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, 450-66 | 5 | 46 |
| 61 | Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73 | 50.4 | 2800 |
| 60 | 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 |
| 59 | Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013 , 499, 43-9 | 50.4 | 2184 |
| 58 | Genomic and transcriptome analysis revealing an oncogenic functional module in meningiomas. <i>Neurosurgical Focus</i> , 2013 , 35, E3 | 4.2 | 17 |
| 57 | Low-level processing of Illumina Infinium DNA Methylation BeadArrays. <i>Nucleic Acids Research</i> , 2013 , 41, e90 | 20.1 | 393 |
| 56 | DNA methylation in the malignant transformation of meningiomas. <i>PLoS ONE</i> , 2013 , 8, e54114 | 3.7 | 53 |
| 55 | Alterations of immune response of Non-Small Cell Lung Cancer with Azacytidine. <i>Oncotarget</i> , 2013 , 4, 2067-79 | 3.3 | 285 |
| 54 | Postmenopausal hormone therapy and colorectal cancer risk by molecularly defined subtypes among older women. <i>Gut</i> , 2012 , 61, 1299-305 | 19.2 | 34 |
| 53 | Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012 , 487, 330-7 | 50.4 | 5640 |
| 52 | Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012 , 490, 61-70 | 50.4 | 8025 |
| 51 | cis-Expression QTL analysis of established colorectal cancer risk variants in colon tumors and adjacent normal tissue. <i>PLoS ONE</i> , 2012 , 7, e30477 | 3.7 | 52 |
| 50 | 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 |
| 49 | Genome-scale analysis of aberrant DNA methylation in colorectal cancer. <i>Genome Research</i> , 2012 , 22, 271-82 | 9.7 | 466 |

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|----|---|------|------|
| 48 | 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 |
| 47 | Genome-scale discovery of DNA-methylation biomarkers for blood-based detection of colorectal cancer. <i>PLoS ONE</i> , 2012 , 7, e50266 | 3.7 | 88 |
| 46 | 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 |
| 45 | Integrated genomic analyses of ovarian carcinoma. <i>Nature</i> , 2011 , 474, 609-15 | 50.4 | 5210 |
| 44 | 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 |
| 43 | 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 |
| 42 | Modeling measurement error in tumor characterization studies. <i>BMC Bioinformatics</i> , 2011 , 12, 284 | 3.6 | 2 |
| 41 | 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 |
| 40 | 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 |
| 39 | Abstract LB-173: Genome-scale analysis of aberrant DNA methylation in colorectal cancer 2011 , | | 4 |
| 38 | 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 |
| 37 | 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 |
| 36 | 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 |
| 35 | 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 |
| 34 | The relationship of DNA methylation with age, gender and genotype in twins and healthy controls. <i>PLoS ONE</i> , 2009 , 4, e6767 | 3.7 | 262 |
| 33 | 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 |
| 32 | 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, 176-84 | 5.7 | 50 |
| 31 | 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 |

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|----|---|------|------|
| 30 | Locking in on the human methylome. <i>Nature Biotechnology</i> , 2009 , 27, 341-2 | 44.5 | 18 |
| 29 | MethyLight. <i>Methods in Molecular Biology</i> , 2009 , 507, 325-37 | 1.4 | 94 |
| 28 | 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 |
| 27 | DNA methylation profiles of gastric carcinoma characterized by quantitative DNA methylation analysis. <i>Laboratory Investigation</i> , 2008 , 88, 161-70 | 5.9 | 139 |
| 26 | DNA methylation profiles in diffuse large B-cell lymphoma and their relationship to gene expression status. <i>Leukemia</i> , 2008 , 22, 1035-43 | 10.7 | 78 |
| 25 | Comprehensive genomic characterization defines human glioblastoma genes and core pathways. <i>Nature</i> , 2008 , 455, 1061-8 | 50.4 | 5669 |
| 24 | 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 |
| 23 | DNA methylation analysis by digital bisulfite genomic sequencing and digital MethyLight. <i>Nucleic Acids Research</i> , 2008 , 36, 4689-98 | 20.1 | 118 |
| 22 | 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 |
| 21 | Epigenetic stem cell signature in cancer. <i>Nature Genetics</i> , 2007 , 39, 157-8 | 36.3 | 909 |
| 20 | 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 |
| 19 | 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, 1000-6 | 19.2 | 274 |
| 18 | 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 |
| 17 | CpG island methylator phenotype underlies sporadic microsatellite instability and is tightly associated with BRAF mutation in colorectal cancer. <i>Nature Genetics</i> , 2006 , 38, 787-93 | 36.3 | 1514 |
| 16 | Quantitative analysis of associations between DNA hypermethylation, hypomethylation, and DNMT RNA levels in ovarian tumors. <i>Oncogene</i> , 2006 , 25, 2636-45 | 9.2 | 118 |
| 15 | 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 | 20.1 | 158 |
| 14 | Prognostic relevance of methylation markers in patients with non-muscle invasive bladder carcinoma. <i>European Journal of Cancer</i> , 2005 , 41, 2769-78 | 7.5 | 101 |
| 13 | Analysis of repetitive element DNA methylation by MethyLight. <i>Nucleic Acids Research</i> , 2005 , 33, 6823-36 | 20.1 | 588 |

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|----|---|------|-----|
| 12 | 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, 1219-23 | 4 | 15 |
| 11 | Continuous zebularine treatment effectively sustains demethylation in human bladder cancer cells. <i>Molecular and Cellular Biology</i> , 2004 , 24, 1270-8 | 4.8 | 183 |
| 10 | Detection of methylated apoptosis-associated genes in urine sediments of bladder cancer patients. <i>Clinical Cancer Research</i> , 2004 , 10, 7457-65 | 12.9 | 186 |
| 9 | 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, 7357-62 | 11.5 | 374 |
| 8 | Preferential response of cancer cells to zebularine. <i>Cancer Cell</i> , 2004 , 6, 151-8 | 24.3 | 255 |
| 7 | DNA Demethylating Agents 2004 , 151-167 | | 2 |
| 6 | Role of the DNA methyltransferase variant DNMT3b3 in DNA methylation. <i>Molecular Cancer Research</i> , 2004 , 2, 62-72 | 6.6 | 72 |
| 5 | Role of the DNA Methyltransferase Variant DNMT3b3 in DNA Methylation. <i>Molecular Cancer Research</i> , 2004 , 2, 62-72 | 6.6 | 108 |
| 4 | Identification and characterization of alternatively spliced variants of DNA methyltransferase 3a in mammalian cells. <i>Gene</i> , 2002 , 298, 91-9 | 3.8 | 45 |
| 3 | Cell division is required for de novo methylation of CpG islands in bladder cancer cells. <i>Cancer Research</i> , 2002 , 62, 2378-84 | 10.1 | 63 |
| 2 | Histone H3-lysine 9 methylation is associated with aberrant gene silencing in cancer cells and is rapidly reversed by 5-aza-2Udeoxycytidine. <i>Cancer Research</i> , 2002 , 62, 6456-61 | 10.1 | 274 |
| 1 | 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, 23948-54 | 5.4 | 56 |