

Zdenko Herceg

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9148723/zdenko-herceg-publications-by-year.pdf>

Version: 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
165	Epigenetic Epidemiology of Cancer 2022 , 325-342		
164	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
163	A Method to Investigate the Helicobacter pylori-Associated DNA Methylome. <i>Methods in Molecular Biology</i> , 2021 , 2283, 75-81	1.4	
162	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
161	IL6 and BCL3 Expression Are Potential Biomarkers in Esophageal Squamous Cell Carcinoma. <i>Frontiers in Oncology</i> , 2021 , 11, 722417	5.3	1
160	Epigenetic remodelling of enhancers in response to estrogen deprivation and re-stimulation. <i>Nucleic Acids Research</i> , 2021 , 49, 9738-9754	20.1	2
159	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
158	A concise review towards defining the exposome of oesophageal cancer in sub-Saharan Africa. <i>Environment International</i> , 2021 , 157, 106880	12.9	1
157	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
156	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
155	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
154	Personalized early detection and prevention of breast cancer: ENVISION consensus statement. <i>Nature Reviews Clinical Oncology</i> , 2020 , 17, 687-705	19.4	64
153	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
152	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
151	DNA hypermethylation is associated with invasive phenotype of malignant melanoma. <i>Experimental Dermatology</i> , 2020 , 29, 39-50	4	7
150	Pan-cancer multi-omics analysis and orthogonal experimental assessment of epigenetic driver genes. <i>Genome Research</i> , 2020 , 30, 1517-1532	9.7	4

149	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
148	Human mitochondrial DNA is extensively methylated in a non-CpG context. <i>Nucleic Acids Research</i> , 2019 , 47, 10072-10085	20.1	68
147	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
146	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
145	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
144	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
143	The Cord Blood Insulin and Mitochondrial DNA Content Related Methylome. <i>Frontiers in Genetics</i> , 2019 , 10, 325	4.5	4
142	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
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	7.5	8
140	Smoking-associated DNA methylation changes: no smoke without fire. <i>Epigenomics</i> , 2019 , 11, 1117-1119	4.4	3
139	Antagonistic and synergistic epigenetic modulation using orthologous CRISPR/dCas9-based modular system. <i>Nucleic Acids Research</i> , 2019 , 47, 9637-9657	20.1	20
138	In vitro transformation of primary human hepatocytes: Epigenetic changes and stemness properties. <i>Experimental Cell Research</i> , 2019 , 384, 111643	4.2	3
137	DNA Methylation and Carcinogenesis: Current and Future Perspectives 2019 , 153-171		2
136	Epigenetic Changes Induced by Environment and Diet in Cancer 2019 , 672-677		
135	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
134	Genome-wide profiling of normal gastric mucosa identifies Helicobacter pylori- and cancer-associated DNA methylome changes. <i>International Journal of Cancer</i> , 2018 , 143, 597-609	7.5	17
133	Identifying and correcting epigenetics measurements for systematic sources of variation. <i>Clinical Epigenetics</i> , 2018 , 10, 38	7.7	13
132	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

131	Cohort Profile: Pregnancy And Childhood Epigenetics (PACE) Consortium. <i>International Journal of Epidemiology</i> , 2018 , 47, 22-23u	7.8	62
130	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018 , 142, 874-882	7.5	46
129	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
128	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
127	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
126	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
125	Novel Predictors of Breast Cancer Survival Derived from miRNA Activity Analysis. <i>Clinical Cancer Research</i> , 2018 , 24, 581-591	12.9	13
124	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
123	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
122	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
121	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
120	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
119	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
118	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
117	Asbestos-associated genome-wide DNA methylation changes in lung cancer. <i>International Journal of Cancer</i> , 2017 , 141, 2014-2029	7.5	32
116	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
115	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
114	Lowly methylated region analysis identifies EBF1 as a potential epigenetic modifier in breast cancer. <i>Epigenetics</i> , 2017 , 12, 964-972	5.7	11

113	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
112	Unique DNA methylation signature in HPV-positive head and neck squamous cell carcinomas. <i>Genome Medicine</i> , 2017 , 9, 33	14.4	43
111	Mechanisms of Histone Modifications 2017 , 25-46		3
110	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
109	Epigenetic Signatures of Cigarette Smoking. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 436-447		442
108	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
107	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
106	Identification of novel long non-coding RNAs deregulated in hepatocellular carcinoma using RNA-sequencing. <i>Oncotarget</i> , 2016 , 7, 31862-77	3.3	60
105	Tobacco smoking-associated genome-wide DNA methylation changes in the EPIC study. <i>Epigenomics</i> , 2016 , 8, 599-618	4.4	145
104	Inhibition of DNA methylation promotes breast tumor sensitivity to netrin-1 interference. <i>EMBO Molecular Medicine</i> , 2016 , 8, 863-77	12	15
103	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
102	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
101	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
100	Genome-wide methylation and transcriptome analysis in penile carcinoma: uncovering new molecular markers. <i>Clinical Epigenetics</i> , 2015 , 7, 46	7.7	32
99	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
98	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
97	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
96	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

95	Genomic responses to hepatitis B virus (HBV) infection in primary human hepatocytes. <i>Oncotarget</i> , 2015 , 6, 44877-91	3.3	7
94	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, 851-73.6	3.6	82
93	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
92	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, 137-42.4	4.4	8
91	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
90	DNA methylation characteristics of primary melanomas with distinct biological behaviour. <i>PLoS ONE</i> , 2014 , 9, e96612	3.7	20
89	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
88	Epstein-Barr virus down-regulates tumor suppressor DOK1 expression. <i>PLoS Pathogens</i> , 2014 , 10, e1004125	4.5	16
87	The epigenome and cancer prevention: A complex story of dietary supplementation. <i>Cancer Letters</i> , 2014 , 342, 275-84	9.9	18
86	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
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, 1369-76	5.3	21
84	Towards incorporating epigenetic mechanisms into carcinogen identification and evaluation. <i>Carcinogenesis</i> , 2013 , 34, 1955-67	4.6	70
83	Chromatin structure in double strand break repair. <i>DNA Repair</i> , 2013 , 12, 800-10	4.3	43
82	Deciphering the epigenetic code: an overview of DNA methylation analysis methods. <i>Antioxidants and Redox Signaling</i> , 2013 , 18, 1972-86	8.4	54
81	Shaping chromatin for repair. <i>Mutation Research - Reviews in Mutation Research</i> , 2013 , 752, 45-60	7	26
80	Parthenolide: from plant shoots to cancer roots. <i>Drug Discovery Today</i> , 2013 , 18, 894-905	8.8	192
79	Reply to GC Burdge. <i>American Journal of Clinical Nutrition</i> , 2013 , 98, 1595-6	7	
78	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

77	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
76	Transforming epidemiology for 21st century medicine and public health. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2013 , 22, 508-16	4	83
75	Modulation of DNA methylation states and infant immune system by dietary supplementation with Ω 3 PUFA during pregnancy in an intervention study. <i>American Journal of Clinical Nutrition</i> , 2013 , 98, 480-7	7	108
74	Integrative genomics identifies gene signature associated with melanoma ulceration. <i>PLoS ONE</i> , 2013 , 8, e54958	3.7	24
73	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
72	Methylome analysis and epigenetic changes associated with menarcheal age. <i>PLoS ONE</i> , 2013 , 8, e79391	3.7	26
71	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
70	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
69	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
68	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
67	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
66	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
65	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
64	DNA methylation changes associated with risk factors in tumors of the upper aerodigestive tract. <i>Epigenetics</i> , 2012 , 7, 270-7	5.7	16
63	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
62	Transcriptional regulation of the human tumor suppressor DOK1 by E2F1. <i>Molecular and Cellular Biology</i> , 2012 , 32, 4877-90	4.8	17
61	Mechanisms of Epigenetic Gene Silencing 2011 , 41-53		
60	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

59	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
58	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
57	The Effects of Diet on Epigenetic Processes 2011 , 449-458		1
56	DNA methylation and cancer: ghosts and angels above the genes. <i>Current Opinion in Oncology</i> , 2011 , 23, 69-76	4.2	46
55	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
54	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
53	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
52	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
51	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
50	Epigenetic mechanisms and cancer: an interface between the environment and the genome. <i>Epigenetics</i> , 2011 , 6, 804-19	5.7	174
49	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
48	Epigenetic Identity in Cancer Stem Cells. <i>Pancreatic Islet Biology</i> , 2011 , 127-139	0.4	1
47	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
46	Mechanisms of Histone Modifications 2011 , 25-45		5
45	Methylome analysis reveals Jak-STAT pathway deregulation in putative breast cancer stem cells. <i>Epigenetics</i> , 2011 , 6, 428-39	5.7	59
44	Chromatin: The Entry to and Exit from DNA Repair 2011 , 387-409		
43	Histone code in the cross-talk during DNA damage signaling. <i>Cell Research</i> , 2010 , 20, 113-5	24.7	6
42	Hepatocellular carcinoma displays distinct DNA methylation signatures with potential as clinical predictors. <i>PLoS ONE</i> , 2010 , 5, e9749	3.7	156

4 ¹	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
4 ⁰	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
39	Epigenetics is a fascinating field of modern biology. Preface. <i>Advances in Genetics</i> , 2010 , 71, xi-xii	3.3	4
38	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
37	Introduction: epigenetics and cancer. <i>Advances in Genetics</i> , 2010 , 70, 1-23	3.3	24
36	Histone modifications and cancer. <i>Advances in Genetics</i> , 2010 , 70, 57-85	3.3	147
35	DNA demethylating agents and epigenetic therapy of cancer. <i>Advances in Genetics</i> , 2010 , 70, 327-40	3.3	37
34	Quantitative detection of DNA methylation states in minute amounts of DNA from body fluids. <i>Methods</i> , 2010 , 52, 242-7	4.6	28
33	Oncogenic microRNAs (OncomiRs) as a new class of cancer biomarkers. <i>BioEssays</i> , 2010 , 32, 894-904	4.1	64
32	Epigenetic Changes in Cancer: Role of Environment 2010 , 153-196		2
3 ¹	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
3 ⁰	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
29	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
28	Histone acetyltransferase cofactor Trapp is essential for maintaining the hematopoietic stem/progenitor cell pool. <i>Journal of Immunology</i> , 2009 , 183, 6422-31	5.3	24
27	Epigenetic information in chromatin and cancer. <i>European Journal of Cancer</i> , 2009 , 45 Suppl 1, 442-4	7.5	7
26	Epigenetic signatures in stem cells and cancer stem cells. <i>Epigenomics</i> , 2009 , 1, 261-80	4.4	15
25	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
24	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

23	Developmental and transplacental genotoxicology: fluconazole. <i>Mutation Research - Genetic Toxicology and Environmental Mutagenesis</i> , 2008 , 657, 43-7	3	12
22	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
21	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
20	Genetic and epigenetic alterations as biomarkers for cancer detection, diagnosis and prognosis. <i>Molecular Oncology</i> , 2007 , 1, 26-41	7.9	134
19	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
18	Epigenetics and cancer: towards an evaluation of the impact of environmental and dietary factors. <i>Mutagenesis</i> , 2007 , 22, 91-103	2.8	271
17	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
16	Epigenetic information in chromatin: the code of entry for DNA repair. <i>Cell Cycle</i> , 2006 , 5, 696-701	4.7	52
15	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
14	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
13	An essential function for NBS1 in the prevention of ataxia and cerebellar defects. <i>Nature Medicine</i> , 2005 , 11, 538-44	50.5	133
12	Rendez-vous at mitosis: TRRAPed in the chromatin. <i>Cell Cycle</i> , 2005 , 4, 383-7	4.7	22
11	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
10	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
9	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
8	HAT cofactor Trrap regulates the mitotic checkpoint by modulation of Mad1 and Mad2 expression. <i>EMBO Journal</i> , 2004 , 23, 4824-34	13	44
7	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
6	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

5	Nbn heterozygosity renders mice susceptible to tumor formation and ionizing radiation-induced tumorigenesis. <i>Cancer Research</i> , 2003 , 63, 7263-9	10.1	94
4	Disruption of Trrap causes early embryonic lethality and defects in cell cycle progression. <i>Nature Genetics</i> , 2001 , 29, 206-11	36.3	106
3	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
2	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
1	Interplay between the epigenetic enzyme lysine (K)-specific demethylase 2B and Epstein-Barr virus infection		1