Eri Arai

List of Publications by Year
in descending order

28 papers	879 citations	471477 17 h-index	526264 27 g-index
28 all docs	28 docs citations	28 times ranked	1334 citing authors

#	Article	IF	Citations
1	The oligodendroglial histological features are not independently predictive of patient prognosis in lower-grade gliomas. Brain Tumor Pathology, 2022, , 1.	1.7	2
2	DNA hypermethylation of the <i>ZNF132</i> gene participates in the clinicopathological aggressiveness of 'pan-negative'-type lung adenocarcinomas. Carcinogenesis, 2021, 42, 169-179.	2.8	9
3	Evaluation of clinical formalin‐fixed paraffin‐embedded tissue quality for targeted‐bisulfite sequencing. Pathology International, 2021, 71, 135-140.	1.3	5
4	Clinicopathological impacts of DNA methylation alterations on pancreatic ductal adenocarcinoma: prediction of early recurrence based on genome-wide DNA methylation profiling. Journal of Cancer Research and Clinical Oncology, 2021, 147, 1341-1354.	2.5	11
5	Aberrant DNA methylation results in altered gene expression in non-alcoholic steatohepatitis-related hepatocellular carcinomas. Journal of Cancer Research and Clinical Oncology, 2020, 146, 2461-2477.	2.5	27
6	Cooperative participation of epigenomic and genomic alterations in the clinicopathological diversity of gastric adenocarcinomas: significance of cell adhesion and epithelial–mesenchymal transition-related signaling pathways. Carcinogenesis, 2020, 41, 1473-1484.	2.8	7
7	Establishment of diagnostic criteria for upper urinary tract urothelial carcinoma based on genome-wide DNA methylation analysis. Epigenetics, 2020, 15, 1289-1301.	2.7	9
8	Establishment of permutation for cancer risk estimation in the urothelium based on genome-wide DNA methylation analysis. Carcinogenesis, 2019, 40, 1308-1319.	2.8	21
9	Genome-wide DNA methylation profile of early-onset endometrial cancer: its correlation with genetic aberrations and comparison with late-onset endometrial cancer. Carcinogenesis, 2019, 40, 611-623.	2.8	42
10	The Japanese Society of Pathology Guidelines on the handling of pathological tissue samples for genomic research: Standard operating procedures based on empirical analyses. Pathology International, 2018, 68, 63-90.	1.3	44
11	Novel method for <scp>DNA</scp> methylation analysis using high‐performance liquid chromatography and its clinical application. Cancer Science, 2018, 109, 1690-1700.	3.9	20
12	Feasibility of methylome analysis using small amounts of genomic DNA from formalin‐fixed paraffin‐embedded tissue. Pathology International, 2018, 68, 633-635.	1.3	12
13	Epigenome mapping of human normal purified hepatocytes: personal epigenome variation and genome–epigenome correlation. Epigenomics, 2018, 10, 955-979.	2.1	3
14	Genome-wide DNA methylation analysis during non-alcoholic steatohepatitis-related multistage hepatocarcinogenesis: comparison with hepatitis virus-related carcinogenesis. Carcinogenesis, 2017, 38, 261-270.	2.8	51
15	Genes involved in development and differentiation are commonly methylated in cancers derived from multiple organs: A single-institutional methylome analysis using 1007 tissue specimens. Carcinogenesis, 2017, 38, bgw209.	2.8	16
16	Alterations of the spindle checkpoint pathway in clinicopathologically aggressive <scp>C</scp>p<scp>G</scp> island methylator phenotype clear cell renal cell carcinomas. International Journal of Cancer, 2015, 137, 2589-2606.	5.1	41
17	Epigenetic clustering of gastric carcinomas based on DNA methylation profiles at the precancerous stage: its correlation with tumor aggressiveness and patient outcome. Carcinogenesis, 2015, 36, 509-520.	2.8	31
18	Multilayer-omics analyses of human cancers: exploration of biomarkers and drug targets based on the activities of the International Human Epigenome Consortium. Frontiers in Genetics, 2014, 5, 24.	2.3	17

#	Article	IF	Citations
19	Epigenetic clustering of lung adenocarcinomas based on DNA methylation profiles in adjacent lung tissue: Its correlation with smoking history and chronic obstructive pulmonary disease. International Journal of Cancer, 2014, 135, 319-334.	5.1	57
20	Prognostication of patients with clear cell renal cell carcinomas based on quantification of DNA methylation levels of CpG island methylator phenotype marker genes. BMC Cancer, 2014, 14, 772.	2.6	47
21	Single-CpG-resolution methylome analysis identifies clinicopathologically aggressive CpG island methylator phenotype clear cell renal cell carcinomas. Carcinogenesis, 2012, 33, 1487-1493.	2.8	116
22	Carcinogenetic risk estimation based on quantification of DNA methylation levels in liver tissue at the precancerous stage. International Journal of Cancer, 2011, 129, 1170-1179.	5.1	38
23	Copy number alterations in urothelial carcinomas: their clinicopathological significance and correlation with DNA methylation alterations. Carcinogenesis, 2011, 32, 462-469.	2.8	13
24	Diagnosis and Prognostication of Ductal Adenocarcinomas of the Pancreas Based on Genome-Wide DNA Methylation Profiling by Bacterial Artificial Chromosome Array-Based Methylated CpG Island Amplification. Journal of Biomedicine and Biotechnology, 2011, 2011, 1-10.	3.0	7
25	Genomeâ€wide DNA methylation profiles in urothelial carcinomas and urothelia at the precancerous stage. Cancer Science, 2010, 101, 231-240.	3.9	44
26	DNA methylation profiles in precancerous tissue and cancers: carcinogenetic risk estimation and prognostication based on DNA methylation status. Epigenomics, 2010, 2, 467-481.	2.1	33
27	Genomeâ€wide DNA methylation profiles in liver tissue at the precancerous stage and in hepatocellular carcinoma. International Journal of Cancer, 2009, 125, 2854-2862.	5.1	58
28	Regional DNA hypermethylation and DNA methyltransferase (DNMT) 1 protein overexpression in both renal tumors and corresponding nontumorous renal tissues. International Journal of Cancer, 2006, 119, 288-296.	5.1	98