

Keith D Robertson

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

13,467
citations

30551

56
h-index

35168

102
g-index

118
all docs

118
docs citations

118
times ranked

20543
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Interferon drives HCV scarring of the epigenome and creates targetable vulnerabilities following viral clearance. <i>Hepatology</i> , 2022, 75, 983-996. | 3.6 | 15 |
| 2 | Oncogenic gene expression and epigenetic remodeling of cis-regulatory elements in ASXL1-mutant chronic myelomonocytic leukemia. <i>Nature Communications</i> , 2022, 13, 1434. | 5.8 | 17 |
| 3 | SHP2 inhibition enhances Yes-associated protein-mediated liver regeneration in murine partial hepatectomy models. <i>JCI Insight</i> , 2022, 7, . | 2.3 | 5 |
| 4 | CpGtools: a python package for DNA methylation analysis. <i>Bioinformatics</i> , 2021, 37, 1598-1599. | 1.8 | 19 |
| 5 | Identification of DNA methylation signatures associated with poor outcome in lower-risk Stage, Size, Grade and Necrosis (SSIGN) score clear cell renal cell cancer. <i>Clinical Epigenetics</i> , 2021, 13, 12. | 1.8 | 8 |
| 6 | Distinguishing Active Versus Passive Using Illumina MethylationEPIC BeadChip Microarrays. <i>Methods in Molecular Biology</i> , 2021, 2272, 97-140. | 0.4 | 1 |
| 7 | Lipid-induced endothelial vascular cell adhesion molecule 1 promotes nonalcoholic steatohepatitis pathogenesis. <i>Journal of Clinical Investigation</i> , 2021, 131, . | 3.9 | 56 |
| 8 | RAS mutations drive proliferative chronic myelomonocytic leukemia via a KMT2A-PLK1 axis. <i>Nature Communications</i> , 2021, 12, 2901. | 5.8 | 44 |
| 9 | Plasma Cell-Free DNA Methylomics of Bipolar Disorder With and Without Rapid Cycling. <i>Frontiers in Neuroscience</i> , 2021, 15, 774037. | 1.4 | 4 |
| 10 | Clinical, molecular, and prognostic correlates of number, type, and functional localization of TET2 mutations in chronic myelomonocytic leukemia (CMML)â€”a study of 1084 patients. <i>Leukemia</i> , 2020, 34, 1407-1421. | 3.3 | 68 |
| 11 | The role of survivin in the progression of pancreatic ductal adenocarcinoma (PDAC) and a novel survivin-targeted therapeutic for PDAC. <i>PLoS ONE</i> , 2020, 15, e0226917. | 1.1 | 18 |
| 12 | Title is missing!. , 2020, 15, e0226917. | | 0 |
| 13 | Title is missing!. , 2020, 15, e0226917. | | 0 |
| 14 | Title is missing!. , 2020, 15, e0226917. | | 0 |
| 15 | Title is missing!. , 2020, 15, e0226917. | | 0 |
| 16 | Loss of SETD2 Induces a Metabolic Switch in Renal Cell Carcinoma Cell Lines toward Enhanced Oxidative Phosphorylation. <i>Journal of Proteome Research</i> , 2019, 18, 331-340. | 1.8 | 27 |
| 17 | Integrating the Epigenome to Identify Drivers of Hepatocellular Carcinoma. <i>Hepatology</i> , 2019, 69, 639-652. | 3.6 | 73 |
| 18 | Genome-wide DNA methylomic differences between dorsolateral prefrontal and temporal pole cortices of bipolar disorder. <i>Journal of Psychiatric Research</i> , 2019, 117, 45-54. | 1.5 | 24 |

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|----|---|-----|-----------|
| 19 | In silico DNA methylation analysis identifies potential prognostic biomarkers in type 2 papillary renal cell carcinoma. <i>Cancer Medicine</i> , 2019, 8, 5760-5768. | 1.3 | 8 |
| 20 | DNA methylation of individual repetitive elements in hepatitis C virus infection-induced hepatocellular carcinoma. <i>Clinical Epigenetics</i> , 2019, 11, 145. | 1.8 | 31 |
| 21 | Genome-wide discovery and validation of diagnostic DNA methylation-based biomarkers for hepatocellular cancer detection in circulating cell free DNA. <i>Theranostics</i> , 2019, 9, 7239-7250. | 4.6 | 59 |
| 22 | Alpha α 1 Antitrypsin Deficiency Liver Disease, Mutational Homogeneity Modulated by Epigenetic Heterogeneity With Links to Obesity. <i>Hepatology</i> , 2019, 70, 51-66. | 3.6 | 26 |
| 23 | Enhanced and controlled chromatin extraction from FFPE tissues and the application to ChIP-seq. <i>BMC Genomics</i> , 2019, 20, 249. | 1.2 | 16 |
| 24 | Phenotypic Correlates and Prognostic Outcomes of TET2 Mutations in Myelodysplastic Syndrome/Myeloproliferative Neoplasm Overlap Syndromes: A Comprehensive Study of 504 Patients. <i>Blood</i> , 2019, 134, 3005-3005. | 0.6 | 0 |
| 25 | Epigenomic Determinants of Transcriptional Activity in ASXL1-Mutant Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2019, 134, 2987-2987. | 0.6 | 0 |
| 26 | Distal Enhancer Elements in ASXL1-Mutant Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2019, 134, 2981-2981. | 0.6 | 0 |
| 27 | Clinical Categorization of Chronic Myelomonocytic Leukemia into Proliferative and Dysplastic Subtypes Correlates with Distinct Genomic, Transcriptomic and Epigenomic Signatures. <i>Blood</i> , 2019, 134, 1710-1710. | 0.6 | 0 |
| 28 | Genetic and Epigenetic Heterogeneity in Normal Liver Homeostasis and Its Implications for Liver Disease and Hepatocellular Cancer. <i>Seminars in Liver Disease</i> , 2018, 38, 041-050. | 1.8 | 25 |
| 29 | Use of the CRISPR/Cas9-based epigenetic gene activation system In Vivo: A new potential therapeutic modality. <i>Hepatology</i> , 2018, 68, 1191-1193. | 3.6 | 1 |
| 30 | Epigenetic Regulations in the Pathogenesis of HCC and the Clinical Application. <i>Molecular Pathology Library</i> , 2018, , 69-93. | 0.1 | 0 |
| 31 | DNA methylation age is accelerated in alcohol dependence. <i>Translational Psychiatry</i> , 2018, 8, 182. | 2.4 | 73 |
| 32 | A Three-pronged Epigenetic Approach to the Treatment of Hepatocellular Carcinoma. <i>Hepatology</i> , 2018, 68, 1226-1228. | 3.6 | 15 |
| 33 | Distinctive epigenomes characterize glioma stem cells and their response to differentiation cues. <i>Genome Biology</i> , 2018, 19, 43. | 3.8 | 81 |
| 34 | ZBTB24 is a transcriptional regulator that coordinates with DNMT3B to control DNA methylation. <i>Nucleic Acids Research</i> , 2018, 46, 10034-10051. | 6.5 | 45 |
| 35 | Association of Clinical Epidemiologic Exposures and Overall Survival with Genome-Wide DNA Methylation Profiles in Acute Myeloid Leukemia: Analysis of the Mayo Clinic AML Epidemiology Cohort. <i>Blood</i> , 2018, 132, 3987-3987. | 0.6 | 1 |
| 36 | Indoleamine 2,3-Dioxygenase-1 Expressing Dendritic Cell Populations Are Associated with Tumor-Induced Immune Tolerance & Aggressive Disease Biology in Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2018, 132, 4344-4344. | 0.6 | 0 |

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|----|---|------|-----------|
| 37 | CAME: identification of chromatin accessibility from nucleosome occupancy and methylome sequencing. <i>Bioinformatics</i> , 2017, 33, 1139-1146. | 1.8 | 4 |
| 38 | Initiation of aberrant DNA methylation patterns and heterogeneity in precancerous lesions of human hepatocellular cancer. <i>Epigenetics</i> , 2017, 12, 215-225. | 1.3 | 23 |
| 39 | Focal adhesion kinase inhibitor PF573228 and death receptor 5 agonist lexatumumab synergistically induce apoptosis in pancreatic carcinoma. <i>Tumor Biology</i> , 2017, 39, 101042831769912. | 0.8 | 6 |
| 40 | Misregulation of DNA Methylation Regulators in Cancer. <i>Cancer Drug Discovery and Development</i> , 2017, , 97-124. | 0.2 | 2 |
| 41 | A Novel Vaccine Targeting Glypican-3 as a Treatment for Hepatocellular Carcinoma. <i>Molecular Therapy</i> , 2017, 25, 2299-2308. | 3.7 | 21 |
| 42 | High fat diet and exercise lead to a disrupted and pathogenic DNA methylome in mouse liver. <i>Epigenetics</i> , 2017, 12, 55-69. | 1.3 | 40 |
| 43 | Purification of nanogram-range immunoprecipitated DNA in ChIP-seq application. <i>BMC Genomics</i> , 2017, 18, 985. | 1.2 | 34 |
| 44 | Nucleosome positioning changes during human embryonic stem cell differentiation. <i>Epigenetics</i> , 2016, 11, 426-437. | 1.3 | 7 |
| 45 | Targeting epigenetic pathways in acute myeloid leukemia and myelodysplastic syndrome: a systematic review of hypomethylating agents trials. <i>Clinical Epigenetics</i> , 2016, 8, 68. | 1.8 | 62 |
| 46 | Number and Type of TET2 Mutations in Chronic Myelomonocytic Leukemia: Clinical and Prognostic Correlates. <i>Blood</i> , 2016, 128, 4343-4343. | 0.6 | 1 |
| 47 | Dynamic reprogramming of DNA methylation in SETD2-deregulated renal cell carcinoma. <i>Oncotarget</i> , 2016, 7, 1927-1946. | 0.8 | 52 |
| 48 | Unique Clinical Epidemiologic Risk Factors Are Associated with Distinct Methylation Subgroups in Newly-Diagnosed Acute Myeloid Leukemia (AML). <i>Blood</i> , 2016, 128, 1719-1719. | 0.6 | 1 |
| 49 | iTagPlot: an accurate computation and interactive drawing tool for tag density plot. <i>Bioinformatics</i> , 2015, 31, 2384-2387. | 1.8 | 0 |
| 50 | Small Molecule Inhibitor YM155-Mediated Activation of Death Receptor 5 Is Crucial for Chemotherapy-Induced Apoptosis in Pancreatic Carcinoma. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 80-89. | 1.9 | 18 |
| 51 | Effects of Alcohol metabolism on Hepatocellular carcinoma progression. <i>FASEB Journal</i> , 2015, 29, . | 0.2 | 0 |
| 52 | Acute Depletion Redefines the Division of Labor among DNA Methyltransferases in Methylating the Human Genome. <i>Cell Reports</i> , 2014, 9, 1554-1566. | 2.9 | 33 |
| 53 | Distinct and overlapping control of 5-methylcytosine and 5-hydroxymethylcytosine by the TET proteins in human cancer cells. <i>Genome Biology</i> , 2014, 15, R81. | 13.9 | 91 |
| 54 | Impact of human MLL/COMPASS and polycomb complexes on the DNA methylome. <i>Oncotarget</i> , 2014, 5, 6338-6352. | 0.8 | 9 |

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|----|---|-----|-----------|
| 55 | Epigenetic signatures of alcohol abuse and hepatitis infection during human hepatocarcinogenesis. <i>Oncotarget</i> , 2014, 5, 9425-9443. | 0.8 | 78 |
| 56 | DNA Methyltransferases, DNA Damage Repair, and Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2013, 754, 3-29. | 0.8 | 361 |
| 57 | Butyrate suppresses colonic inflammation through HDAC1-dependent Fas upregulation and Fas-mediated apoptosis of T cells. <i>American Journal of Physiology - Renal Physiology</i> , 2012, 302, G1405-G1415. | 1.6 | 218 |
| 58 | Linking DNA Methyltransferases to Epigenetic Marks and Nucleosome Structure Genome-wide in Human Tumor Cells. <i>Cell Reports</i> , 2012, 2, 1411-1424. | 2.9 | 96 |
| 59 | Molecular Modeling of Inhibitors of Human DNA Methyltransferase with a Crystal Structure. <i>Advances in Protein Chemistry and Structural Biology</i> , 2012, 87, 219-247. | 1.0 | 53 |
| 60 | DNA Methylation: Superior or Subordinate in the Epigenetic Hierarchy?. <i>Genes and Cancer</i> , 2011, 2, 607-617. | 0.6 | 564 |
| 61 | DNA Methylation Suppresses Expression of the Urea Cycle Enzyme Carbamoyl Phosphate Synthetase 1 (CPS1) in Human Hepatocellular Carcinoma. <i>American Journal of Pathology</i> , 2011, 178, 652-661. | 1.9 | 95 |
| 62 | SIRT1 Deacetylates the DNA Methyltransferase 1 (DNMT1) Protein and Alters Its Activities. <i>Molecular and Cellular Biology</i> , 2011, 31, 4720-4734. | 1.1 | 178 |
| 63 | The transglutaminase 2 gene is aberrantly hypermethylated in glioma. <i>Journal of Neuro-Oncology</i> , 2011, 101, 429-440. | 1.4 | 38 |
| 64 | Epigenetic mechanisms and genome stability. <i>Clinical Epigenetics</i> , 2011, 2, 299-314. | 1.8 | 96 |
| 65 | Rapid and transient recruitment of DNMT1 to DNA double-strand breaks is mediated by its interaction with multiple components of the DNA damage response machinery. <i>Human Molecular Genetics</i> , 2011, 20, 126-140. | 1.4 | 94 |
| 66 | Modulation of Dnmt3b function in vitro by interactions with Dnmt3L, Dnmt3a and Dnmt3b splice variants. <i>Nucleic Acids Research</i> , 2011, 39, 4984-5002. | 6.5 | 67 |
| 67 | Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. <i>Nucleic Acids Research</i> , 2011, 39, e127-e127. | 6.5 | 61 |
| 68 | Verticillin A Overcomes Apoptosis Resistance in Human Colon Carcinoma through DNA Methylation-Dependent Upregulation of BNIP3. <i>Cancer Research</i> , 2011, 71, 6807-6816. | 0.4 | 52 |
| 69 | DNMT1 and DNMT3B Modulate Distinct Polycomb-Mediated Histone Modifications in Colon Cancer. <i>Cancer Research</i> , 2009, 69, 7412-7421. | 0.4 | 92 |
| 70 | DNMT3B interacts with constitutive centromere protein CENP-C to modulate DNA methylation and the histone code at centromeric regions. <i>Human Molecular Genetics</i> , 2009, 18, 3178-3193. | 1.4 | 132 |
| 71 | Comparative epigenomics of human and mouse mammary tumors. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 83-97. | 1.5 | 65 |
| 72 | Slow progressive conduction and contraction defects in loss of Nkx2-5 mice after cardiomyocyte terminal differentiation. <i>Laboratory Investigation</i> , 2009, 89, 983-993. | 1.7 | 42 |

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|----|--|-----|-----------|
| 73 | A Novel DNMT3B Splice Variant Expressed in Tumor and Pluripotent Cells Modulates Genomic DNA Methylation Patterns and Displays Altered DNA Binding. <i>Molecular Cancer Research</i> , 2009, 7, 1622-1634. | 1.5 | 78 |
| 74 | Missteps in α -tango for epigenome targeting. <i>Blood</i> , 2009, 114, 2569-2570. | 0.6 | 2 |
| 75 | Specific Loss of Histone H3 Lysine 9 Trimethylation and HP1 ³ /Cohesin Binding at D4Z4 Repeats Is Associated with Facioscapulohumeral Dystrophy (FSHD). <i>PLoS Genetics</i> , 2009, 5, e1000559. | 1.5 | 234 |
| 76 | Invasion suppressor cystatin E/M (CST6): high-level cell type-specific expression in normal brain and epigenetic silencing in gliomas. <i>Laboratory Investigation</i> , 2008, 88, 910-925. | 1.7 | 55 |
| 77 | DNA methylation in development and human disease. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 647, 30-38. | 0.4 | 222 |
| 78 | DNA methyltransferase 3B (DNMT3B) mutations in ICF syndrome lead to altered epigenetic modifications and aberrant expression of genes regulating development, neurogenesis and immune function. <i>Human Molecular Genetics</i> , 2008, 17, 690-709. | 1.4 | 216 |
| 79 | DNA Methylation Inhibitor 5-Aza-2-Deoxycytidine Induces Reversible Genome-Wide DNA Damage That Is Distinctly Influenced by DNA Methyltransferases 1 and 3B. <i>Molecular and Cellular Biology</i> , 2008, 28, 752-771. | 1.1 | 321 |
| 80 | Epigenetic Control of Tumor Suppression. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2007, 17, 295-316. | 0.4 | 34 |
| 81 | DNMT1 knockout delivers a strong blow to genome stability and cell viability. <i>Nature Genetics</i> , 2007, 39, 289-290. | 9.4 | 51 |
| 82 | The tumor suppressor Wnt inhibitory factor 1 is frequently methylated in nasopharyngeal and esophageal carcinomas. <i>Laboratory Investigation</i> , 2007, 87, 644-650. | 1.7 | 93 |
| 83 | Potential advantages of DNA methyltransferase 1 (DNMT1)-targeted inhibition for cancer therapy. <i>Journal of Molecular Medicine</i> , 2007, 85, 1137-1148. | 1.7 | 58 |
| 84 | The DNA methylation inhibitor 5-azadeoxycytidine (5-azadC) induces reversible genome-wide DNA damage that is distinctly influenced by DNA methyltransferases (DNMTs) 1 and 3B. <i>FASEB Journal</i> , 2007, 21, A660. | 0.2 | 0 |
| 85 | Histone Deacetylase Inhibitors for Cancer Therapy. <i>Epigenetics</i> , 2006, 1, 15-24. | 1.3 | 61 |
| 86 | Inactivation of Wnt inhibitory factor-1 (WIF1) expression by epigenetic silencing is a common event in breast cancer. <i>Carcinogenesis</i> , 2006, 27, 1341-1348. | 1.3 | 169 |
| 87 | Epigenomic Profiling Reveals Novel and Frequent Targets of Aberrant DNA Methylation-Mediated Silencing in Malignant Glioma. <i>Cancer Research</i> , 2006, 66, 7490-7501. | 0.4 | 153 |
| 88 | Epigenetic Silencing of the Tumor Suppressor Cystatin M Occurs during Breast Cancer Progression. <i>Cancer Research</i> , 2006, 66, 7899-7909. | 0.4 | 89 |
| 89 | An EBF3-Mediated Transcriptional Program That Induces Cell Cycle Arrest and Apoptosis. <i>Cancer Research</i> , 2006, 66, 9445-9452. | 0.4 | 64 |
| 90 | DNA methylation and human disease. <i>Nature Reviews Genetics</i> , 2005, 6, 597-610. | 7.7 | 2,449 |

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| 91 | Epigenetic Mechanisms of Gene Regulation. , 2005, , 13-30. | | 5 |
| 92 | Azacitidine Induces Demethylation of the Epstein-Barr Virus Genome in Tumors. Journal of Clinical Oncology, 2004, 22, 1373-1381. | 0.8 | 129 |
| 93 | Doxorubicin Inhibits DNMT1, Resulting in Conditional Apoptosis. Molecular Pharmacology, 2004, 66, 1415-1420. | 1.0 | 93 |
| 94 | Isolation and characterization of a novel DNA methyltransferase complex linking DNMT3B with components of the mitotic chromosome condensation machinery. Nucleic Acids Research, 2004, 32, 2716-2729. | 6.5 | 109 |
| 95 | Human DNA Methyltransferase 1 Is Required for Maintenance of the Histone H3 Modification Pattern. Journal of Biological Chemistry, 2004, 279, 37175-37184. | 1.6 | 171 |
| 96 | Modification of de novo DNA methyltransferase 3a (Dnmt3a) by SUMO-1 modulates its interaction with histone deacetylases (HDACs) and its capacity to repress transcription. Nucleic Acids Research, 2004, 32, 598-610. | 6.5 | 117 |
| 97 | Dimethyl sulfoxide stimulates the catalytic activity of de novo DNA methyltransferase 3a (Dnmt3a) in vitro. Bioorganic Chemistry, 2004, 32, 234-243. | 2.0 | 17 |
| 98 | DNMT3B interacts with hSNF2H chromatin remodeling enzyme, HDACs 1 and 2, and components of the histone methylation system. Biochemical and Biophysical Research Communications, 2004, 318, 544-555. | 1.0 | 108 |
| 99 | Effects of chromatin structure on the enzymatic and DNA binding functions of DNA methyltransferases DNMT1 and Dnmt3a in vitro. Biochemical and Biophysical Research Communications, 2004, 322, 110-118. | 1.0 | 67 |
| 100 | Stealth technology: how Epstein-Barr virus utilizes DNA methylation to cloak itself from immune detection. Clinical Immunology, 2003, 109, 53-63. | 1.4 | 84 |
| 101 | Defective de novo methylation of viral and cellular DNA sequences in ICF syndrome cells. Human Molecular Genetics, 2002, 11, 2091-2102. | 1.4 | 131 |
| 102 | Preferential Methylation of Unmethylated DNA by Mammalian de Novo DNA Methyltransferase Dnmt3a. Journal of Biological Chemistry, 2002, 277, 11735-11745. | 1.6 | 134 |
| 103 | Chromatin remodeling, histone modifications, and DNA methylation?how does it all fit together?. Journal of Cellular Biochemistry, 2002, 87, 117-125. | 1.2 | 281 |
| 104 | DNA methylation and chromatin " unraveling the tangled web. Oncogene, 2002, 21, 5361-5379. | 2.6 | 408 |
| 105 | DNA methylation, methyltransferases, and cancer. Oncogene, 2001, 20, 3139-3155. | 2.6 | 660 |
| 106 | DNMT1 forms a complex with Rb, E2F1 and HDAC1 and represses transcription from E2F-responsive promoters. Nature Genetics, 2000, 25, 338-342. | 9.4 | 884 |
| 107 | DNA methylation in health and disease. Nature Reviews Genetics, 2000, 1, 11-19. | 7.7 | 959 |
| 108 | Differential mRNA expression of the human DNA methyltransferases (DNMTs) 1, 3a and 3b during the G0/G1 to S phase transition in normal and tumor cells. Nucleic Acids Research, 2000, 28, 2108-2113. | 6.5 | 170 |

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|-----|--|-----|-----------|
| 109 | Tissue-specific alternative splicing in the human INK4a/ARF cell cycle regulatory locus. <i>Oncogene</i> , 1999, 18, 3810-3820. | 2.6 | 99 |
| 110 | DNA methylation and the Epstein-Barr virus. <i>Seminars in Cancer Biology</i> , 1999, 9, 369-375. | 4.3 | 82 |
| 111 | Methylation Status of the Epstein-Barr Virus Major Latent Promoter C in Iatrogenic B Cell Lymphoproliferative Disease. <i>American Journal of Pathology</i> , 1999, 155, 619-625. | 1.9 | 100 |
| 112 | Roles of Cell Division and Gene Transcription in the Methylation of CpG Islands. <i>Molecular and Cellular Biology</i> , 1999, 19, 6690-6698. | 1.1 | 120 |
| 113 | The Human ARF Cell Cycle Regulatory Gene Promoter Is a CpG Island Which Can Be Silenced by DNA Methylation and Down-Regulated by Wild-Type p53. <i>Molecular and Cellular Biology</i> , 1998, 18, 6457-6473. | 1.1 | 323 |
| 114 | Epstein-Barr Virus (EBV) in Endemic Burkitt's Lymphoma: Molecular Analysis of Primary Tumor Tissue. <i>Blood</i> , 1998, 91, 1373-1381. | 0.6 | 169 |
| 115 | The Epstein-Barr Virus Major Latent Promoter Qp Is Constitutively Active, Hypomethylated, and Methylation Sensitive. <i>Journal of Virology</i> , 1998, 72, 7075-7083. | 1.5 | 69 |
| 116 | Dynamic Interrelationships between DNA Replication, Methylation, and Repair. <i>American Journal of Human Genetics</i> , 1997, 61, 1220-1224. | 2.6 | 20 |
| 117 | Methylation of the Epstein-Barr Virus Genome in Normal Lymphocytes. <i>Blood</i> , 1997, 90, 4480-4484. | 0.6 | 60 |