

Manel Esteller

List of Publications by Year in descending order

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Version: 2024-02-01

599
papers

86,043
citations

576

129
h-index

536

272
g-index

626
all docs

626
docs citations

626
times ranked

94926
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Non-coding RNAs in human disease. <i>Nature Reviews Genetics</i> , 2011, 12, 861-874. | 7.7 | 4,159 |
| 2 | Epigenetics in Cancer. <i>New England Journal of Medicine</i> , 2008, 358, 1148-1159. | 13.9 | 3,251 |
| 3 | From The Cover: Epigenetic differences arise during the lifetime of monozygotic twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10604-10609. | 3.3 | 3,169 |
| 4 | Epigenetic modifications and human disease. <i>Nature Biotechnology</i> , 2010, 28, 1057-1068. | 9.4 | 2,328 |
| 5 | Inactivation of the DNA-Repair Gene MGMT and the Clinical Response of Gliomas to Alkylating Agents. <i>New England Journal of Medicine</i> , 2000, 343, 1350-1354. | 13.9 | 2,323 |
| 6 | The Polycomb group protein EZH2 directly controls DNA methylation. <i>Nature</i> , 2006, 439, 871-874. | 13.7 | 1,964 |
| 7 | Cancer epigenomics: DNA methylomes and histone-modification maps. <i>Nature Reviews Genetics</i> , 2007, 8, 286-298. | 7.7 | 1,916 |
| 8 | Loss of acetylation at Lys16 and trimethylation at Lys20 of histone H4 is a common hallmark of human cancer. <i>Nature Genetics</i> , 2005, 37, 391-400. | 9.4 | 1,710 |
| 9 | Gene-Expression Profiles in Hereditary Breast Cancer. <i>New England Journal of Medicine</i> , 2001, 344, 539-548. | 13.9 | 1,669 |
| 10 | Global Epigenomic Reconfiguration During Mammalian Brain Development. <i>Science</i> , 2013, 341, 1237-1245. | 6.0 | 1,609 |
| 11 | A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016, 166, 740-754. | 13.5 | 1,518 |
| 12 | DNA Methylation and Cancer. <i>Advances in Genetics</i> , 2010, 70, 27-56. | 0.8 | 1,238 |
| 13 | CpG island hypermethylation and tumor suppressor genes: a booming present, a brighter future. <i>Oncogene</i> , 2002, 21, 5427-5440. | 2.6 | 1,103 |
| 14 | Cancer epigenetics reaches mainstream oncology. <i>Nature Medicine</i> , 2011, 17, 330-339. | 15.2 | 1,102 |
| 15 | The transcription factor Slug represses E-cadherin expression and induces epithelial to mesenchymal transitions: a comparison with Snail and E47 repressors. <i>Journal of Cell Science</i> , 2003, 116, 499-511. | 1.2 | 1,021 |
| 16 | A microRNA DNA methylation signature for human cancer metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 13556-13561. | 3.3 | 990 |
| 17 | Validation of a DNA methylation microarray for 450,000 CpG sites in the human genome. <i>Epigenetics</i> , 2011, 6, 692-702. | 1.3 | 908 |
| 18 | Inactivation of the apoptosis effector Apaf-1 in malignant melanoma. <i>Nature</i> , 2001, 409, 207-211. | 13.7 | 901 |

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|----|---|------|-----------|
| 19 | Genetic Unmasking of an Epigenetically Silenced microRNA in Human Cancer Cells. <i>Cancer Research</i> , 2007, 67, 1424-1429. | 0.4 | 883 |
| 20 | The role of histone deacetylases (HDACs) in human cancer. <i>Molecular Oncology</i> , 2007, 1, 19-25. | 2.1 | 796 |
| 21 | Distinct DNA methylomes of newborns and centenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10522-10527. | 3.3 | 687 |
| 22 | Cancer as an epigenetic disease: DNA methylation and chromatin alterations in human tumours. <i>Journal of Pathology</i> , 2002, 196, 1-7. | 2.1 | 679 |
| 23 | DNA methylation profiling in the clinic: applications and challenges. <i>Nature Reviews Genetics</i> , 2012, 13, 679-692. | 7.7 | 675 |
| 24 | Snail Mediates E-Cadherin Repression by the Recruitment of the Sin3A/Histone Deacetylase 1 (HDAC1)/HDAC2 Complex. <i>Molecular and Cellular Biology</i> , 2004, 24, 306-319. | 1.1 | 672 |
| 25 | Identification of an Immune-specific Class of Hepatocellular Carcinoma, Based on Molecular Features. <i>Gastroenterology</i> , 2017, 153, 812-826. | 0.6 | 650 |
| 26 | Epigenetics and aging: the targets and the marks. <i>Trends in Genetics</i> , 2007, 23, 413-418. | 2.9 | 611 |
| 27 | Epigenetic gene silencing in cancer: the DNA hypermethylome. <i>Human Molecular Genetics</i> , 2007, 16, R50-R59. | 1.4 | 604 |
| 28 | Toward understanding and exploiting tumor heterogeneity. <i>Nature Medicine</i> , 2015, 21, 846-853. | 15.2 | 604 |
| 29 | Changes in the pattern of DNA methylation associate with twin discordance in systemic lupus erythematosus. <i>Genome Research</i> , 2010, 20, 170-179. | 2.4 | 569 |
| 30 | DNA methyltransferases control telomere length and telomere recombination in mammalian cells. <i>Nature Cell Biology</i> , 2006, 8, 416-424. | 4.6 | 538 |
| 31 | Aberrant Epigenetic Landscape in Cancer: How Cellular Identity Goes Awry. <i>Developmental Cell</i> , 2010, 19, 698-711. | 3.1 | 529 |
| 32 | Validation of a DNA methylation microarray for 850,000 CpG sites of the human genome enriched in enhancer sequences. <i>Epigenomics</i> , 2016, 8, 389-399. | 1.0 | 529 |
| 33 | Epigenetic mechanisms in neurological diseases: genes, syndromes, and therapies. <i>Lancet Neurology</i> , 2009, 8, 1056-1072. | 4.9 | 528 |
| 34 | CpG Island Hypermethylation of the DNA Repair Enzyme Methyltransferase Predicts Response to Temozolomide in Primary Gliomas. <i>Clinical Cancer Research</i> , 2004, 10, 4933-4938. | 3.2 | 523 |
| 35 | ABERRANT DNA METHYLATION AS A CANCER-INDUCING MECHANISM. <i>Annual Review of Pharmacology and Toxicology</i> , 2005, 45, 629-656. | 4.2 | 490 |
| 36 | lncRNAs and microRNAs with a role in cancer development. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 169-176. | 0.9 | 449 |

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|----|---|------|-----------|
| 37 | MLH1 promoter hypermethylation is associated with the microsatellite instability phenotype in sporadic endometrial carcinomas. <i>Oncogene</i> , 1998, 17, 2413-2417. | 2.6 | 442 |
| 38 | Notch Signaling Is Essential for Ventricular Chamber Development. <i>Developmental Cell</i> , 2007, 12, 415-429. | 3.1 | 422 |
| 39 | Cancer epigenomics: beyond genomics. <i>Current Opinion in Genetics and Development</i> , 2012, 22, 50-55. | 1.5 | 421 |
| 40 | The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149. | 13.5 | 404 |
| 41 | Cis-acting noncoding RNAs: friends and foes. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1068-1075. | 3.6 | 384 |
| 42 | DNA methylation-based prognosis and epidrivers in hepatocellular carcinoma. <i>Hepatology</i> , 2015, 61, 1945-1956. | 3.6 | 367 |
| 43 | DNA Methylation: A Profile of Methods and Applications. <i>BioTechniques</i> , 2002, 33, 632-649. | 0.8 | 359 |
| 44 | Epigenetic profiling to classify cancer of unknown primary: a multicentre, retrospective analysis. <i>Lancet Oncology</i> , The, 2016, 17, 1386-1395. | 5.1 | 357 |
| 45 | A TARBP2 mutation in human cancer impairs microRNA processing and DICER1 function. <i>Nature Genetics</i> , 2009, 41, 365-370. | 9.4 | 355 |
| 46 | DNA methylation contributes to natural human variation. <i>Genome Research</i> , 2013, 23, 1363-1372. | 2.4 | 353 |
| 47 | Clinical epigenetics: seizing opportunities for translation. <i>Nature Reviews Genetics</i> , 2019, 20, 109-127. | 7.7 | 353 |
| 48 | A DNA methylation fingerprint of 1628 human samples. <i>Genome Research</i> , 2012, 22, 407-419. | 2.4 | 341 |
| 49 | A Role for RNAi in the Selective Correction of DNA Methylation Defects. <i>Science</i> , 2009, 323, 1600-1604. | 6.0 | 338 |
| 50 | BLUEPRINT to decode the epigenetic signature written in blood. <i>Nature Biotechnology</i> , 2012, 30, 224-226. | 9.4 | 323 |
| 51 | Role of the RB1 family in stabilizing histone methylation at constitutive heterochromatin. <i>Nature Cell Biology</i> , 2005, 7, 420-428. | 4.6 | 314 |
| 52 | Genome-wide parent-of-origin DNA methylation analysis reveals the intricacies of human imprinting and suggests a germline methylation-independent mechanism of establishment. <i>Genome Research</i> , 2014, 24, 554-569. | 2.4 | 311 |
| 53 | A Genetic Defect in Exportin-5 Traps Precursor MicroRNAs in the Nucleus of Cancer Cells. <i>Cancer Cell</i> , 2010, 18, 303-315. | 7.7 | 299 |
| 54 | Methyl-CpG binding proteins identify novel sites of epigenetic inactivation in human cancer. <i>EMBO Journal</i> , 2003, 22, 6335-6345. | 3.5 | 294 |

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|----|--|-----|-----------|
| 55 | Relevance of DNA methylation in the management of cancer. <i>Lancet Oncology</i> , The, 2003, 4, 351-358. | 5.1 | 293 |
| 56 | Generating mutations but providing chemosensitivity: the role of O6-methylguanine DNA methyltransferase in human cancer. <i>Oncogene</i> , 2004, 23, 1-8. | 2.6 | 289 |
| 57 | Chromosomal Instability Correlates with Genome-wide DNA Demethylation in Human Primary Colorectal Cancers. <i>Cancer Research</i> , 2006, 66, 8462-9468. | 0.4 | 286 |
| 58 | SOCS-1, a negative regulator of cytokine signaling, is frequently silenced by methylation in multiple myeloma. <i>Blood</i> , 2003, 101, 2784-2788. | 0.6 | 285 |
| 59 | DNA methylomes, histone codes and miRNAs: Tying it all together. <i>International Journal of Biochemistry and Cell Biology</i> , 2009, 41, 87-95. | 1.2 | 283 |
| 60 | hMLH1 Promoter Hypermethylation Is an Early Event in Human Endometrial Tumorigenesis. <i>American Journal of Pathology</i> , 1999, 155, 1767-1772. | 1.9 | 280 |
| 61 | DNA Methylation Polymorphisms Precede Any Histological Sign of Atherosclerosis in Mice Lacking Apolipoprotein E. <i>Journal of Biological Chemistry</i> , 2004, 279, 29147-29154. | 1.6 | 279 |
| 62 | Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. <i>Nature Biotechnology</i> , 2016, 34, 726-737. | 9.4 | 270 |
| 63 | Dysregulation of microRNAs in cancer: Playing with fire. <i>FEBS Letters</i> , 2011, 585, 2087-2099. | 1.3 | 264 |
| 64 | DNA methylation loss promotes immune evasion of tumours with high mutation and copy number load. <i>Nature Communications</i> , 2019, 10, 4278. | 5.8 | 263 |
| 65 | Loss of the glycine N-methyltransferase gene leads to steatosis and hepatocellular carcinoma in mice. <i>Hepatology</i> , 2008, 47, 1191-1199. | 3.6 | 262 |
| 66 | Hypermethylation of the DNA Repair Gene O6-Methylguanine DNA Methyltransferase and Survival of Patients With Diffuse Large B-Cell Lymphoma. <i>Journal of the National Cancer Institute</i> , 2002, 94, 26-32. | 3.0 | 261 |
| 67 | Tumor Cell-Specific BRCA1 and RASSF1A Hypermethylation in Serum, Plasma, and Peritoneal Fluid from Ovarian Cancer Patients. <i>Cancer Research</i> , 2004, 64, 6476-6481. | 0.4 | 259 |
| 68 | A truncating mutation of HDAC2 in human cancers confers resistance to histone deacetylase inhibition. <i>Nature Genetics</i> , 2006, 38, 566-569. | 9.4 | 254 |
| 69 | Abnormalities of the APC/β-catenin pathway in endometrial cancer. <i>Oncogene</i> , 2002, 21, 7981-7990. | 2.6 | 252 |
| 70 | A Prognostic DNA Methylation Signature for Stage I Non-Small-Cell Lung Cancer. <i>Journal of Clinical Oncology</i> , 2013, 31, 4140-4147. | 0.8 | 250 |
| 71 | Histone deacetylase inhibitors: Understanding a new wave of anticancer agents. <i>International Journal of Cancer</i> , 2004, 112, 171-178. | 2.3 | 241 |
| 72 | Epigenetic inactivation of the premature aging Werner syndrome gene in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8822-8827. | 3.3 | 240 |

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|----|---|-----|-----------|
| 73 | Bromodomain inhibitors and cancer therapy: From structures to applications. <i>Epigenetics</i> , 2017, 12, 323-339. | 1.3 | 239 |
| 74 | Tumor-Related Molecular Mechanisms of Oxaliplatin Resistance. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 1767-1776. | 1.9 | 237 |
| 75 | Sarcoma classification by DNA methylation profiling. <i>Nature Communications</i> , 2021, 12, 498. | 5.8 | 237 |
| 76 | GATA-4 and GATA-5 Transcription Factor Genes and Potential Downstream Antitumor Target Genes Are Epigenetically Silenced in Colorectal and Gastric Cancer. <i>Molecular and Cellular Biology</i> , 2003, 23, 8429-8439. | 1.1 | 234 |
| 77 | RNA-RNA interactions in gene regulation: the coding and noncoding players. <i>Trends in Biochemical Sciences</i> , 2015, 40, 248-256. | 3.7 | 230 |
| 78 | Small molecule enoxacin is a cancer-specific growth inhibitor that acts by enhancing TAR RNA-binding protein 2-mediated microRNA processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4394-4399. | 3.3 | 222 |
| 79 | Cross-Talk between Aging and Cancer: The Epigenetic Language. <i>Annals of the New York Academy of Sciences</i> , 2007, 1100, 60-74. | 1.8 | 221 |
| 80 | The dynamic DNA methylomes of double-stranded DNA viruses associated with human cancer. <i>Genome Research</i> , 2009, 19, 438-451. | 2.4 | 218 |
| 81 | Genetic analysis of p38 MAP kinases in myogenesis: fundamental role of p38 β in abrogating myoblast proliferation. <i>EMBO Journal</i> , 2007, 26, 1245-1256. | 3.5 | 217 |
| 82 | Genomic DNA hypomethylation as a biomarker for bladder cancer susceptibility in the Spanish Bladder Cancer Study: a case-control study. <i>Lancet Oncology</i> , The, 2008, 9, 359-366. | 5.1 | 211 |
| 83 | DNA Methylation Map of Human Atherosclerosis. <i>Circulation: Cardiovascular Genetics</i> , 2014, 7, 692-700. | 5.1 | 207 |
| 84 | The Epigenetic Face of Systemic Lupus Erythematosus. <i>Journal of Immunology</i> , 2006, 176, 7143-7147. | 0.4 | 203 |
| 85 | The affinity of different MBD proteins for a specific methylated locus depends on their intrinsic binding properties. <i>Nucleic Acids Research</i> , 2003, 31, 1765-1774. | 6.5 | 202 |
| 86 | Lung cancer epigenetics: From knowledge to applications. <i>Seminars in Cancer Biology</i> , 2018, 51, 116-128. | 4.3 | 202 |
| 87 | Heterozygous disruption of Hic1 predisposes mice to a gender-dependent spectrum of malignant tumors. <i>Nature Genetics</i> , 2003, 33, 197-202. | 9.4 | 200 |
| 88 | Allele-specific histone lysine methylation marks regulatory regions at imprinted mouse genes. <i>EMBO Journal</i> , 2002, 21, 6560-6570. | 3.5 | 198 |
| 89 | Epigenetic biomarkers for human cancer: The time is now. <i>Critical Reviews in Oncology/Hematology</i> , 2008, 68, 1-11. | 2.0 | 197 |
| 90 | Head-to-head antisense transcription and R-loop formation promotes transcriptional activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5785-5790. | 3.3 | 194 |

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|-----|--|------|-----------|
| 91 | A Mouse Skin Multistage Carcinogenesis Model Reflects the Aberrant DNA Methylation Patterns of Human Tumors. <i>Cancer Research</i> , 2004, 64, 5527-5534. | 0.4 | 193 |
| 92 | Epigenetic inactivation of the Sotos overgrowth syndrome gene histone methyltransferase NSD1 in human neuroblastoma and glioma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21830-21835. | 3.3 | 190 |
| 93 | Discovery of methylated circulating DNA biomarkers for comprehensive non-invasive monitoring of treatment response in metastatic colorectal cancer. <i>Gut</i> , 2018, 67, 1995-2005. | 6.1 | 188 |
| 94 | Epigenetic and genetic alterations of APC and CDH1 genes in lobular breast cancer: Relationships with abnormal E-cadherin and catenin expression and microsatellite instability. <i>International Journal of Cancer</i> , 2003, 106, 208-215. | 2.3 | 186 |
| 95 | Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016, 17, 11. | 3.8 | 184 |
| 96 | The Epigenetic Basis of Twin Discordance in Age-Related Diseases. <i>Pediatric Research</i> , 2007, 61, 38R-42R. | 1.1 | 183 |
| 97 | Point mutation and homozygous deletion of PTEN/MMAC1 in primary bladder cancers. <i>Oncogene</i> , 1998, 16, 3215-3218. | 2.6 | 175 |
| 98 | Methyl-DNA immunoprecipitation (MeDIP): Hunting down the DNA methylome. <i>BioTechniques</i> , 2008, 44, 35-43. | 0.8 | 175 |
| 99 | Epigenetic inactivation of LKB1 in primary tumors associated with the Peutz-Jeghers syndrome. <i>Oncogene</i> , 2000, 19, 164-168. | 2.6 | 171 |
| 100 | Human DNA Methyltransferase 1 Is Required for Maintenance of the Histone H3 Modification Pattern. <i>Journal of Biological Chemistry</i> , 2004, 279, 37175-37184. | 1.6 | 171 |
| 101 | Genome-Wide Analysis of DNA Methylation Differences in Muscle and Fat from Monozygotic Twins Discordant for Type 2 Diabetes. <i>PLoS ONE</i> , 2012, 7, e51302. | 1.1 | 171 |
| 102 | Breast Cancer Epigenetics: From DNA Methylation to microRNAs. <i>Journal of Mammary Gland Biology and Neoplasia</i> , 2010, 15, 5-17. | 1.0 | 167 |
| 103 | Epigenetic alterations involved in cancer stem cell reprogramming. <i>Molecular Oncology</i> , 2012, 6, 620-636. | 2.1 | 167 |
| 104 | An Adenine Code for DNA: A Second Life for N6-Methyladenine. <i>Cell</i> , 2015, 161, 710-713. | 13.5 | 167 |
| 105 | Epigenetic prediction of response to anti-PD-1 treatment in non-small-cell lung cancer: a multicentre, retrospective analysis. <i>Lancet Respiratory Medicine</i> , 2018, 6, 771-781. | 5.2 | 167 |
| 106 | The Wnt antagonist DICKKOPF-1 gene is induced by 1 α ,25-dihydroxyvitamin D3 associated to the differentiation of human colon cancer cells. <i>Carcinogenesis</i> , 2007, 28, 1877-1884. | 1.3 | 166 |
| 107 | E47 phosphorylation by p38 MAPK promotes MyoD/E47 association and muscle-specific gene transcription. <i>EMBO Journal</i> , 2005, 24, 974-984. | 3.5 | 165 |
| 108 | Epigenetic Inactivation of the Circadian Clock Gene <i>BMAL1</i> in Hematologic Malignancies. <i>Cancer Research</i> , 2009, 69, 8447-8454. | 0.4 | 161 |

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|-----|---|-----|-----------|
| 109 | DNA methylation and cancer therapy: new developments and expectations. <i>Current Opinion in Oncology</i> , 2005, 17, 55-60. | 1.1 | 159 |
| 110 | Intronic RNAs mediate EZH2 regulation of epigenetic targets. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 664-670. | 3.6 | 159 |
| 111 | Mechanisms of Therapy Resistance in Patient-Derived Xenograft Models of BRCA1-Deficient Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2016, 108, djw148. | 3.0 | 157 |
| 112 | A DNA methylation-based definition of biologically distinct breast cancer subtypes. <i>Molecular Oncology</i> , 2015, 9, 555-568. | 2.1 | 156 |
| 113 | A microarray-based DNA methylation study of glioblastoma multiforme. <i>Epigenetics</i> , 2009, 4, 255-264. | 1.3 | 155 |
| 114 | EMP3, a Myelin-Related Gene Located in the Critical 19q13.3 Region, Is Epigenetically Silenced and Exhibits Features of a Candidate Tumor Suppressor in Glioma and Neuroblastoma. <i>Cancer Research</i> , 2005, 65, 2565-2571. | 0.4 | 154 |
| 115 | Sirtuin 1 regulation of developmental genes during differentiation of stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 13736-13741. | 3.3 | 154 |
| 116 | <i>BRCA1</i> CpG Island Hypermethylation Predicts Sensitivity to Poly(Adenosine Diphosphate)- Ribose Polymerase Inhibitors. <i>Journal of Clinical Oncology</i> , 2010, 28, e563-e564. | 0.8 | 152 |
| 117 | Towards the Human Cancer Epigenome: A First Draft of Histone Modifications. <i>Cell Cycle</i> , 2005, 4, 1377-1381. | 1.3 | 149 |
| 118 | The necessity of a human epigenome project. <i>Carcinogenesis</i> , 2006, 27, 1121-1125. | 1.3 | 149 |
| 119 | Genome-wide profiling of p53-regulated enhancer RNAs uncovers a subset of enhancers controlled by a lncRNA. <i>Nature Communications</i> , 2015, 6, 6520. | 5.8 | 149 |
| 120 | CSL-MAML-dependent Notch1 signaling controls T lineage-specific IL-7R α gene expression in early human thymopoiesis and leukemia. <i>Journal of Experimental Medicine</i> , 2009, 206, 779-791. | 4.2 | 145 |
| 121 | How epigenetics can explain human metastasis: A new role for microRNAs. <i>Cell Cycle</i> , 2009, 8, 377-382. | 1.3 | 143 |
| 122 | Whole-Exome Sequencing Identifies MDH2 as a New Familial Paraganglioma Gene. <i>Journal of the National Cancer Institute</i> , 2015, 107, . | 3.0 | 143 |
| 123 | High-performance capillary electrophoretic method for the quantification of 5-methyl 2'-deoxycytidine in genomic DNA: Application to plant, animal and human cancer tissues. <i>Electrophoresis</i> , 2002, 23, 1677. | 1.3 | 142 |
| 124 | Genetic syndromes caused by mutations in epigenetic genes. <i>Human Genetics</i> , 2013, 132, 359-383. | 1.8 | 141 |
| 125 | A CpG island hypermethylation profile of primary colorectal carcinomas and colon cancer cell lines. <i>Molecular Cancer</i> , 2004, 3, 28. | 7.9 | 140 |
| 126 | Epigenetic inactivation of the p53-induced long noncoding RNA TP53 target 1 in human cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7535-E7544. | 3.3 | 140 |

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|-----|---|------|-----------|
| 127 | Differential DNA hypermethylation and hypomethylation signatures in colorectal cancer. <i>Human Molecular Genetics</i> , 2005, 14, 319-326. | 1.4 | 138 |
| 128 | MGMT hypermethylation: A prognostic foe, a predictive friend. <i>DNA Repair</i> , 2007, 6, 1155-1160. | 1.3 | 138 |
| 129 | Characterization of 8p21.3 chromosomal deletions in B-cell lymphoma: TRAIL-R1 and TRAIL-R2 as candidate dosage-dependent tumor suppressor genes. <i>Blood</i> , 2005, 106, 3214-3222. | 0.6 | 137 |
| 130 | Regulation of pri-miRNA Processing by a Long Noncoding RNA Transcribed from an Ultraconserved Region. <i>Molecular Cell</i> , 2014, 55, 138-147. | 4.5 | 137 |
| 131 | Human DNA methylomes of neurodegenerative diseases show common epigenomic patterns. <i>Translational Psychiatry</i> , 2016, 6, e718-e718. | 2.4 | 137 |
| 132 | Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , 2014, 512, 87-90. | 13.7 | 136 |
| 133 | DNA methylation profiling in breast cancer discordant identical twins identifies DOK7 as novel epigenetic biomarker. <i>Carcinogenesis</i> , 2013, 34, 102-108. | 1.3 | 135 |
| 134 | New insights into the biology and origin of mature aggressive B-cell lymphomas by combined epigenomic, genomic, and transcriptional profiling. <i>Blood</i> , 2009, 113, 2488-2497. | 0.6 | 133 |
| 135 | The Contribution of Epigenetics to Cancer Immunotherapy. <i>Trends in Immunology</i> , 2020, 41, 676-691. | 2.9 | 133 |
| 136 | The Epitranscriptome of Noncoding RNAs in Cancer. <i>Cancer Discovery</i> , 2017, 7, 359-368. | 7.7 | 132 |
| 137 | DNA methylation map of mouse and human brain identifies target genes in Alzheimer's disease. <i>Brain</i> , 2013, 136, 3018-3027. | 3.7 | 129 |
| 138 | Epigenetic disruption of ribosomal RNA genes and nucleolar architecture in DNA methyltransferase 1 (Dnmt1) deficient cells. <i>Nucleic Acids Research</i> , 2007, 35, 2191-2198. | 6.5 | 128 |
| 139 | Normative Data on Angular Vestibulo-Ocular Responses in the Yaw Axis Measured Using the Video Head Impulse Test. <i>Otology and Neurotology</i> , 2015, 36, 466-471. | 0.7 | 128 |
| 140 | Disrupted microRNA expression caused by Mecp2 loss in a mouse model of Rett syndrome. <i>Epigenetics</i> , 2010, 5, 656-663. | 1.3 | 125 |
| 141 | A mutation in the POT1 gene is responsible for cardiac angiosarcoma in TP53-negative Li-Fraumeni-like families. <i>Nature Communications</i> , 2015, 6, 8383. | 5.8 | 124 |
| 142 | Mutator pathways unleashed by epigenetic silencing in human cancer. <i>Mutagenesis</i> , 2007, 22, 247-253. | 1.0 | 123 |
| 143 | Identification of inflammatory mediators in patients with Crohn's disease unresponsive to anti-TNF α therapy. <i>Gut</i> , 2015, 64, 233-242. | 6.1 | 123 |
| 144 | IL-4 orchestrates STAT6-mediated DNA demethylation leading to dendritic cell differentiation. <i>Genome Biology</i> , 2016, 17, 4. | 3.8 | 122 |

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|-----|---|-----|-----------|
| 145 | Abnormalities of E- and P-cadherin and catenin (β -, γ -catenin, and p120 ^{ctn}) expression in endometrial cancer and endometrial atypical hyperplasia. <i>Journal of Pathology</i> , 2003, 199, 471-478. | 2.1 | 121 |
| 146 | MicroRNAs and cancer epigenetics: a macrorevolution. <i>Current Opinion in Oncology</i> , 2010, 22, 35-45. | 1.1 | 121 |
| 147 | Profiling aberrant DNA methylation in hematologic neoplasms: a view from the tip of the iceberg. <i>Clinical Immunology</i> , 2003, 109, 80-88. | 1.4 | 120 |
| 148 | Epigenetic inactivation of the putative DNA/RNA helicase SLFN11 in human cancer confers resistance to platinum drugs. <i>Oncotarget</i> , 2016, 7, 3084-3097. | 0.8 | 120 |
| 149 | Clustering of Gene Hypermethylation Associated With Clinical Risk Groups in Neuroblastoma. <i>Journal of the National Cancer Institute</i> , 2004, 96, 1208-1219. | 3.0 | 119 |
| 150 | Inactivation of the Lamin A/C Gene by CpG Island Promoter Hypermethylation in Hematologic Malignancies, and Its Association With Poor Survival in Nodal Diffuse Large B-Cell Lymphoma. <i>Journal of Clinical Oncology</i> , 2005, 23, 3940-3947. | 0.8 | 119 |
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