

Keith D Robertson

List of Publications by Year in descending order

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Version: 2024-02-01

117
papers

13,467
citations

26630

56
h-index

30922

102
g-index

118
all docs

118
docs citations

118
times ranked

18587
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.	7.3	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.	12.8	17
3	SHP2 inhibition enhances Yes-associated protein-mediated liver regeneration in murine partial hepatectomy models. <i>JCI Insight</i> , 2022, 7, .	5.0	5
4	CpGtools: a python package for DNA methylation analysis. <i>Bioinformatics</i> , 2021, 37, 1598-1599.	4.1	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.	4.1	8
6	Distinguishing Active Versus Passive Using Illumina MethylationEPIC BeadChip Microarrays. <i>Methods in Molecular Biology</i> , 2021, 2272, 97-140.	0.9	1
7	Lipid-induced endothelial vascular cell adhesion molecule 1 promotes nonalcoholic steatohepatitis pathogenesis. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	56
8	RAS mutations drive proliferative chronic myelomonocytic leukemia via a KMT2A-PLK1 axis. <i>Nature Communications</i> , 2021, 12, 2901.	12.8	44
9	Plasma Cell-Free DNA Methylomics of Bipolar Disorder With and Without Rapid Cycling. <i>Frontiers in Neuroscience</i> , 2021, 15, 774037.	2.8	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.	7.2	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.	2.5	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.	3.7	27
17	Integrating the Epigenome to Identify Drivers of Hepatocellular Carcinoma. <i>Hepatology</i> , 2019, 69, 639-652.	7.3	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.	3.1	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.	2.8	8
20	DNA methylation of individual repetitive elements in hepatitis C virus infection-induced hepatocellular carcinoma. <i>Clinical Epigenetics</i> , 2019, 11, 145.	4.1	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.	10.0	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.	7.3	26
23	Enhanced and controlled chromatin extraction from FFPE tissues and the application to ChIP-seq. <i>BMC Genomics</i> , 2019, 20, 249.	2.8	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.	1.4	0
25	Epigenomic Determinants of Transcriptional Activity in ASXL1-Mutant Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2019, 134, 2987-2987.	1.4	0
26	Distal Enhancer Elements in ASXL1-Mutant Chronic Myelomonocytic Leukemia. <i>Blood</i> , 2019, 134, 2981-2981.	1.4	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.	1.4	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.	3.6	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.	7.3	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.	4.8	73
32	A Three-pronged Epigenetic Approach to the Treatment of Hepatocellular Carcinoma. <i>Hepatology</i> , 2018, 68, 1226-1228.	7.3	15
33	Distinctive epigenomes characterize glioma stem cells and their response to differentiation cues. <i>Genome Biology</i> , 2018, 19, 43.	8.8	81
34	ZBTB24 is a transcriptional regulator that coordinates with DNMT3B to control DNA methylation. <i>Nucleic Acids Research</i> , 2018, 46, 10034-10051.	14.5	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.	1.4	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.	1.4	0

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37	CAME: identification of chromatin accessibility from nucleosome occupancy and methylome sequencing. <i>Bioinformatics</i> , 2017, 33, 1139-1146.	4.1	4
38	Initiation of aberrant DNA methylation patterns and heterogeneity in precancerous lesions of human hepatocellular cancer. <i>Epigenetics</i> , 2017, 12, 215-225.	2.7	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.	1.8	6
40	Misregulation of DNA Methylation Regulators in Cancer. <i>Cancer Drug Discovery and Development</i> , 2017, , 97-124.	0.4	2
41	A Novel Vaccine Targeting Glypican-3 as a Treatment for Hepatocellular Carcinoma. <i>Molecular Therapy</i> , 2017, 25, 2299-2308.	8.2	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.	2.7	40
43	Purification of nanogram-range immunoprecipitated DNA in ChIP-seq application. <i>BMC Genomics</i> , 2017, 18, 985.	2.8	34
44	Nucleosome positioning changes during human embryonic stem cell differentiation. <i>Epigenetics</i> , 2016, 11, 426-437.	2.7	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.	4.1	62
46	Number and Type of TET2 Mutations in Chronic Myelomonocytic Leukemia: Clinical and Prognostic Correlates. <i>Blood</i> , 2016, 128, 4343-4343.	1.4	1
47	Dynamic reprogramming of DNA methylation in SETD2-deregulated renal cell carcinoma. <i>Oncotarget</i> , 2016, 7, 1927-1946.	1.8	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.	1.4	1
49	iTagPlot: an accurate computation and interactive drawing tool for tag density plot. <i>Bioinformatics</i> , 2015, 31, 2384-2387.	4.1	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.	4.1	18
51	Effects of Alcohol metabolism on Hepatocellular carcinoma progression. <i>FASEB Journal</i> , 2015, 29, .	0.5	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.	6.4	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.	9.6	91
54	Impact of human MLL/COMPASS and polycomb complexes on the DNA methylome. <i>Oncotarget</i> , 2014, 5, 6338-6352.	1.8	9

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55	Epigenetic signatures of alcohol abuse and hepatitis infection during human hepatocarcinogenesis. <i>Oncotarget</i> , 2014, 5, 9425-9443.	1.8	78
56	DNA Methyltransferases, DNA Damage Repair, and Cancer. <i>Advances in Experimental Medicine and Biology</i> , 2013, 754, 3-29.	1.6	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.	3.4	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.	6.4	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.	2.3	53
60	DNA Methylation: Superior or Subordinate in the Epigenetic Hierarchy?. <i>Genes and Cancer</i> , 2011, 2, 607-617.	1.9	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.	3.8	95
62	SIRT1 Deacetylates the DNA Methyltransferase 1 (DNMT1) Protein and Alters Its Activities. <i>Molecular and Cellular Biology</i> , 2011, 31, 4720-4734.	2.3	178
63	The transglutaminase 2 gene is aberrantly hypermethylated in glioma. <i>Journal of Neuro-Oncology</i> , 2011, 101, 429-440.	2.9	38
64	Epigenetic mechanisms and genome stability. <i>Clinical Epigenetics</i> , 2011, 2, 299-314.	4.1	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.	2.9	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.	14.5	67
67	Targeted bisulfite sequencing by solution hybrid selection and massively parallel sequencing. <i>Nucleic Acids Research</i> , 2011, 39, e127-e127.	14.5	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.	0.9	52
69	DNMT1 and DNMT3B Modulate Distinct Polycomb-Mediated Histone Modifications in Colon Cancer. <i>Cancer Research</i> , 2009, 69, 7412-7421.	0.9	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.	2.9	132
71	Comparative epigenomics of human and mouse mammary tumors. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 83-97.	2.8	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.	3.7	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.	3.4	78
74	Missteps in α -tango for epigenome targeting. <i>Blood</i> , 2009, 114, 2569-2570.	1.4	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.	3.5	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.	3.7	55
77	DNA methylation in development and human disease. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 647, 30-38.	1.0	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.	2.9	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.	2.3	321
80	Epigenetic Control of Tumor Suppression. <i>Critical Reviews in Eukaryotic Gene Expression</i> , 2007, 17, 295-316.	0.9	34
81	DNMT1 knockout delivers a strong blow to genome stability and cell viability. <i>Nature Genetics</i> , 2007, 39, 289-290.	21.4	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.	3.7	93
83	Potential advantages of DNA methyltransferase 1 (DNMT1)-targeted inhibition for cancer therapy. <i>Journal of Molecular Medicine</i> , 2007, 85, 1137-1148.	3.9	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.	0.5	0
85	Histone Deacetylase Inhibitors for Cancer Therapy. <i>Epigenetics</i> , 2006, 1, 15-24.	2.7	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.	2.8	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.	0.9	153
88	Epigenetic Silencing of the Tumor Suppressor Cystatin M Occurs during Breast Cancer Progression. <i>Cancer Research</i> , 2006, 66, 7899-7909.	0.9	89
89	An EBF3-Mediated Transcriptional Program That Induces Cell Cycle Arrest and Apoptosis. <i>Cancer Research</i> , 2006, 66, 9445-9452.	0.9	64
90	DNA methylation and human disease. <i>Nature Reviews Genetics</i> , 2005, 6, 597-610.	16.3	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.	1.6	129
93	Doxorubicin Inhibits DNMT1, Resulting in Conditional Apoptosis. Molecular Pharmacology, 2004, 66, 1415-1420.	2.3	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.	14.5	109
95	Human DNA Methyltransferase 1 Is Required for Maintenance of the Histone H3 Modification Pattern. Journal of Biological Chemistry, 2004, 279, 37175-37184.	3.4	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.	14.5	117
97	Dimethyl sulfoxide stimulates the catalytic activity of de novo DNA methyltransferase 3a (Dnmt3a) in vitro. Bioorganic Chemistry, 2004, 32, 234-243.	4.1	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.	2.1	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.	2.1	67
100	Stealth technology: how Epstein-Barr virus utilizes DNA methylation to cloak itself from immune detection. Clinical Immunology, 2003, 109, 53-63.	3.2	84
101	Defective de novo methylation of viral and cellular DNA sequences in ICF syndrome cells. Human Molecular Genetics, 2002, 11, 2091-2102.	2.9	131
102	Preferential Methylation of Unmethylated DNA by Mammalian de Novo DNA Methyltransferase Dnmt3a. Journal of Biological Chemistry, 2002, 277, 11735-11745.	3.4	134
103	Chromatin remodeling, histone modifications, and DNA methylation—how does it all fit together?. Journal of Cellular Biochemistry, 2002, 87, 117-125.	2.6	281
104	DNA methylation and chromatin — unraveling the tangled web. Oncogene, 2002, 21, 5361-5379.	5.9	408
105	DNA methylation, methyltransferases, and cancer. Oncogene, 2001, 20, 3139-3155.	5.9	660
106	DNMT1 forms a complex with Rb, E2F1 and HDAC1 and represses transcription from E2F-responsive promoters. Nature Genetics, 2000, 25, 338-342.	21.4	884
107	DNA methylation in health and disease. Nature Reviews Genetics, 2000, 1, 11-19.	16.3	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.	14.5	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.	5.9	99
110	DNA methylation and the Epstein-Barr virus. <i>Seminars in Cancer Biology</i> , 1999, 9, 369-375.	9.6	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.	3.8	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.	2.3	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.	2.3	323
114	Epstein-Barr Virus (EBV) in Endemic Burkitt's Lymphoma: Molecular Analysis of Primary Tumor Tissue. <i>Blood</i> , 1998, 91, 1373-1381.	1.4	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.	3.4	69
116	Dynamic Interrelationships between DNA Replication, Methylation, and Repair. <i>American Journal of Human Genetics</i> , 1997, 61, 1220-1224.	6.2	20
117	Methylation of the Epstein-Barr Virus Genome in Normal Lymphocytes. <i>Blood</i> , 1997, 90, 4480-4484.	1.4	60