

Toshikazu Ushijima

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.

153
papers

7,623
citations

47
h-index

82
g-index

159
ext. papers

8,551
ext. citations

7.6
avg, IF

6.03
L-index

#	Paper	IF	Citations
153	High levels of aberrant DNA methylation in <i>Helicobacter pylori</i> -infected gastric mucosae and its possible association with gastric cancer risk. <i>Clinical Cancer Research</i> , 2006 , 12, 989-95	12.9	517
152	Detection and interpretation of altered methylation patterns in cancer cells. <i>Nature Reviews Cancer</i> , 2005 , 5, 223-31	31.3	392
151	Inflammatory processes triggered by <i>Helicobacter pylori</i> infection cause aberrant DNA methylation in gastric epithelial cells. <i>Cancer Research</i> , 2010 , 70, 1430-40	10.1	305
150	Focus on gastric cancer. <i>Cancer Cell</i> , 2004 , 5, 121-5	24.3	235
149	DNA methylation of microRNA genes in gastric mucosae of gastric cancer patients: its possible involvement in the formation of epigenetic field defect. <i>International Journal of Cancer</i> , 2009 , 124, 2367-74	7.5	230
148	Chemical genomic screening for methylation-silenced genes in gastric cancer cell lines using 5-aza-2-Deoxycytidine treatment and oligonucleotide microarray. <i>Cancer Science</i> , 2006 , 97, 64-71	6.9	208
147	Epigenetic mechanisms of chronic pain. <i>Trends in Neurosciences</i> , 2015 , 38, 237-46	13.3	193
146	Aberrant methylations in cancer cells: where do they come from?. <i>Cancer Science</i> , 2005 , 96, 206-11	6.9	155
145	Epigenetic field for cancerization. <i>BMB Reports</i> , 2007 , 40, 142-50	5.5	155
144	Silencing of Peroxiredoxin 2 and aberrant methylation of 33 CpG islands in putative promoter regions in human malignant melanomas. <i>Cancer Research</i> , 2006 , 66, 6080-6	10.1	146
143	Fidelity of the methylation pattern and its variation in the genome. <i>Genome Research</i> , 2003 , 13, 868-74	9.7	125
142	Genome-wide profiling of promoter methylation in human. <i>Oncogene</i> , 2006 , 25, 3059-64	9.2	121
141	Identification of 20 genes aberrantly methylated in human breast cancers. <i>International Journal of Cancer</i> , 2005 , 116, 407-14	7.5	119
140	Recurrent mutations of CD79B and MYD88 are the hallmark of primary central nervous system lymphomas. <i>Neuropathology and Applied Neurobiology</i> , 2016 , 42, 279-90	5.2	118
139	The presence of aberrant DNA methylation in noncancerous esophageal mucosae in association with smoking history: a target for risk diagnosis and prevention of esophageal cancers. <i>Cancer</i> , 2009 , 115, 3412-26	6.4	109
138	Frequent hypomethylation in multiple promoter CpG islands is associated with global hypomethylation, but not with frequent promoter hypermethylation. <i>Cancer Science</i> , 2004 , 95, 58-64	6.9	109
137	Diagnostic and therapeutic applications of epigenetics. <i>Japanese Journal of Clinical Oncology</i> , 2005 , 35, 293-301	2.8	108

136	Epigenetic transcriptional activation of monocyte chemotactic protein 3 contributes to long-lasting neuropathic pain. <i>Brain</i> , 2013 , 136, 828-43	11.2	101
135	Molecular pathways: involvement of Helicobacter pylori-triggered inflammation in the formation of an epigenetic field defect, and its usefulness as cancer risk and exposure markers. <i>Clinical Cancer Research</i> , 2012 , 18, 923-9	12.9	98
134	Cancer development based on chronic active gastritis and resulting gastric atrophy as assessed by serum levels of pepsinogen and Helicobacter pylori antibody titer. <i>International Journal of Cancer</i> , 2014 , 134, 1445-57	7.5	97
133	Inflammation-induced repression of tumor suppressor miR-7 in gastric tumor cells. <i>Oncogene</i> , 2012 , 31, 3949-60	9.2	97
132	Persistence of a component of DNA methylation in gastric mucosae after Helicobacter pylori eradication. <i>Journal of Gastroenterology</i> , 2010 , 45, 37-44	6.9	96
131	Identification of 27 5TCpG islands aberrantly methylated and 13 genes silenced in human pancreatic cancers. <i>Oncogene</i> , 2004 , 23, 8705-10	9.2	96
130	The presence of a methylation fingerprint of Helicobacter pylori infection in human gastric mucosae. <i>International Journal of Cancer</i> , 2009 , 124, 905-10	7.5	93
129	Promoter methylation profiling of 30 genes in human malignant melanoma. <i>Cancer Science</i> , 2004 , 95, 962-8	6.9	88
128	Silencing of the UCHL1 gene in human colorectal and ovarian cancers. <i>International Journal of Cancer</i> , 2006 , 119, 1338-44	7.5	83
127	Methylation-associated silencing of the Wnt antagonist SFRP1 gene in human ovarian cancers. <i>Cancer Science</i> , 2004 , 95, 741-4	6.9	82
126	Aberrant DNA methylation in contrast with mutations. <i>Cancer Science</i> , 2010 , 101, 300-5	6.9	81
125	Integrated analysis of cancer-related pathways affected by genetic and epigenetic alterations in gastric cancer. <i>Gastric Cancer</i> , 2015 , 18, 65-76	7.6	77
124	Epigenetic impact of infection on carcinogenesis: mechanisms and applications. <i>Genome Medicine</i> , 2016 , 8, 10	14.4	75
123	Insufficient role of cell proliferation in aberrant DNA methylation induction and involvement of specific types of inflammation. <i>Carcinogenesis</i> , 2011 , 32, 35-41	4.6	68
122	Accumulation of genetic and epigenetic alterations in normal cells and cancer risk. <i>Npj Precision Oncology</i> , 2019 , 3, 7	9.8	67
121	Development of gastric cancer in nonatrophic stomach with highly active inflammation identified by serum levels of pepsinogen and Helicobacter pylori antibody together with endoscopic rugal hyperplastic gastritis. <i>International Journal of Cancer</i> , 2012 , 131, 2632-42	7.5	65
120	Large-scale characterization of DNA methylation changes in human gastric carcinomas with and without metastasis. <i>Clinical Cancer Research</i> , 2014 , 20, 4598-612	12.9	64
119	Decreased expression of the seven ARP2/3 complex genes in human gastric cancers. <i>Cancer Letters</i> , 2004 , 212, 203-10	9.9	63

118	Mechanisms for the induction of gastric cancer by <i>Helicobacter pylori</i> infection: aberrant DNA methylation pathway. <i>Gastric Cancer</i> , 2017 , 20, 8-15	7.6	62
117	Incidence of and risk factors for metachronous gastric cancer after endoscopic resection and successful <i>Helicobacter pylori</i> eradication: results of a large-scale, multicenter cohort study in Japan. <i>Gastric Cancer</i> , 2016 , 19, 911-8	7.6	60
116	Role of transcriptional and posttranscriptional regulation of methionine adenosyltransferases in liver cancer progression. <i>Hepatology</i> , 2012 , 56, 165-75	11.2	57
115	Interleukin-1 β induced by <i>Helicobacter pylori</i> infection enhances mouse gastric carcinogenesis. <i>Cancer Letters</i> , 2013 , 340, 141-7	9.9	56
114	Prevention of <i>Helicobacter pylori</i> -induced gastric cancers in gerbils by a DNA demethylating agent. <i>Cancer Prevention Research</i> , 2013 , 6, 263-70	3.2	55
113	Dose-dependent roles for canonical Wnt signalling in de novo crypt formation and cell cycle properties of the colonic epithelium. <i>Development (Cambridge)</i> , 2013 , 140, 66-75	6.6	54
112	Comprehensive analyses using next-generation sequencing and immunohistochemistry enable precise treatment in advanced gastric cancer. <i>Annals of Oncology</i> , 2016 , 27, 127-33	10.3	52
111	Identification of coexistence of DNA methylation and H3K27me3 specifically in cancer cells as a promising target for epigenetic therapy. <i>Carcinogenesis</i> , 2015 , 36, 192-201	4.6	52
110	Alu and SatI hypomethylation in <i>Helicobacter pylori</i> -infected gastric mucosae. <i>International Journal of Cancer</i> , 2011 , 128, 33-9	7.5	51
109	Lack of association between CpG island methylator phenotype in human gastric cancers and methylation in their background non-cancerous gastric mucosae. <i>Cancer Science</i> , 2007 , 98, 1853-61	6.9	51
108	Genetic and epigenetic alterations in normal tissues have differential impacts on cancer risk among tissues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 1328-1333	11.5	50
107	Silencing of tissue factor pathway inhibitor-2 gene in malignant melanomas. <i>International Journal of Cancer</i> , 2007 , 121, 301-7	7.5	48
106	Roadmap for investigating epigenome deregulation and environmental origins of cancer. <i>International Journal of Cancer</i> , 2018 , 142, 874-882	7.5	46
105	Identification of genes targeted by CpG island methylator phenotype in neuroblastomas, and their possible integrative involvement in poor prognosis. <i>Oncology</i> , 2008 , 74, 50-60	3.6	45
104	Down-regulated expression of prostasin in high-grade or hormone-refractory human prostate cancers. <i>Prostate</i> , 2003 , 54, 187-93	4.2	45
103	WNT Pathway Gene Mutations Are Associated With the Presence of Dysplasia in Colorectal Sessile Serrated Adenoma/Polyps. <i>American Journal of Surgical Pathology</i> , 2017 , 41, 1188-1197	6.7	44
102	ANGPTL4 is a secreted tumor suppressor that inhibits angiogenesis. <i>Oncogene</i> , 2014 , 33, 2273-8	9.2	44
101	Revisit of field cancerization in squamous cell carcinoma of upper aerodigestive tract: better risk assessment with epigenetic markers. <i>Cancer Prevention Research</i> , 2011 , 4, 1982-92	3.2	44

100	No-observed effect levels for carcinogenicity and for in vivo mutagenicity of a genotoxic carcinogen. <i>Toxicological Sciences</i> , 2004 , 81, 273-9	4.4	44
99	Methylation-sensitive representational difference analysis and its application to cancer research. <i>Annals of the New York Academy of Sciences</i> , 2003 , 983, 131-41	6.5	44
98	Compendium of aberrant DNA methylation and histone modifications in cancer. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 455, 3-9	3.4	43
97	Methylation silencing of transforming growth factor-beta receptor type II in rat prostate cancers. <i>Cancer Research</i> , 2008 , 68, 2112-21	10.1	43
96	Overexpression of PIK3CA is associated with lymph node metastasis in esophageal squamous cell carcinoma. <i>International Journal of Oncology</i> , 2009 , 34, 767-75	1	42
95	Identification of a TLR2-regulated gene signature associated with tumor cell growth in gastric cancer. <i>Oncogene</i> , 2017 , 36, 5134-5144	9.2	41
94	Marked and independent prognostic significance of the CpG island methylator phenotype in neuroblastomas. <i>Cancer Letters</i> , 2007 , 247, 253-8	9.9	41
93	Frequent involvement of chromatin remodeler alterations in gastric field cancerization. <i>Cancer Letters</i> , 2015 , 357, 328-338	9.9	39
92	Reduced expression of the insulin-induced protein 1 and p41 Arp2/3 complex genes in human gastric cancers. <i>International Journal of Cancer</i> , 2002 , 100, 57-62	7.5	39
91	Genome-wide methylation profiles in primary intracranial germ cell tumors indicate a primordial germ cell origin for germinomas. <i>Acta Neuropathologica</i> , 2017 , 133, 445-462	14.3	38
90	Autophagy impairment by Helicobacter pylori-induced methylation silencing of MAP1LC3Av1 promotes gastric carcinogenesis. <i>International Journal of Cancer</i> , 2017 , 140, 2272-2283	7.5	38
89	Recurrent neomorphic mutations of MTOR in central nervous system and testicular germ cell tumors may be targeted for therapy. <i>Acta Neuropathologica</i> , 2016 , 131, 889-901	14.3	38
88	Methylation and expression analysis of 15 genes and three normally-methylated genes in 13 Ovarian cancer cell lines. <i>Cancer Letters</i> , 2006 , 241, 213-20	9.9	38
87	DNA methylation of microRNA-124a is a potential risk marker of colitis-associated cancer in patients with ulcerative colitis. <i>Digestive Diseases and Sciences</i> , 2014 , 59, 2444-51	4	37
86	Promoter hypermethylation and post-transcriptional mechanisms for reduced BRCA1 immunoreactivity in sporadic human breast cancers. <i>Japanese Journal of Clinical Oncology</i> , 2002 , 32, 79-84 ⁸	3.8	37
85	Adenomatous polyposis coli 1A is likely to be methylated as a passenger in human gastric carcinogenesis. <i>Cancer Letters</i> , 2009 , 285, 182-9	9.9	36
84	Dependence receptor UNC5D mediates nerve growth factor depletion-induced neuroblastoma regression. <i>Journal of Clinical Investigation</i> , 2013 , 123, 2935-47	15.9	36
83	Cancer cell niche factors secreted from cancer-associated fibroblast by loss of H3K27me3. <i>Gut</i> , 2020 , 69, 243-251	19.2	35

82	Development of a novel output value for quantitative assessment in methylated DNA immunoprecipitation-CpG island microarray analysis. <i>DNA Research</i> , 2009 , 16, 275-86	4.5	33
81	Identification of gastric cancer risk markers that are informative in individuals with past H. pylori infection. <i>Gastric Cancer</i> , 2012 , 15, 382-8	7.6	32
80	FHL1 on chromosome X is a single-hit gastrointestinal tumor-suppressor gene and contributes to the formation of an epigenetic field defect. <i>Oncogene</i> , 2013 , 32, 2140-9	9.2	32
79	Global expression analysis of N-methyl-N-nitro-N-nitrosoguanidine-induced rat stomach carcinomas using oligonucleotide microarrays. <i>Carcinogenesis</i> , 2003 , 24, 861-7	4.6	32
78	Visualization of multivalent histone modification in a single cell reveals highly concerted epigenetic changes on differentiation of embryonic stem cells. <i>Nucleic Acids Research</i> , 2013 , 41, 7231-9	20.1	30
77	Development of a novel approach, the epigenome-based outlier approach, to identify tumor-suppressor genes silenced by aberrant DNA methylation. <i>Cancer Letters</i> , 2012 , 322, 204-12	9.9	29
76	Induction of aberrant trimethylation of histone H3 lysine 27 by inflammation in mouse colonic epithelial cells. <i>Carcinogenesis</i> , 2012 , 33, 2384-90	4.6	28
75	Expression quantitative trait loci analysis of 13 genes in the rat prostate. <i>Genetics</i> , 2005 , 171, 1231-8	4	28
74	A tissue microRNA signature that predicts the prognosis of breast cancer in young women. <i>PLoS ONE</i> , 2017 , 12, e0187638	3.7	27
73	Identification of PRTFDC1 silencing and aberrant promoter methylation of GPR150, ITGA8 and HOXD11 in ovarian cancers. <i>Life Sciences</i> , 2007 , 80, 1458-65	6.8	26
72	Estimation of the fraction of cancer cells in a tumor DNA sample using DNA methylation. <i>PLoS ONE</i> , 2013 , 8, e82302	3.7	25
71	Epigenetic inactivation of FAT4 contributes to gastric field cancerization. <i>Gastric Cancer</i> , 2017 , 20, 136-145	4.5	24
70	Novel epigenetic markers for gastric cancer risk stratification in individuals after Helicobacter pylori eradication. <i>Gastric Cancer</i> , 2018 , 21, 745-755	7.6	24
69	Association of gastric cancer risk factors with DNA methylation levels in gastric mucosa of healthy Japanese: a cross-sectional study. <i>Carcinogenesis</i> , 2015 , 36, 1291-8	4.6	24
68	Association between frequent CpG island methylation and HER2 amplification in human breast cancers. <i>Carcinogenesis</i> , 2009 , 30, 466-71	4.6	23
67	Methylation of multiple genes in gastric glands with intestinal metaplasia: A disorder with polyclonal origins. <i>American Journal of Pathology</i> , 2006 , 169, 1643-51	5.8	23
66	Whole-genome analyses of loss of heterozygosity and methylation analysis of four tumor-suppressor genes in N-methyl-N-nitro-N-nitrosoguanidine-induced rat stomach carcinomas. <i>Cancer Science</i> , 2005 , 96, 409-13	6.9	23
65	Cloning of the 5Tupstream region of the rat p16 gene and its role in silencing. <i>Japanese Journal of Cancer Research</i> , 2002 , 93, 1100-6		22

64	Targeting of super-enhancers and mutant BRAF can suppress growth of BRAF-mutant colon cancer cells via repression of MAPK signaling pathway. <i>Cancer Letters</i> , 2017 , 402, 100-109	9.9	21
63	Altered mucosal DNA methylation in parallel with highly active Helicobacter pylori-related gastritis. <i>Gastric Cancer</i> , 2013 , 16, 488-97	7.6	21
62	Methylation destiny: Moira takes account of histones and RNA polymerase II. <i>Epigenetics</i> , 2010 , 5, 89-95	5.7	21
61	Linkage and microarray analyses of susceptibility genes in ACI/Seg rats: a model for prostate cancers in the aged. <i>Cancer Research</i> , 2005 , 65, 2610-6	10.1	20
60	Chronic treatment of non-small-cell lung cancer cells with gefitinib leads to an epigenetic loss of epithelial properties associated with reductions in microRNA-155 and -200c. <i>PLoS ONE</i> , 2017 , 12, e0172115	3.7	20
59	Integrated analysis of DNA methylation and mutations in esophageal squamous cell carcinoma. <i>Molecular Carcinogenesis</i> , 2016 , 55, 2077-2088	5	19
58	Identification and validation of DNA methylation markers to predict lymph node metastasis of esophageal squamous cell carcinomas. <i>Annals of Surgical Oncology</i> , 2011 , 18, 1185-94	3.1	19
57	TET repression and increased DNMT activity synergistically induce aberrant DNA methylation. <i>Journal of Clinical Investigation</i> , 2020 , 130, 5370-5379	15.9	19
56	RNF208, an estrogen-inducible E3 ligase, targets soluble Vimentin to suppress metastasis in triple-negative breast cancers. <i>Nature Communications</i> , 2019 , 10, 5805	17.4	19
55	Establishment of a DNA methylation marker to evaluate cancer cell fraction in gastric cancer. <i>Gastric Cancer</i> , 2016 , 19, 361-369	7.6	18
54	PRC2-Mediated Transcriptomic Alterations at the Embryonic Stage Govern Tumorigenesis and Clinical Outcome in MYCN-Driven Neuroblastoma. <i>Cancer Research</i> , 2017 , 77, 5259-5271	10.1	18
53	Genome-wide analysis of DNA methylation changes induced by gestational arsenic exposure in liver tumors. <i>Cancer Science</i> , 2013 , 104, 1575-85	6.9	18
52	Pathological complete response of HER2-positive breast cancer to trastuzumab and chemotherapy can be predicted by HSD17B4 methylation. <i>Oncotarget</i> , 2017 , 8, 19039-19048	3.3	18
51	Hypomethylation of Alu repetitive elements in esophageal mucosa, and its potential contribution to the epigenetic field for cancerization. <i>Cancer Causes and Control</i> , 2012 , 23, 865-73	2.8	17
50	Methylation silencing of angiotensin-like 4 in rat and human mammary carcinomas. <i>Cancer Science</i> , 2011 , 102, 1337-43	6.9	17
49	ZNF695 methylation predicts a response of esophageal squamous cell carcinoma to definitive chemoradiotherapy. <i>Journal of Cancer Research and Clinical Oncology</i> , 2015 , 141, 453-63	4.9	16
48	Gene expression profiling distinguishes between spontaneous and radiation-induced rat mammary carcinomas. <i>Journal of Radiation Research</i> , 2008 , 49, 349-60	2.4	16
47	Systemic Administration of Small Interfering RNA Targeting Human Nestin Inhibits Pancreatic Cancer Cell Proliferation and Metastasis. <i>Pancreas</i> , 2016 , 45, 93-100	2.6	16

46	Epigenetic priming sensitizes gastric cancer cells to irinotecan and cisplatin by restoring multiple pathways. <i>Gastric Cancer</i> , 2020 , 23, 105-115	7.6	16
45	Persistence of gene expression changes in stomach mucosae induced by short-term N-methyl-N-nitro-N-nitrosoguanidine treatment and their presence in stomach cancers. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2004 , 549, 185-93	3.3	15
44	Genome-wide DNA methylation profiling identifies primary central nervous system lymphoma as a distinct entity different from systemic diffuse large B-cell lymphoma. <i>Acta Neuropathologica</i> , 2017 , 133, 321-324	14.3	14
43	Presacral malignant teratoid neoplasm in association with pathogenic DICER1 variation. <i>Modern Pathology</i> , 2019 , 32, 1744-1750	9.8	14
42	Clinical application of the CpG island methylator phenotype to prognostic diagnosis in neuroblastomas. <i>Journal of Human Genetics</i> , 2013 , 58, 428-33	4.3	14
41	Antibiotics suppress colon tumorigenesis through inhibition of aberrant DNA methylation in an azoxymethane and dextran sulfate sodium colitis model. <i>Cancer Science</i> , 2019 , 110, 147-156	6.9	14
40	Metabolomic profiling reveals salivary hypotaurine as a potential early detection marker for medication-related osteonecrosis of the jaw. <i>PLoS ONE</i> , 2019 , 14, e0220712	3.7	13
39	Effects of genome architecture and epigenetic factors on susceptibility of promoter CpG islands to aberrant DNA methylation induction. <i>Genomics</i> , 2011 , 98, 182-8	4.3	13
38	Distinct DNA methylation targets by aging and chronic inflammation: a pilot study using gastric mucosa infected with <i>Helicobacter pylori</i> . <i>Clinical Epigenetics</i> , 2019 , 11, 191	7.7	13
37	Novel prodrugs of decitabine with greater metabolic stability and less toxicity. <i>Clinical Epigenetics</i> , 2019 , 11, 111	7.7	12
36	Early-Stage Induction of SWI/SNF Mutations during Esophageal Squamous Cell Carcinogenesis. <i>PLoS ONE</i> , 2016 , 11, e0147372	3.7	12
35	Degree of methylation burden is determined by the exposure period to carcinogenic factors. <i>Cancer Science</i> , 2017 , 108, 316-321	6.9	11
34	LINC00162 confers sensitivity to 5-Aza-2'deoxyctidine via modulation of an RNA splicing protein, HNRNPH1. <i>Oncogene</i> , 2019 , 38, 5281-5293	9.2	11
33	Targeting aberrant DNA hypermethylation as a driver of ATL leukemogenesis by using the new oral demethylating agent OR-2100. <i>Blood</i> , 2020 , 136, 871-884	2.2	11
32	Establishment of a detection system for demethylating agents using an endogenous promoter CpG island. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2004 , 568, 187-94	3.3	11
31	Exclusive KRAS mutation in microsatellite-unstable human colorectal carcinomas with sequence alterations in the DNA mismatch repair gene, MLH1. <i>Gene</i> , 2008 , 423, 188-93	3.8	10
30	Stronger prognostic power of the CpG island methylator phenotype than methylation of individual genes in neuroblastomas. <i>Japanese Journal of Clinical Oncology</i> , 2013 , 43, 641-5	2.8	9
29	The absence of Mth1 inactivation and DNA polymerase kappa overexpression in rat mammary carcinomas with frequent A:T to C:G transversions. <i>Japanese Journal of Cancer Research</i> , 2002 , 93, 501-6		9

28	Epigenetic reprogramming underlies efficacy of DNA demethylation therapy in osteosarcomas. <i>Scientific Reports</i> , 2019 , 9, 20360	4.9	9
27	Establishment of a high-throughput detection system for DNA demethylating agents. <i>Epigenetics</i> , 2018 , 13, 147-155	5.7	8
26	A 5Tregion polymorphism modulates promoter activity of the tumor suppressor gene MFSD2A. <i>Molecular Cancer</i> , 2011 , 10, 81	42.1	8
25	The Origin of CIMP, At Last. <i>Cancer Cell</i> , 2019 , 35, 165-167	24.3	7
24	A novel method to quantify base substitution mutations at the 10 per bp level in DNA samples. <i>Cancer Letters</i> , 2017 , 403, 152-158	9.9	6
23	Differential expression of genes related to levels of mucosal cell proliferation among multiple rat strains by using oligonucleotide microarrays. <i>Mammalian Genome</i> , 2003 , 14, 845-52	3.2	6
22	Genetic and epigenetic profiling indicates the proximal tubule origin of renal cancers in end-stage renal disease. <i>Cancer Science</i> , 2020 , 111, 4276-4287	6.9	6
21	The Moment that KRAS Mutation Started to Evolve into Precision Medicine in Metastatic Colorectal Cancer. <i>Cancer Research</i> , 2016 , 76, 6443-6444	10.1	6
20	DNA methylation marker to estimate the breast cancer cell fraction in DNA samples. <i>Medical Oncology</i> , 2018 , 35, 147	3.7	6
19	FGF5 methylation is a sensitivity marker of esophageal squamous cell carcinoma to definitive chemoradiotherapy. <i>Scientific Reports</i> , 2019 , 9, 13347	4.9	5
18	Analysis of DNA Methylation in Tissues Exposed to Inflammation. <i>Methods in Molecular Biology</i> , 2018 , 1725, 185-199	1.4	5
17	SAA1 is upregulated in gastric cancer-associated fibroblasts possibly by its enhancer activation. <i>Carcinogenesis</i> , 2021 , 42, 180-189	4.6	5
16	Multi-omics analyses identify HSD17B4 methylation-silencing as a predictive and response marker of HER2-positive breast cancer to HER2-directed therapy. <i>Scientific Reports</i> , 2020 , 10, 15530	4.9	5
15	Methylation changes and aberrant expression of FGFR3 in Lewy body disease neurons. <i>Brain Research</i> , 2018 , 1697, 59-66	3.7	4
14	Low-dose DNA demethylating therapy induces reprogramming of diverse cancer-related pathways at the single-cell level. <i>Clinical Epigenetics</i> , 2020 , 12, 142	7.7	4
13	Increased H-ras mutation frequency in mammary tumors of rats initiated with N-methyl-N-nitrosourea (MNU) and treated with acrylamide. <i>Journal of Toxicological Sciences</i> , 2009 , 34, 407-12	1.9	3
12	Sparse and wavy hair: a new model for hypoplasia of hair follicle and mammary glands on rat chromosome 17. <i>Journal of Heredity</i> , 2005 , 96, 339-45	2.4	3
11	Predictive value of genetic analysis for pathological complete response to preoperative treatment in HER2 positive, HR negative early breast cancer (PASSION trial). <i>Japanese Journal of Clinical Oncology</i> , 2018 , 48, 388-391	2.8	2

10	Influence of degree of DNA degradation in formalin-fixed and paraffin-embedded tissue samples on accuracy of genome-wide DNA methylation analysis. <i>Epigenomics</i> , 2021 , 13, 565-576	4.4	2
9	Silylation of Deoxynucleotide Analog Yields an Orally Available Drug with Antileukemia Effects. <i>Molecular Cancer Therapeutics</i> , 2021 , 20, 1412-1421	6.1	2
8	BRCA1 promoter methylation in breast cancer patients is associated with response to olaparib/eribulin combination therapy. <i>Breast Cancer Research and Treatment</i> , 2020 , 181, 323-329	4.4	2
7	Mapping genomic and epigenomic evolution in cancer ecosystems. <i>Science</i> , 2021 , 373, 1474-1479	33.3	2
6	Prediction of tissue origin of adenocarcinomas in the esophagogastric junction by DNA methylation. <i>Gastric Cancer</i> , 2021 , 1	7.6	1
5	Autoimmune gastritis induces aberrant DNA methylation reflecting its carcinogenic potential.. <i>Journal of Gastroenterology</i> , 2022 , 57, 144	6.9	0
4	DNA methylation marker to estimate ovarian cancer cell fraction.. <i>Medical Oncology</i> , 2022 , 39, 78	3.7	0
3	ARID1A loss-of-function induces CpG island methylator phenotype.. <i>Cancer Letters</i> , 2022 , 532, 215587	9.9	
2	Combination of a synthetic retinoid and a DNA demethylating agent induced differentiation of neuroblastoma through retinoic acid signal reprogramming. <i>British Journal of Cancer</i> , 2021 , 125, 1647-1656	8.7	
1	Comparable genetic alteration profiles between gastric cancers with current and past <i>Helicobacter pylori</i> infection. <i>Scientific Reports</i> , 2021 , 11, 23443	4.9	