

Zdenko Herceg

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

166 papers	9,314 citations	52 h-index	92 g-index
177 ext. papers	10,871 ext. citations	7.7 avg, IF	6.11 L-index

#	Paper	IF	Citations
166	DNA Methylation in Newborns and Maternal Smoking in Pregnancy: Genome-wide Consortium Meta-analysis. <i>American Journal of Human Genetics</i> , 2016 , 98, 680-96	11	489
165	Histone acetylation by Trrap-Tip60 modulates loading of repair proteins and repair of DNA double-strand breaks. <i>Nature Cell Biology</i> , 2006 , 8, 91-9	23.4	465
164	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
163	Epigenetic interplay between histone modifications and DNA methylation in gene silencing. <i>Mutation Research - Reviews in Mutation Research</i> , 2008 , 659, 40-8	7	425
162	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, 314-9	50.5	324
161	Epigenetics and cancer: towards an evaluation of the impact of environmental and dietary factors. <i>Mutagenesis</i> , 2007 , 22, 91-103	2.8	271
160	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, 5124-33	4.8	197
159	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, 243-52	10.1	193
158	Parthenolide: from plant shoots to cancer roots. <i>Drug Discovery Today</i> , 2013 , 18, 894-905	8.8	192
157	Epigenetic mechanisms and cancer: an interface between the environment and the genome. <i>Epigenetics</i> , 2011 , 6, 804-19	5.7	174
156	Hepatocellular carcinoma displays distinct DNA methylation signatures with potential as clinical predictors. <i>PLoS ONE</i> , 2010 , 5, e9749	3.7	156
155	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	5.6	151
154	Histone modifications and cancer. <i>Advances in Genetics</i> , 2010 , 70, 57-85	3.3	147
153	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, 7163-78	4.8	146
152	Tobacco smoking-associated genome-wide DNA methylation changes in the EPIC study. <i>Epigenomics</i> , 2016 , 8, 599-618	4.4	145
151	Measuring the exposome: a powerful basis for evaluating environmental exposures and cancer risk. <i>Environmental and Molecular Mutagenesis</i> , 2013 , 54, 480-99	3.2	142
150	PR-Set7-dependent lysine methylation ensures genome replication and stability through S phase. <i>Journal of Cell Biology</i> , 2007 , 179, 1413-26	7.3	138

149	Genetic and epigenetic alterations as biomarkers for cancer detection, diagnosis and prognosis. <i>Molecular Oncology</i> , 2007 , 1, 26-41	7.9	134
148	Epigenetic mechanisms in hepatocellular carcinoma: how environmental factors influence the epigenome. <i>Mutation Research - Reviews in Mutation Research</i> , 2011 , 727, 55-61	7	133
147	An essential function for NBS1 in the prevention of ataxia and cerebellar defects. <i>Nature Medicine</i> , 2005 , 11, 538-44	50.5	133
146	Aberrant DNA methylation distinguishes hepatocellular carcinoma associated with HBV and HCV infection and alcohol intake. <i>Journal of Hepatology</i> , 2011 , 54, 705-15	13.4	127
145	Independent genomewide screens identify the tumor suppressor VTRNA2-1 as a human epiallele responsive to periconceptional environment. <i>Genome Biology</i> , 2015 , 16, 118	18.3	119
144	Epigenetic drivers and genetic passengers on the road to cancer. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2008 , 642, 1-13	3.3	114
143	Modulation of DNA methylation states and infant immune system by dietary supplementation with EB PUFA during pregnancy in an intervention study. <i>American Journal of Clinical Nutrition</i> , 2013 , 98, 480-7	7	108
142	Disruption of Trpap causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001 , 29, 206-11	36.3	106
141	DNA methylome analysis identifies accelerated epigenetic ageing associated with postmenopausal breast cancer susceptibility. <i>European Journal of Cancer</i> , 2017 , 75, 299-307	7.5	104
140	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	3.7	99
139	Nbn heterozygosity renders mice susceptible to tumor formation and ionizing radiation-induced tumorigenesis. <i>Cancer Research</i> , 2003 , 63, 7263-9	10.1	94
138	Transforming epidemiology for 21st century medicine and public health. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 508-16	4	83
137	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, 851-7	3.6	82
136	Towards incorporating epigenetic mechanisms into carcinogen identification and evaluation. <i>Carcinogenesis</i> , 2013 , 34, 1955-67	4.6	70
135	Mammalian Ino80 mediates double-strand break repair through its role in DNA end strand resection. <i>Molecular and Cellular Biology</i> , 2011 , 31, 4735-45	4.8	70
134	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, 5527-38	13	70
133	Exposure to aflatoxin B1 in utero is associated with DNA methylation in white blood cells of infants in The Gambia. <i>International Journal of Epidemiology</i> , 2015 , 44, 1238-48	7.8	69
132	DNA methylation in peripheral blood measured by LUMA is associated with breast cancer in a population-based study. <i>FASEB Journal</i> , 2012 , 26, 2657-66	0.9	69

131	Human mitochondrial DNA is extensively methylated in a non-CpG context. <i>Nucleic Acids Research</i> , 2019 , 47, 10072-10085	20.1	68
130	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020 , 17, 687-705	19.4	64
129	Oncogenic microRNAs (OncomiRs) as a new class of cancer biomarkers. <i>BioEssays</i> , 2010 , 32, 894-904	4.1	64
128	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, 3017-22	11.5	63
127	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, 402-12	4.8	63
126	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 22-23u	7.8	62
125	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, 2058-65	4.6	61
124	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	3.3	61
123	Oxidative stress and inflammation mediate the effect of air pollution on cardio- and cerebrovascular disease: A prospective study in nonsmokers. <i>Environmental and Molecular Mutagenesis</i> , 2018 , 59, 234-246	3.2	61
122	Identification of novel long non-coding RNAs deregulated in hepatocellular carcinoma using RNA-sequencing. <i>Oncotarget</i> , 2016 , 7, 31862-77	3.3	60
121	Aberrant DNA methylation links cancer susceptibility locus 15q25.1 to apoptotic regulation and lung cancer. <i>Cancer Research</i> , 2010 , 70, 2779-88	10.1	59
120	Methylome analysis reveals Jak-STAT pathway deregulation in putative breast cancer stem cells. <i>Epigenetics</i> , 2011 , 6, 428-39	5.7	59
119	The Fanconi anemia group A protein modulates homologous repair of DNA double-strand breaks in mammalian cells. <i>Carcinogenesis</i> , 2005 , 26, 1731-40	4.6	59
118	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	9.9	56
117	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, 2385-97	5.6	56
116	Deciphering the epigenetic code: an overview of DNA methylation analysis methods. <i>Antioxidants and Redox Signaling</i> , 2013 , 18, 1972-86	8.4	54
115	Epigenetic information in chromatin: the code of entry for DNA repair. <i>Cell Cycle</i> , 2006 , 5, 696-701	4.7	52
114	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	5.7	51

113	Perturbation of metabolic pathways mediates the association of air pollutants with asthma and cardiovascular diseases. <i>Environment International</i> , 2018 , 119, 334-345	12.9	49
112	Quantitative analysis of DNA methylation after whole bisulfite amplification of a minute amount of DNA from body fluids. <i>Epigenetics</i> , 2009 , 4, 221-30	5.7	48
111	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018 , 142, 874-882	7.5	46
110	DNA methylation and cancer: ghosts and angels above the genes. <i>Current Opinion in Oncology</i> , 2011 , 23, 69-76	4.2	46
109	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, 700-4	7	46
108	Maternal Gestational Diabetes Mellitus and Newborn DNA Methylation: Findings From the Pregnancy and Childhood Epigenetics Consortium. <i>Diabetes Care</i> , 2020 , 43, 98-105	14.6	45
107	HAT cofactor Trapp regulates the mitotic checkpoint by modulation of Mad1 and Mad2 expression. <i>EMBO Journal</i> , 2004 , 23, 4824-34	13	44
106	Chromatin structure in double strand break repair. <i>DNA Repair</i> , 2013 , 12, 800-10	4.3	43
105	Unique DNA methylation signature in HPV-positive head and neck squamous cell carcinomas. <i>Genome Medicine</i> , 2017 , 9, 33	14.4	43
104	Identification of a DNA methylome signature of esophageal squamous cell carcinoma and potential epigenetic biomarkers. <i>Epigenetics</i> , 2011 , 6, 1217-27	5.7	43
103	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	6.5	40
102	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, 325-36	2.9	39
101	Noncleavable poly(ADP-ribose) polymerase-1 regulates the inflammation response in mice. <i>Journal of Clinical Investigation</i> , 2004 , 114, 1072-81	15.9	38
100	DNA demethylating agents and epigenetic therapy of cancer. <i>Advances in Genetics</i> , 2010 , 70, 327-40	3.3	37
99	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	3.7	37
98	Targeted deep DNA methylation analysis of circulating cell-free DNA in plasma using massively parallel semiconductor sequencing. <i>Epigenomics</i> , 2015 , 7, 353-62	4.4	36
97	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	8.5	36
96	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, 1114-9	5.7	36

95	Acute changes in DNA methylation in relation to 24 h personal air pollution exposure measurements: A panel study in four European countries. <i>Environment International</i> , 2018 , 120, 11-21	12.9	35
94	Trrap-dependent histone acetylation specifically regulates cell-cycle gene transcription to control neural progenitor fate decisions. <i>Cell Stem Cell</i> , 2014 , 14, 632-43	18	35
93	From hepatitis to hepatocellular carcinoma: a proposed model for cross-talk between inflammation and epigenetic mechanisms. <i>Genome Medicine</i> , 2012 , 4, 8	14.4	35
92	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	5.6	33
91	Genome-wide methylation and transcriptome analysis in penile carcinoma: uncovering new molecular markers. <i>Clinical Epigenetics</i> , 2015 , 7, 46	7.7	32
90	Asbestos-associated genome-wide DNA methylation changes in lung cancer. <i>International Journal of Cancer</i> , 2017 , 141, 2014-2029	7.5	32
89	Epigenetic silencing of HNF1A associates with changes in the composition of the human plasma N-glycome. <i>Epigenetics</i> , 2012 , 7, 164-72	5.7	31
88	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	6.5	31
87	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, 1388-95	4.6	29
86	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	8.4	28
85	Quantitative detection of DNA methylation states in minute amounts of DNA from body fluids. <i>Methods</i> , 2010 , 52, 242-7	4.6	28
84	Challenges and opportunities in research on early-life events/exposures and cancer development later in life. <i>Cancer Causes and Control</i> , 2012 , 23, 983-90	2.8	27
83	The Promises and Challenges of Toxic-Epigenomics: Environmental Chemicals and Their Impacts on the Epigenome. <i>Environmental Health Perspectives</i> , 2020 , 128, 15001	8.4	26
82	Shaping chromatin for repair. <i>Mutation Research - Reviews in Mutation Research</i> , 2013 , 752, 45-60	7	26
81	Translational cancer research: balancing prevention and treatment to combat cancer globally. <i>Journal of the National Cancer Institute</i> , 2015 , 107, 353	9.7	26
80	Methylome analysis and epigenetic changes associated with menarcheal age. <i>PLoS ONE</i> , 2013 , 8, e79391	3.7	26
79	Inactivation of the putative suppressor gene DOK1 by promoter hypermethylation in primary human cancers. <i>International Journal of Cancer</i> , 2012 , 130, 2484-94	7.5	25
78	Comparison of smoking-related DNA methylation between newborns from prenatal exposure and adults from personal smoking. <i>Epigenomics</i> , 2019 , 11, 1487-1500	4.4	24

77	Integrative genomics identifies gene signature associated with melanoma ulceration. <i>PLoS ONE</i> , 2013 , 8, e54958	3.7	24
76	Introduction: epigenetics and cancer. <i>Advances in Genetics</i> , 2010 , 70, 1-23	3.3	24
75	Histone acetyltransferase cofactor Trrap is essential for maintaining the hematopoietic stem/progenitor cell pool. <i>Journal of Immunology</i> , 2009 , 183, 6422-31	5.3	24
74	Histone deacetylase inhibitors potentiate photodynamic therapy in colon cancer cells marked by chromatin-mediated epigenetic regulation of. <i>Clinical Epigenetics</i> , 2017 , 9, 62	7.7	23
73	TET-Catalyzed 5-Hydroxymethylation Precedes HNF4A Promoter Choice during Differentiation of Bipotent Liver Progenitors. <i>Stem Cell Reports</i> , 2017 , 9, 264-278	8	23
72	Rendez-vous at mitosis: TRRAPed in the chromatin. <i>Cell Cycle</i> , 2005 , 4, 383-7	4.7	22
71	Dynamic imbalance between cancer cell subpopulations induced by transforming growth factor beta (TGF- β) is associated with a DNA methylome switch. <i>BMC Genomics</i> , 2014 , 15, 435	4.5	21
70	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, 1369-76	5.3	21
69	Histone acetyltransferase cofactor Trrap maintains self-renewal and restricts differentiation of embryonic stem cells. <i>Stem Cells</i> , 2013 , 31, 979-91	5.8	21
68	Genome-wide analysis of gene expression regulated by the HAT cofactor Trrap in conditional knockout cells. <i>Nucleic Acids Research</i> , 2003 , 31, 7011-23	20.1	21
67	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	7.8	21
66	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. <i>Breast Cancer Research</i> , 2019 , 21, 62	8.3	20
65	Antagonistic and synergistic epigenetic modulation using orthologous CRISPR/dCas9-based modular system. <i>Nucleic Acids Research</i> , 2019 , 47, 9637-9657	20.1	20
64	DNA methylation characteristics of primary melanomas with distinct biological behaviour. <i>PLoS ONE</i> , 2014 , 9, e96612	3.7	20
63	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, 733-42	2.8	19
62	The epigenome and cancer prevention: A complex story of dietary supplementation. <i>Cancer Letters</i> , 2014 , 342, 275-84	9.9	18
61	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, 178-85	5	18
60	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	7.5	17

59	DNA Methylome Marks of Exposure to Particulate Matter at Three Time Points in Early Life. <i>Environmental Science & Technology</i> , 2018 , 52, 5427-5437	10.3	17
58	Epigenetic Mechanisms as an Interface Between the Environment and Genome. <i>Advances in Experimental Medicine and Biology</i> , 2016 , 903, 3-15	3.6	17
57	Detection of cancer-specific epigenomic changes in biofluids: powerful tools in biomarker discovery and application. <i>Molecular Oncology</i> , 2012 , 6, 704-15	7.9	17
56	Transcriptional regulation of the human tumor suppressor DOK1 by E2F1. <i>Molecular and Cellular Biology</i> , 2012 , 32, 4877-90	4.8	17
55	Epstein-Barr virus down-regulates tumor suppressor DOK1 expression. <i>PLoS Pathogens</i> , 2014 , 10, e1004125	12.5	16
54	DNA methylation changes associated with risk factors in tumors of the upper aerodigestive tract. <i>Epigenetics</i> , 2012 , 7, 270-7	5.7	16
53	Epigenetic signatures in cancer: Implications for the control of cancer in the clinic. <i>Current Opinion in Molecular Therapeutics</i> , 2010 , 12, 316-24		16
52	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	4.9	15
51	Epigenetic signatures in stem cells and cancer stem cells. <i>Epigenomics</i> , 2009 , 1, 261-80	4.4	15
50	HAT cofactor TRRAP mediates beta-catenin ubiquitination on the chromatin and the regulation of the canonical Wnt pathway. <i>Cell Cycle</i> , 2008 , 7, 3908-14	4.7	15
49	Inhibition of DNA methylation promotes breast tumor sensitivity to netrin-1 interference. <i>EMBO Molecular Medicine</i> , 2016 , 8, 863-77	12	15
48	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	7.7	14
47	Loss of histone acetyltransferase cofactor transformation/transcription domain-associated protein impairs liver regeneration after toxic injury. <i>Hepatology</i> , 2011 , 53, 954-63	11.2	14
46	Identifying and correcting epigenetics measurements for systematic sources of variation. <i>Clinical Epigenetics</i> , 2018 , 10, 38	7.7	13
45	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	10.1	13
44	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018 , 24, 581-591	12.9	13
43	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	2.7	13
42	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. <i>Clinical Epigenetics</i> , 2019 , 11, 66	7.7	12

41	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	12.7	12
40	Developmental and transplacental genotoxicology: fluconazole. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2008 , 657, 43-7	3	12
39	Lowly methylated region analysis identifies EBF1 as a potential epigenetic modifier in breast cancer. <i>Epigenetics</i> , 2017 , 12, 964-972	5.7	11
38	Interplay between the Epigenetic Enzyme Lysine (K)-Specific Demethylase 2B and Epstein-Barr Virus Infection. <i>Journal of Virology</i> , 2019 , 93,	6.6	10
37	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	5.3	10
36	hypermethylation and decreased expression in esophageal squamous cell carcinoma and histologically normal tumor surrounding esophageal cells. <i>Clinical Epigenetics</i> , 2017 , 9, 130	7.7	10
35	Transposable hypomethylation is associated with metastatic capacity of primary melanomas. <i>International Journal of Clinical and Experimental Pathology</i> , 2013 , 6, 2943-8	1.4	10
34	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,	4.6	8
33	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	7.5	8
32	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, 137-42	2.4	8
31	Epigenetic information in chromatin and cancer. <i>European Journal of Cancer</i> , 2009 , 45 Suppl 1, 442-4	7.5	7
30	Genomic responses to hepatitis B virus (HBV) infection in primary human hepatocytes. <i>Oncotarget</i> , 2015 , 6, 44877-91	3.3	7
29	DNA hypermethylation is associated with invasive phenotype of malignant melanoma. <i>Experimental Dermatology</i> , 2020 , 29, 39-50	4	7
28	Identification of novel dysregulated circular RNAs in early-stage breast cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2021 , 25, 3912-3921	5.6	7
27	Histone code in the cross-talk during DNA damage signaling. <i>Cell Research</i> , 2010 , 20, 113-5	24.7	6
26	Mechanisms of Histone Modifications 2011 , 25-45		5
25	The Cord Blood Insulin and Mitochondrial DNA Content Related Methylome. <i>Frontiers in Genetics</i> , 2019 , 10, 325	4.5	4
24	Epigenetics is a fascinating field of modern biology. Preface. <i>Advances in Genetics</i> , 2010 , 71, xi-xii	3.3	4

23	Pan-cancer multi-omics analysis and orthogonal experimental assessment of epigenetic driver genes. <i>Genome Research</i> , 2020 , 30, 1517-1532	9.7	4
22	Smoking-associated DNA methylation changes: no smoke without fire. <i>Epigenomics</i> , 2019 , 11, 1117-1119	4.4	3
21	In vitro transformation of primary human hepatocytes: Epigenetic changes and stemness properties. <i>Experimental Cell Research</i> , 2019 , 384, 111643	4.2	3
20	Mechanisms of Histone Modifications 2017 , 25-46		3
19	Tissue-specific inactivation of HAT cofactor TRRAP reveals its essential role in B cells. <i>Cell Cycle</i> , 2014 , 13, 1583-9	4.7	2
18	DNA Methylation and Carcinogenesis: Current and Future Perspectives 2019 , 153-171		2
17	Epigenetic Changes in Cancer: Role of Environment 2010 , 153-196		2
16	Antiproliferative Effects of Epigenetic Modifier Drugs Through E-cadherin Up-regulation in Liver Cancer Cell Lines. <i>Annals of Hepatology</i> , 2018 , 17, 444-460	3.1	2
15	Epigenetic remodelling of enhancers in response to estrogen deprivation and re-stimulation. <i>Nucleic Acids Research</i> , 2021 , 49, 9738-9754	20.1	2
14	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	7	2
13	The Effects of Diet on Epigenetic Processes 2011 , 449-458		1
12	Epigenetic Identity in Cancer Stem Cells. <i>Pancreatic Islet Biology</i> , 2011 , 127-139	0.4	1
11	Interplay between the epigenetic enzyme lysine (K)-specific demethylase 2B and Epstein-Barr virus infection		1
10	IL6 and BCL3 Expression Are Potential Biomarkers in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021 , 11, 722417	5.3	1
9	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,	6.3	1
8	A concise review towards defining the exposome of oesophageal cancer in sub-Saharan Africa. <i>Environment International</i> , 2021 , 157, 106880	12.9	1
7	An epigenetic aging analysis of randomized metformin and weight loss interventions in overweight postmenopausal breast cancer survivors.. <i>Clinical Epigenetics</i> , 2021 , 13, 224	7.7	1
6	Reply to GC Burdge. <i>American Journal of Clinical Nutrition</i> , 2013 , 98, 1595-6	7	

5 Mechanisms of Epigenetic Gene Silencing **2011**, 41-53

4 Chromatin: The Entry to and Exit from DNA Repair **2011**, 387-409

3 Epigenetic Changes Induced by Environment and Diet in Cancer **2019**, 672-677

2 A Method to Investigate the Helicobacter pylori-Associated DNA Methylome. *Methods in Molecular Biology*, **2021**, 2283, 75-81 1.4

1 Epigenetic Epidemiology of Cancer **2022**, 325-342