

Zdenko Herceg

List of Publications by Year in descending order

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Version: 2024-02-01

170
papers

12,190
citations

26630

56
h-index

30087

103
g-index

177
all docs

177
docs citations

177
times ranked

19484
citing authors

#	ARTICLE	IF	CITATIONS
1	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016, 98, 680-696.	6.2	717
2	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
3	Histone acetylation by Tip60 modulates loading of repair proteins and repair of DNA double-strand breaks. <i>Nature Cell Biology</i> , 2006, 8, 91-99.	10.3	529
4	Epigenetic interplay between histone modifications and DNA methylation in gene silencing. <i>Mutation Research - Reviews in Mutation Research</i> , 2008, 659, 40-48.	5.5	515
5	Mice lacking the poly(ADP-ribose) polymerase gene are resistant to pancreatic beta-cell destruction and diabetes development induced by streptozocin. <i>Nature Medicine</i> , 1999, 5, 314-319.	30.7	348
6	Epigenetics and cancer: towards an evaluation of the impact of environmental and dietary factors. <i>Mutagenesis</i> , 2007, 22, 91-103.	2.6	307
7	Parthenolide: from plant shoots to cancer roots. <i>Drug Discovery Today</i> , 2013, 18, 894-905.	6.4	248
8	Quantitative Analysis of DNA Methylation Profiles in Lung Cancer Identifies Aberrant DNA Methylation of Specific Genes and Its Association with Gender and Cancer Risk Factors. <i>Cancer Research</i> , 2009, 69, 243-252.	0.9	231
9	Carcinogenicity of night shift work. <i>Lancet Oncology</i> , The, 2019, 20, 1058-1059.	10.7	219
10	Failure of Poly(ADP-Ribose) Polymerase Cleavage by Caspases Leads to Induction of Necrosis and Enhanced Apoptosis. <i>Molecular and Cellular Biology</i> , 1999, 19, 5124-5133.	2.3	218
11	Maternal BMI at the start of pregnancy and offspring epigenome-wide DNA methylation: findings from the pregnancy and childhood epigenetics (PACE) consortium. <i>Human Molecular Genetics</i> , 2017, 26, 4067-4085.	2.9	211
12	Genetic and epigenetic alterations as biomarkers for cancer detection, diagnosis and prognosis. <i>Molecular Oncology</i> , 2007, 1, 26-41.	4.6	206
13	Epigenetic mechanisms and cancer: An interface between the environment and the genome. <i>Epigenetics</i> , 2011, 6, 804-819.	2.7	204
14	Measuring the exposome: A powerful basis for evaluating environmental exposures and cancer risk. <i>Environmental and Molecular Mutagenesis</i> , 2013, 54, 480-499.	2.2	196
15	Tobacco smoking-associated genome-wide DNA methylation changes in the EPIC study. <i>Epigenomics</i> , 2016, 8, 599-618.	2.1	192
16	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	27.6	178
17	Hepatocellular Carcinoma Displays Distinct DNA Methylation Signatures with Potential as Clinical Predictors. <i>PLoS ONE</i> , 2010, 5, e9749.	2.5	175
18	Histone Modifications and Cancer. <i>Advances in Genetics</i> , 2010, 70, 57-85.	1.8	174

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19	Depletion of the 110-Kilodalton Isoform of Poly(ADP-Ribose) Glycohydrolase Increases Sensitivity to Genotoxic and Endotoxic Stress in Mice. <i>Molecular and Cellular Biology</i> , 2004, 24, 7163-7178.	2.3	160
20	PR-Set7-dependent lysine methylation ensures genome replication and stability through S phase. <i>Journal of Cell Biology</i> , 2007, 179, 1413-1426.	5.2	156
21	An essential function for NBS1 in the prevention of ataxia and cerebellar defects. <i>Nature Medicine</i> , 2005, 11, 538-544.	30.7	155
22	DNA methylome analysis identifies accelerated epigenetic ageing associated with postmenopausal breast cancer susceptibility. <i>European Journal of Cancer</i> , 2017, 75, 299-307.	2.8	154
23	Aberrant DNA methylation distinguishes hepatocellular carcinoma associated with HBV and HCV infection and alcohol intake. <i>Journal of Hepatology</i> , 2011, 54, 705-715.	3.7	153
24	Independent genomewide screens identify the tumor suppressor VTRNA2-1 as a human epiallele responsive to periconceptual environment. <i>Genome Biology</i> , 2015, 16, 118.	9.6	149
25	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , 2020, 43, 98-105.	8.6	145
26	Epigenetic mechanisms in hepatocellular carcinoma: How environmental factors influence the epigenome. <i>Mutation Research - Reviews in Mutation Research</i> , 2011, 727, 55-61.	5.5	144
27	Modulation of DNA methylation states and infant immune system by dietary supplementation with ̳-3 PUFA during pregnancy in an intervention study. <i>American Journal of Clinical Nutrition</i> , 2013, 98, 480-487.	4.7	142
28	Epigenetic drivers and genetic passengers on the road to cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 642, 1-13.	1.0	137
29	Disruption of Trapp causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001, 29, 206-211.	21.4	122
30	Comparisons of microRNA Patterns in Plasma before and after Tumor Removal Reveal New Biomarkers of Lung Squamous Cell Carcinoma. <i>PLoS ONE</i> , 2013, 8, e78649.	2.5	112
31	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
32	Transforming Epidemiology for 21st Century Medicine and Public Health. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013, 22, 508-516.	2.5	104
33	Human mitochondrial DNA is extensively methylated in a non-CpG context. <i>Nucleic Acids Research</i> , 2019, 47, 10072-10085.	14.5	103
34	Dietary supplementation with polyunsaturated fatty acid during pregnancy modulates DNA methylation at IGF2/H19 imprinted genes and growth of infants. <i>Physiological Genomics</i> , 2014, 46, 851-857.	2.3	101
35	Nbn heterozygosity renders mice susceptible to tumor formation and ionizing radiation-induced tumorigenesis. <i>Cancer Research</i> , 2003, 63, 7263-9.	0.9	100
36	Towards incorporating epigenetic mechanisms into carcinogen identification and evaluation. <i>Carcinogenesis</i> , 2013, 34, 1955-1967.	2.8	88

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37	Exposure to aflatoxin B ₁ in utero is associated with DNA methylation in white blood cells of infants in The Gambia. <i>International Journal of Epidemiology</i> , 2015, 44, 1238-1248.	1.9	88
38	Oxidative stress and inflammation mediate the effect of air pollution on cardiovascular disease: A prospective study in nonsmokers. <i>Environmental and Molecular Mutagenesis</i> , 2018, 59, 234-246.	2.2	88
39	Mammalian Ino80 Mediates Double-Strand Break Repair through Its Role in DNA End Strand Resection. <i>Molecular and Cellular Biology</i> , 2011, 31, 4735-4745.	2.3	85
40	Dependence receptor TrkC is a putative colon cancer tumor suppressor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3017-3022.	7.1	85
41	Oncogenic microRNAs (OncomiRs) as a new class of cancer biomarkers. <i>BioEssays</i> , 2010, 32, 894-904.	2.5	83
42	Histone acetylation and chromatin signature in stem cell identity and cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008, 637, 1-15.	1.0	77
43	DNA methylation in peripheral blood measured by LUMA is associated with breast cancer in a population-based study. <i>FASEB Journal</i> , 2012, 26, 2657-2666.	0.5	76
44	Identification of novel long non-coding RNAs deregulated in hepatocellular carcinoma using RNA-sequencing. <i>Oncotarget</i> , 2016, 7, 31862-31877.	1.8	74
45	Perturbation of metabolic pathways mediates the association of air pollutants with asthma and cardiovascular diseases. <i>Environment International</i> , 2018, 119, 334-345.	10.0	73
46	Conditional deletion of Nbs1 in murine cells reveals its role in branching repair pathways of DNA double-strand breaks. <i>EMBO Journal</i> , 2006, 25, 5527-5538.	7.8	72
47	An inducible null mutant murine model of Nijmegen breakage syndrome proves the essential function of NBS1 in chromosomal stability and cell viability. <i>Human Molecular Genetics</i> , 2004, 13, 2385-2397.	2.9	70
48	Methylome analysis reveals Jak-STAT pathway deregulation in putative breast cancer stem cells. <i>Epigenetics</i> , 2011, 6, 428-439.	2.7	70
49	The Fanconi anemia group A protein modulates homologous repair of DNA double-strand breaks in mammalian cells. <i>Carcinogenesis</i> , 2005, 26, 1731-1740.	2.8	69
50	The Transcriptional Histone Acetyltransferase Cofactor TRRAP Associates with the MRN Repair Complex and Plays a Role in DNA Double-Strand Break Repair. <i>Molecular and Cellular Biology</i> , 2006, 26, 402-412.	2.3	68
51	Unique DNA methylation signature in HPV-positive head and neck squamous cell carcinomas. <i>Genome Medicine</i> , 2017, 9, 33.	8.2	68
52	Deciphering the Epigenetic Code: An Overview of DNA Methylation Analysis Methods. <i>Antioxidants and Redox Signaling</i> , 2013, 18, 1972-1986.	5.4	66
53	Deletion of the nuclear isoform of poly(ADP-ribose) glycohydrolase (PARG) reveals its function in DNA repair, genomic stability and tumorigenesis. <i>Carcinogenesis</i> , 2010, 31, 2058-2065.	2.8	64
54	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018, 142, 874-882.	5.1	64

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55	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019, 11, 1487-1500.	2.1	64
56	Aberrant DNA Methylation Links Cancer Susceptibility Locus 15q25.1 to Apoptotic Regulation and Lung Cancer. <i>Cancer Research</i> , 2010, 70, 2779-2788.	0.9	62
57	Aberrant DNA methylation of cancer-associated genes in gastric cancer in the European Prospective Investigation into Cancer and Nutrition (EPIC“EURGAST). <i>Cancer Letters</i> , 2011, 311, 85-95.	7.2	62
58	Molecular landscape of esophageal cancer: implications for early detection and personalized therapy. <i>Annals of the New York Academy of Sciences</i> , 2018, 1434, 342-359.	3.8	56
59	Genome-Wide DNA Methylation in Peripheral Blood and Long-Term Exposure to Source-Specific Transportation Noise and Air Pollution: The SAPALDIA Study. <i>Environmental Health Perspectives</i> , 2020, 128, 67003.	6.0	56
60	Targeted deep sequencing of plasma circulating cell-free DNA reveals Vimentin and Fibulin 1 as potential epigenetic biomarkers for hepatocellular carcinoma. <i>PLoS ONE</i> , 2017, 12, e0174265.	2.5	56
61	DNA Methylation of Hepatitis B Virus (HBV) Genome Associated with the Development of Hepatocellular Carcinoma and Occult HBV Infection. <i>Journal of Infectious Diseases</i> , 2010, 202, 700-704.	4.0	55
62	DNA methylation changes associated with cancer risk factors and blood levels of vitamin metabolites in a prospective study. <i>Epigenetics</i> , 2011, 6, 195-201.	2.7	55
63	Epigenetic Information in Chromatin: the Code of Entry for DNA Repair. <i>Cell Cycle</i> , 2006, 5, 696-701.	2.6	54
64	The Impact of Air Pollution on Our Epigenome: How Far Is the Evidence? (A Systematic Review). <i>Current Environmental Health Reports</i> , 2018, 5, 544-578.	6.7	54
65	Identification of a DNA methylome signature of esophageal squamous cell carcinoma and potential epigenetic biomarkers. <i>Epigenetics</i> , 2011, 6, 1217-1227.	2.7	53
66	DNA methylation and cancer: ghosts and angels above the genes. <i>Current Opinion in Oncology</i> , 2011, 23, 69-76.	2.4	53
67	HAT cofactor Trrap regulates the mitotic checkpoint by modulation of Mad1 and Mad2 expression. <i>EMBO Journal</i> , 2004, 23, 4824-4834.	7.8	51
68	Quantitative analysis of DNA methylation after whole bisulfite amplification of a minute amount of DNA from body fluids. <i>Epigenetics</i> , 2009, 4, 221-230.	2.7	51
69	DNA Demethylating Agents and Epigenetic Therapy of Cancer. <i>Advances in Genetics</i> , 2010, 70, 327-340.	1.8	51
70	Role of a polyphenol-enriched preparation on chemoprevention of mammary carcinoma through cancer stem cells and inflammatory pathways modulation. <i>Journal of Translational Medicine</i> , 2016, 14, 13.	4.4	51
71	Noncleavable poly(ADP-ribose) polymerase-1 regulates the inflammation response in mice. <i>Journal of Clinical Investigation</i> , 2004, 114, 1072-1081.	8.2	51
72	Chromatin structure in double strand break repair. <i>DNA Repair</i> , 2013, 12, 800-810.	2.8	48

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73	Genome-wide methylation and transcriptome analysis in penile carcinoma: uncovering new molecular markers. <i>Clinical Epigenetics</i> , 2015, 7, 46.	4.1	48
74	Acute changes in DNA methylation in relation to 24h personal air pollution exposure measurements: A panel study in four European countries. <i>Environment International</i> , 2018, 120, 11-21.	10.0	48
75	Epigenetic silencing of sFRP1 activates the canonical Wnt pathway and contributes to increased cell growth and proliferation in hepatocellular carcinoma. <i>Tumor Biology</i> , 2012, 33, 325-336.	1.8	47
76	Trrap-Dependent Histone Acetylation Specifically Regulates Cell-Cycle Gene Transcription to Control Neural Progenitor Fate Decisions. <i>Cell Stem Cell</i> , 2014, 14, 632-643.	11.1	47
77	The Promises and Challenges of Toxic-Epigenomics: Environmental Chemicals and Their Impacts on the Epigenome. <i>Environmental Health Perspectives</i> , 2020, 128, 15001.	6.0	47
78	Prognostic Classifier Based on Genome-Wide DNA Methylation Profiling in Well-Differentiated Thyroid Tumors. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2017, 102, 4089-4099.	3.6	45
79	Methylation patterns in sentinel genes in peripheral blood cells of heavy smokers: Influence of cruciferous vegetables in an intervention study. <i>Epigenetics</i> , 2011, 6, 1114-1119.	2.7	43
80	Asbestos-associated genome-wide DNA methylation changes in lung cancer. <i>International Journal of Cancer</i> , 2017, 141, 2014-2029.	5.1	42
81	Socioeconomic position during pregnancy and DNA methylation signatures at three stages across early life: epigenome-wide association studies in the ALSPAC birth cohort. <i>International Journal of Epidemiology</i> , 2019, 48, 30-44.	1.9	41
82	CHRNA5 as negative regulator of nicotine signaling in normal and cancer bronchial cells: effects on motility, migration and p63 expression. <i>Carcinogenesis</i> , 2011, 32, 1388-1395.	2.8	39
83	From hepatitis to hepatocellular carcinoma: a proposed model for cross-talk between inflammation and epigenetic mechanisms. <i>Genome Medicine</i> , 2012, 4, 8.	8.2	39
84	Antagonistic and synergistic epigenetic modulation using orthologous CRISPR/dCas9-based modular system. <i>Nucleic Acids Research</i> , 2019, 47, 9637-9657.	14.5	38
85	Epigenetic silencing of HNF1A associates with changes in the composition of the human plasma N-glycome. <i>Epigenetics</i> , 2012, 7, 164-172.	2.7	37
86	Targeted deep DNA methylation analysis of circulating cell-free DNA in plasma using massively parallel semiconductor sequencing. <i>Epigenomics</i> , 2015, 7, 353-362.	2.1	36
87	Methylome Analysis and Epigenetic Changes Associated with Menarcheal Age. <i>PLoS ONE</i> , 2013, 8, e79391.	2.5	36
88	Translational Cancer Research: Balancing Prevention and Treatment to Combat Cancer Globally. <i>Journal of the National Cancer Institute</i> , 2015, 107, 1-5.	6.3	34
89	TET-Catalyzed 5-Hydroxymethylation Precedes HNF4A Promoter Choice during Differentiation of Bipotent Liver Progenitors. <i>Stem Cell Reports</i> , 2017, 9, 264-278.	4.8	34
90	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. <i>Breast Cancer Research</i> , 2019, 21, 62.	5.0	34

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91	Quantitative detection of DNA methylation states in minute amounts of DNA from body fluids. <i>Methods</i> , 2010, 52, 242-247.	3.8	32
92	Challenges and opportunities in research on early-life events/exposures and cancer development later in life. <i>Cancer Causes and Control</i> , 2012, 23, 983-990.	1.8	31
93	DNA hypermethylation is associated with invasive phenotype of malignant melanoma. <i>Experimental Dermatology</i> , 2020, 29, 39-50.	2.9	30
94	Histone Acetyltransferase Cofactor Trrap Is Essential for Maintaining the Hematopoietic Stem/Progenitor Cell Pool. <i>Journal of Immunology</i> , 2009, 183, 6422-6431.	0.8	29
95	Introduction. <i>Advances in Genetics</i> , 2010, 70, 1-23.	1.8	29
96	Inactivation of the putative suppressor gene <i>DOK1</i> by promoter hypermethylation in primary human cancers. <i>International Journal of Cancer</i> , 2012, 130, 2484-2494.	5.1	29
97	Histone deacetylase inhibitors potentiate photodynamic therapy in colon cancer cells marked by chromatin-mediated epigenetic regulation of CDKN1A. <i>Clinical Epigenetics</i> , 2017, 9, 62.	4.1	29
98	Identifying and correcting epigenetics measurements for systematic sources of variation. <i>Clinical Epigenetics</i> , 2018, 10, 38.	4.1	29
99	Shaping chromatin for repair. <i>Mutation Research - Reviews in Mutation Research</i> , 2013, 752, 45-60.	5.5	28
100	Integrative Genomics Identifies Gene Signature Associated with Melanoma Ulceration. <i>PLoS ONE</i> , 2013, 8, e54958.	2.5	28
101	Rendez-vous at Mitosis: TRRAPed in the Chromatin. <i>Cell Cycle</i> , 2005, 4, 383-387.	2.6	27
102	DNA Methylation Characteristics of Primary Melanomas with Distinct Biological Behaviour. <i>PLoS ONE</i> , 2014, 9, e96612.	2.5	27
103	Dynamic imbalance between cancer cell subpopulations induced by Transforming Growth Factor Beta (TGF- β 2) is associated with a DNA methylome switch. <i>BMC Genomics</i> , 2014, 15, 435.	2.8	27
104	Genome-Wide DNA Methylation Profiling of Esophageal Squamous Cell Carcinoma from Global High-Incidence Regions Identifies Crucial Genes and Potential Cancer Markers. <i>Cancer Research</i> , 2021, 81, 2612-2624.	0.9	27
105	Genome-wide analysis of gene expression regulated by the HAT cofactor Trrap in conditional knockout cells. <i>Nucleic Acids Research</i> , 2003, 31, 7011-7023.	14.5	25
106	Germline copy number variation of genes involved in chromatin remodelling in families suggestive of Li-Fraumeni syndrome with brain tumours. <i>European Journal of Human Genetics</i> , 2013, 21, 1369-1376.	2.8	25
107	Histone Acetyltransferase Cofactor Trrap Maintains Self-Renewal and Restricts Differentiation of Embryonic Stem Cells. <i>Stem Cells</i> , 2013, 31, 979-991.	3.2	25
108	Genome-wide profiling of normal gastric mucosa identifies <i>Helicobacter pylori</i> - and cancer-associated DNA methylome changes. <i>International Journal of Cancer</i> , 2018, 143, 597-609.	5.1	25

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109	A multi-omic analysis of birthweight in newborn cord blood reveals new underlying mechanisms related to cholesterol metabolism. <i>Metabolism: Clinical and Experimental</i> , 2020, 110, 154292.	3.4	25
110	Aberrant DNA methylation of imprinted loci in hepatocellular carcinoma and after in vitro exposure to common risk factors. <i>Clinical Epigenetics</i> , 2015, 7, 15.	4.1	24
111	Meta-analysis of epigenome-wide association studies in newborns and children show widespread sex differences in blood DNA methylation. <i>Mutation Research - Reviews in Mutation Research</i> , 2022, 789, 108415.	5.5	24
112	Intensity-dependent constitutional MLH1 promoter methylation leads to early onset of colorectal cancer by affecting both alleles. <i>Genes Chromosomes and Cancer</i> , 2011, 50, 178-185.	2.8	23
113	Characterising the epigenome as a key component of the fetal exposome in evaluating in utero exposures and childhood cancer risk. <i>Mutagenesis</i> , 2015, 30, 733-742.	2.6	23
114	Viral driven epigenetic events alter the expression of cancer-related genes in Epstein-Barr-virus naturally infected Burkitt lymphoma cell lines. <i>Scientific Reports</i> , 2017, 7, 5852.	3.3	22
115	DNA methylation changes associated with risk factors in tumors of the upper aerodigestive tract. <i>Epigenetics</i> , 2012, 7, 270-277.	2.7	21
116	Inhibition of DNA methylation promotes breast tumor sensitivity to netrin-1 interference. <i>EMBO Molecular Medicine</i> , 2016, 8, 863-877.	6.9	21
117	Epigenetic Mechanisms as an Interface Between the Environment and Genome. <i>Advances in Experimental Medicine and Biology</i> , 2016, 903, 3-15.	1.6	21
118	DNA Methylome Marks of Exposure to Particulate Matter at Three Time Points in Early Life. <i>Environmental Science & Technology</i> , 2018, 52, 5427-5437.	10.0	21
119	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018, 24, 581-591.	7.0	21
120	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. <i>Clinical Epigenetics</i> , 2019, 11, 66.	4.1	21
121	Detection of cancer-specific epigenomic changes in biofluids: Powerful tools in biomarker discovery and application. <i>Molecular Oncology</i> , 2012, 6, 704-715.	4.6	20
122	Pan-cancer multi-omics analysis and orthogonal experimental assessment of epigenetic driver genes. <i>Genome Research</i> , 2020, 30, 1517-1532.	5.5	20
123	Identification of novel dysregulated circular RNAs in early-stage breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 3912-3921.	3.6	20
124	Epigenetic signatures in stem cells and cancer stem cells. <i>Epigenomics</i> , 2009, 1, 261-280.	2.1	19
125	The epigenome and cancer prevention: A complex story of dietary supplementation. <i>Cancer Letters</i> , 2014, 342, 275-284.	7.2	19
126	The International Childhood Cancer Cohort Consortium (I4C): A research platform of prospective cohorts for studying the aetiology of childhood cancers. <i>Paediatric and Perinatal Epidemiology</i> , 2018, 32, 568-583.	1.7	19

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127	Arguments to Support a Viral Origin of Oral Squamous Cell Carcinoma in Non-Smoker and Non-Drinker Patients. <i>Frontiers in Oncology</i> , 2020, 10, 822.	2.8	19
128	Epigenetic signatures in cancer: Implications for the control of cancer in the clinic. <i>Current Opinion in Molecular Therapeutics</i> , 2010, 12, 316-24.	2.8	18
129	Transcriptional Regulation of the Human Tumor Suppressor <i>DOK1</i> by E2F1. <i>Molecular and Cellular Biology</i> , 2012, 32, 4877-4890.	2.3	17
130	Epstein-Barr Virus Down-Regulates Tumor Suppressor <i>DOK1</i> Expression. <i>PLoS Pathogens</i> , 2014, 10, e1004125.	4.7	17
131	Interplay between the Epigenetic Enzyme Lysine (K)-Specific Demethylase 2B and Epstein-Barr Virus Infection. <i>Journal of Virology</i> , 2019, 93, .	3.4	17
132	HAT cofactor TRRAP mediates β -Catenin ubiquitination on the chromatin and the regulation of the canonical Wnt pathway. <i>Cell Cycle</i> , 2008, 7, 3908-3914.	2.6	16
133	Lowly methylated region analysis identifies EBF1 as a potential epigenetic modifier in breast cancer. <i>Epigenetics</i> , 2017, 12, 964-972.	2.7	16
134	TFF1 hypermethylation and decreased expression in esophageal squamous cell carcinoma and histologically normal tumor surrounding esophageal cells. <i>Clinical Epigenetics</i> , 2017, 9, 130.	4.1	15
135	Loss of histone acetyltransferase cofactor transformation/transcription domain-associated protein impairs liver regeneration after toxic injury. <i>Hepatology</i> , 2011, 53, 954-963.	7.3	14
136	Evaluation of DNA Methylation Changes and Micronuclei in Workers Exposed to a Construction Environment. <i>International Journal of Environmental Research and Public Health</i> , 2019, 16, 902.	2.6	14
137	Developmental and transplacental genotoxicology: Fluconazole. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2008, 657, 43-47.	1.7	12
138	Transposable hypomethylation is associated with metastatic capacity of primary melanomas. <i>International Journal of Clinical and Experimental Pathology</i> , 2013, 6, 2943-8.	0.5	12
139	HBV protein as a double-barrel shot-gun targets epigenetic landscape in liver cancer. <i>Journal of Hepatology</i> , 2009, 50, 252-255.	3.7	10
140	New concepts of old epigenetic phenomena and their implications for selecting specific cell populations for epigenomic research. <i>Epigenomics</i> , 2011, 3, 383-386.	2.1	10
141	The association between birth order and childhood leukemia may be modified by paternal age and birth weight. Pooled results from the International Childhood Cancer Cohort Consortium (I4C). <i>International Journal of Cancer</i> , 2019, 144, 26-33.	5.1	10
142	Update on hepatocellular carcinoma breakthroughs: Poly(ADP-ribose) polymerase inhibitors as a promising therapeutic strategy. <i>Clinics and Research in Hepatology and Gastroenterology</i> , 2014, 38, 137-142.	1.5	9
143	Genomic responses to hepatitis B virus (HBV) infection in primary human hepatocytes. <i>Oncotarget</i> , 2015, 6, 44877-44891.	1.8	9
144	Epigenetic information in chromatin and cancer. <i>European Journal of Cancer</i> , 2009, 45, 442-444.	2.8	8

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145	Epigenetic remodelling of enhancers in response to estrogen deprivation and re-stimulation. <i>Nucleic Acids Research</i> , 2021, 49, 9738-9754.	14.5	8
146	Mechanisms of Histone Modifications. , 2011, , 25-45.		7
147	The Cord Blood Insulin and Mitochondrial DNA Content Related Methylome. <i>Frontiers in Genetics</i> , 2019, 10, 325.	2.3	7
148	IL6 and BCL3 Expression Are Potential Biomarkers in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 722417.	2.8	7
149	An epigenetic aging analysis of randomized metformin and weight loss interventions in overweight postmenopausal breast cancer survivors. <i>Clinical Epigenetics</i> , 2021, 13, 224.	4.1	7
150	Cutaneous and acral melanoma cross-OMICs reveals prognostic cancer drivers associated with pathobiology and ultraviolet exposure. <i>Nature Communications</i> , 2022, 13, .	12.8	7
151	Histone code in the cross-talk during DNA damage signaling. <i>Cell Research</i> , 2010, 20, 113-115.	12.0	6
152	Smoking-associated DNA methylation changes: no smoke without fire. <i>Epigenomics</i> , 2019, 11, 1117-1119.	2.1	5
153	Aflatoxin Exposure during Early Life Is Associated with Differential DNA Methylation in Two-Year-Old Gambian Children. <i>International Journal of Molecular Sciences</i> , 2021, 22, 8967.	4.1	5
154	A concise review towards defining the exposome of oesophageal cancer in sub-Saharan Africa. <i>Environment International</i> , 2021, 157, 106880.	10.0	5
155	Preface. <i>Advances in Genetics</i> , 2010, 71, xi-xii.	1.8	4
156	In vitro transformation of primary human hepatocytes: Epigenetic changes and stemness properties. <i>Experimental Cell Research</i> , 2019, 384, 111643.	2.6	4
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