

# 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 Methylome Changes of Muscle- and Neuronal-Related Processes Precede Bladder Cancer Invasiveness. <i>Cancers</i> , 2022, 14, 487.	3.7	2
2	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
3	Epigenetic Alteration of the Cancer-Related Gene TGFBI in B Cells Infected with Epstein-Barr Virus and Exposed to Aflatoxin B1: Potential Role in Burkitt Lymphoma Development. <i>Cancers</i> , 2022, 14, 1284.	3.7	2
4	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
5	A Method to Investigate the Helicobacter pylori-Associated DNA Methylome. <i>Methods in Molecular Biology</i> , 2021, 2283, 75-81.	0.9	0
6	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
7	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
8	IL6 and BCL3 Expression Are Potential Biomarkers in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021, 11, 722417.	2.8	7
9	Epigenetic remodelling of enhancers in response to estrogen deprivation and re-stimulation. <i>Nucleic Acids Research</i> , 2021, 49, 9738-9754.	14.5	8
10	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
11	A concise review towards defining the exposome of oesophageal cancer in sub-Saharan Africa. <i>Environment International</i> , 2021, 157, 106880.	10.0	5
12	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
13	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
14	DNA hypermethylation is associated with invasive phenotype of malignant melanoma. <i>Experimental Dermatology</i> , 2020, 29, 39-50.	2.9	30
15	Pan-cancer multi-omics analysis and orthogonal experimental assessment of epigenetic driver genes. <i>Genome Research</i> , 2020, 30, 1517-1532.	5.5	20
16	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
17	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
18	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020, 17, 687-705.	27.6	178

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19	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
20	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
21	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
22	Smoking-associated DNA methylation changes: no smoke without fire. <i>Epigenomics</i> , 2019, 11, 1117-1119.	2.1	5
23	Antagonistic and synergistic epigenetic modulation using orthologous CRISPR/dCas9-based modular system. <i>Nucleic Acids Research</i> , 2019, 47, 9637-9657.	14.5	38
24	Carcinogenicity of night shift work. <i>Lancet Oncology</i> , The, 2019, 20, 1058-1059.	10.7	219
25	In vitro transformation of primary human hepatocytes: Epigenetic changes and stemness properties. <i>Experimental Cell Research</i> , 2019, 384, 111643.	2.6	4
26	Human mitochondrial DNA is extensively methylated in a non-CpG context. <i>Nucleic Acids Research</i> , 2019, 47, 10072-10085.	14.5	103
27	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
28	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
29	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
30	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
31	The Cord Blood Insulin and Mitochondrial DNA Content Related Methylome. <i>Frontiers in Genetics</i> , 2019, 10, 325.	2.3	7
32	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
33	Epigenetic Changes Induced by Environment and Diet in Cancer. , 2019, , 672-677.		0
34	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
35	DNA Methylation and Carcinogenesis: Current and Future Perspectives. , 2019, , 153-171.		4
36	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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37	Identifying and correcting epigenetics measurements for systematic sources of variation. <i>Clinical Epigenetics</i> , 2018, 10, 38.	4.1	29
38	DNA Methylome Marks of Exposure to Particulate Matter at Three Time Points in Early Life. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5427-5437.	10.0	21
39	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 22-23u.	1.9	105
40	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018, 142, 874-882.	5.1	64
41	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.	2.2	88
42	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018, 24, 581-591.	7.0	21
43	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.	1.5	3
44	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
45	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
46	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.	10.0	48
47	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
48	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
49	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
50	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
51	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
52	Asbestos&associated genome&wide DNA methylation changes in lung cancer. <i>International Journal of Cancer</i> , 2017, 141, 2014-2029.	5.1	42
53	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
54	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

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55	Lowly methylated region analysis identifies EBF1 as a potential epigenetic modifier in breast cancer. <i>Epigenetics</i> , 2017, 12, 964-972.	2.7	16
56	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
57	Unique DNA methylation signature in HPV-positive head and neck squamous cell carcinomas. <i>Genome Medicine</i> , 2017, 9, 33.	8.2	68
58	Mechanisms of Histone Modifications. , 2017, , 25-46.		3
59	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
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	Tobacco smoking-associated genome-wide DNA methylation changes in the EPIC study. <i>Epigenomics</i> , 2016, 8, 599-618.	2.1	192
62	Inhibition of <sc>DNA</sc> methylation promotes breast tumor sensitivity to netrinâ€1 interference. <i>EMBO Molecular Medicine</i> , 2016, 8, 863-877.	6.9	21
63	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
64	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016, 9, 436-447.	5.1	678
65	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
66	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
67	Identification of novel long non-coding RNAs deregulated in hepatocellular carcinoma using RNA-sequencing. <i>Oncotarget</i> , 2016, 7, 31862-31877.	1.8	74
68	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
69	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
70	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
71	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
72	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

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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	Exposure to aflatoxin B <sub>1</sub> 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
75	Genomic responses to hepatitis B virus (HBV) infection in primary human hepatocytes. <i>Oncotarget</i> , 2015, 6, 44877-44891.	1.8	9
76	DNA Methylation Characteristics of Primary Melanomas with Distinct Biological Behaviour. <i>PLoS ONE</i> , 2014, 9, e96612.	2.5	27
77	Tissue-specific inactivation of HAT cofactor TRRAP reveals its essential role in B cells. <i>Cell Cycle</i> , 2014, 13, 1583-1589.	2.6	3
78	Epstein-Barr Virus Down-Regulates Tumor Suppressor DOK1 Expression. <i>PLoS Pathogens</i> , 2014, 10, e1004125.	4.7	17
79	The epigenome and cancer prevention: A complex story of dietary supplementation. <i>Cancer Letters</i> , 2014, 342, 275-284.	7.2	19
80	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
81	Dynamic imbalance between cancer cell subpopulations induced by Transforming Growth Factor Beta (TGF- $\beta$ 2) is associated with a DNA methylome switch. <i>BMC Genomics</i> , 2014, 15, 435.	2.8	27
82	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
83	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
84	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
85	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
86	Towards incorporating epigenetic mechanisms into carcinogen identification and evaluation. <i>Carcinogenesis</i> , 2013, 34, 1955-1967.	2.8	88
87	Chromatin structure in double strand break repair. <i>DNA Repair</i> , 2013, 12, 800-810.	2.8	48
88	Deciphering the Epigenetic Code: An Overview of DNA Methylation Analysis Methods. <i>Antioxidants and Redox Signaling</i> , 2013, 18, 1972-1986.	5.4	66
89	Shaping chromatin for repair. <i>Mutation Research - Reviews in Mutation Research</i> , 2013, 752, 45-60.	5.5	28
90	Parthenolide: from plant shoots to cancer roots. <i>Drug Discovery Today</i> , 2013, 18, 894-905.	6.4	248

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91	Reply to GC Burdge. American Journal of Clinical Nutrition, 2013, 98, 1595-1596.	4.7	0
92	Dependence receptor TrkC is a putative colon cancer tumor suppressor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 3017-3022.	7.1	85
93	Histone Acetyltransferase Cofactor Trrap Maintains Self-Renewal and Restricts Differentiation of Embryonic Stem Cells. Stem Cells, 2013, 31, 979-991.	3.2	25
94	Transforming Epidemiology for 21st Century Medicine and Public Health. Cancer Epidemiology Biomarkers and Prevention, 2013, 22, 508-516.	2.5	104
95	Modulation of DNA methylation states and infant immune system by dietary supplementation with ̳-3 PUFA during pregnancy in an intervention study. American Journal of Clinical Nutrition, 2013, 98, 480-487.	4.7	142
96	Integrative Genomics Identifies Gene Signature Associated with Melanoma Ulceration. PLoS ONE, 2013, 8, e54958.	2.5	28
97	Comparisons of microRNA Patterns in Plasma before and after Tumor Removal Reveal New Biomarkers of Lung Squamous Cell Carcinoma. PLoS ONE, 2013, 8, e78649.	2.5	112
98	Methylome Analysis and Epigenetic Changes Associated with Menarcheal Age. PLoS ONE, 2013, 8, e79391.	2.5	36
99	Transposable hypomethylation is associated with metastatic capacity of primary melanomas. International Journal of Clinical and Experimental Pathology, 2013, 6, 2943-8.	0.5	12
100	DNA methylation changes associated with risk factors in tumors of the upper aerodigestive tract. Epigenetics, 2012, 7, 270-277.	2.7	21
101	Epigenetic silencing of <i>HNF1A</i> associates with changes in the composition of the human plasma N-glycome. Epigenetics, 2012, 7, 164-172.	2.7	37
102	Transcriptional Regulation of the Human Tumor Suppressor <i>DOK1</i> by E2F1. Molecular and Cellular Biology, 2012, 32, 4877-4890.	2.3	17
103	Detection of cancer-specific epigenomic changes in biofluids: Powerful tools in biomarker discovery and application. Molecular Oncology, 2012, 6, 704-715.	4.6	20
104	From hepatitis to hepatocellular carcinoma: a proposed model for cross-talk between inflammation and epigenetic mechanisms. Genome Medicine, 2012, 4, 8.	8.2	39
105	Inactivation of the putative suppressor gene <i>DOK1</i> by promoter hypermethylation in primary human cancers. International Journal of Cancer, 2012, 130, 2484-2494.	5.1	29
106	DNA methylation in peripheral blood measured by LUMA is associated with breast cancer in a population-based study. FASEB Journal, 2012, 26, 2657-2666.	0.5	76
107	Challenges and opportunities in research on early-life events/exposures and cancer development later in life. Cancer Causes and Control, 2012, 23, 983-990.	1.8	31
108	Epigenetic silencing of sFRP1 activates the canonical Wnt pathway and contributes to increased cell growth and proliferation in hepatocellular carcinoma. Tumor Biology, 2012, 33, 325-336.	1.8	47

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109	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
110	Mechanisms of Epigenetic Gene Silencing. , 2011, , 41-53.		0
111	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
112	Aberrant DNA methylation of cancer-associated genes in gastric cancer in the European Prospective Investigation into Cancer and Nutrition (EPICâ€“EURGAST). <i>Cancer Letters</i> , 2011, 311, 85-95.	7.2	62
113	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
114	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
115	The Effects of Diet on Epigenetic Processes. , 2011, , 449-458.		1
116	DNA methylation and cancer: ghosts and angels above the genes. <i>Current Opinion in Oncology</i> , 2011, 23, 69-76.	2.4	53
117	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
118	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
119	Intensityâ€“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
120	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
121	Epigenetic mechanisms and cancer: An interface between the environment and the genome. <i>Epigenetics</i> , 2011, 6, 804-819.	2.7	204
122	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
123	Epigenetic Identity in Cancer Stem Cells. <i>Pancreatic Islet Biology</i> , 2011, , 127-139.	0.3	1
124	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
125	Mechanisms of Histone Modifications. , 2011, , 25-45.		7
126	Methylome analysis reveals Jak-STAT pathway deregulation in putative breast cancer stem cells. <i>Epigenetics</i> , 2011, 6, 428-439.	2.7	70



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127	Chromatin: The Entry to and Exit from DNA Repair. , 2011, , 387-409.		1
128	Oncogenic microRNAs (OncomiRs) as a new class of cancer biomarkers. BioEssays, 2010, 32, 894-904.	2.5	83
129	Histone code in the cross-talk during DNA damage signaling. Cell Research, 2010, 20, 113-115.	12.0	6
130	Hepatocellular Carcinoma Displays Distinct DNA Methylation Signatures with Potential as Clinical Predictors. PLoS ONE, 2010, 5, e9749.	2.5	175
131	DNA Methylation of Hepatitis B Virus (HBV) Genome Associated with the Development of Hepatocellular Carcinoma and Occult HBV Infection. Journal of Infectious Diseases, 2010, 202, 700-704.	4.0	55
132	Deletion of the nuclear isoform of poly(ADP-ribose) glycohydrolase (PARG) reveals its function in DNA repair, genomic stability and tumorigenesis. Carcinogenesis, 2010, 31, 2058-2065.	2.8	64
133	Preface. Advances in Genetics, 2010, 71, xi-xii.	1.8	4
134	Aberrant DNA Methylation Links Cancer Susceptibility Locus 15q25.1 to Apoptotic Regulation and Lung Cancer. Cancer Research, 2010, 70, 2779-2788.	0.9	62
135	Introduction. Advances in Genetics, 2010, 70, 1-23.	1.8	29
136	Histone Modifications and Cancer. Advances in Genetics, 2010, 70, 57-85.	1.8	174
137	DNA Demethylating Agents and Epigenetic Therapy of Cancer. Advances in Genetics, 2010, 70, 327-340.	1.8	51
138	Quantitative detection of DNA methylation states in minute amounts of DNA from body fluids. Methods, 2010, 52, 242-247.	3.8	32
139	Epigenetic Changes in Cancer: Role of Environment. , 2010, , 153-196.		2
140	Epigenetic signatures in cancer: Implications for the control of cancer in the clinic. Current Opinion in Molecular Therapeutics, 2010, 12, 316-24.	2.8	18
141	Quantitative analysis of DNA methylation after whole bisulfite amplification of a minute amount of DNA from body fluids. Epigenetics, 2009, 4, 221-230.	2.7	51
142	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. Cancer Research, 2009, 69, 243-252.	0.9	231
143	Histone Acetyltransferase Cofactor Trapp Is Essential for Maintaining the Hematopoietic Stem/Progenitor Cell Pool. Journal of Immunology, 2009, 183, 6422-6431.	0.8	29
144	HBV protein as a double-barrel shot-gun targets epigenetic landscape in liver cancer. Journal of Hepatology, 2009, 50, 252-255.	3.7	10

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145	Epigenetic information in chromatin and cancer. <i>European Journal of Cancer</i> , 2009, 45, 442-444.	2.8	8
146	Epigenetic signatures in stem cells and cancer stem cells. <i>Epigenomics</i> , 2009, 1, 261-280.	2.1	19
147	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
148	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
149	Developmental and transplacental genotoxicology: Fluconazole. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2008, 657, 43-47.	1.7	12
150	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
151	HAT cofactor TRRAP mediates $\beta$ -Catenin ubiquitination on the chromatin and the regulation of the canonical Wnt pathway. <i>Cell Cycle</i> , 2008, 7, 3908-3914.	2.6	16
152	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
153	Epigenetics and cancer: towards an evaluation of the impact of environmental and dietary factors. <i>Mutagenesis</i> , 2007, 22, 91-103.	2.6	307
154	Genetic and epigenetic alterations as biomarkers for cancer detection, diagnosis and prognosis. <i>Molecular Oncology</i> , 2007, 1, 26-41.	4.6	206
155	Histone acetylation by Trrap-dependent 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
156	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
157	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
158	Epigenetic Information in Chromatin: the Code of Entry for DNA Repair. <i>Cell Cycle</i> , 2006, 5, 696-701.	2.6	54
159	An essential function for NBS1 in the prevention of ataxia and cerebellar defects. <i>Nature Medicine</i> , 2005, 11, 538-544.	30.7	155
160	Rendez-vous at Mitosis: TRRAPed in the Chromatin. <i>Cell Cycle</i> , 2005, 4, 383-387.	2.6	27
161	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
162	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

#	ARTICLE	IF	CITATIONS
163	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
164	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
165	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
166	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
167	Nbn heterozygosity renders mice susceptible to tumor formation and ionizing radiation-induced tumorigenesis. <i>Cancer Research</i> , 2003, 63, 7263-9.	0.9	100
168	Disruption of Trrap causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001, 29, 206-211.	21.4	122
169	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
170	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