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Epigenetic clustering of gastric carcinomas based on DNA methylation profiles at the precancerous stage: its correlation with tumor aggressiveness and patient outcome

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#	Paper	IF	Citations
28	Genomic-Wide Analysis with Microarrays in Human Oncology. <i>Microarrays (Basel, Switzerland)</i> , 2015 , 4, 454-73		9
27	Clinical effect of DAPK promoter methylation in gastric cancer: A systematic meta-analysis. <i>Medicine (United States)</i> , 2016 , 95, e5040	1.8	6
26	The epigenetic effects of aspirin: the modification of histone H3 lysine 27 acetylation in the prevention of colon carcinogenesis in azoxymethane- and dextran sulfate sodium-treated CF-1 mice. <i>Carcinogenesis</i> , 2016 , 37, 616-624	4.6	33
25	A truncated splice variant of human lysyl oxidase-like 2 promotes migration and invasion in esophageal squamous cell carcinoma. <i>International Journal of Biochemistry and Cell Biology</i> , 2016 , 75, 85-98	5.6	20
24	Epigenetic impact of infection on carcinogenesis: mechanisms and applications. <i>Genome Medicine</i> , 2016 , 8, 10	14.4	75
23	Emerging role of long noncoding RNAs in lung cancer: Current status and future prospects. <i>Respiratory Medicine</i> , 2016 , 110, 12-9	4.6	29
22	Genome-wide DNA methylation analysis during non-alcoholic steatohepatitis-related multistage hepatocarcinogenesis: comparison with hepatitis virus-related carcinogenesis. <i>Carcinogenesis</i> , 2017 , 38, 261-270	4.6	31
21	Genes involved in development and differentiation are commonly methylated in cancers derived from multiple organs: a single-institutional methylome analysis using 1007 tissue specimens. <i>Carcinogenesis</i> , 2017 , 38, 241-251	4.6	10
20	Reduced O-GlcNAc glycosylation on gastric gland mucin is a biomarker of malignant potential for gastric cancer, Barrett's adenocarcinoma, and pancreatic cancer. <i>Histochemistry and Cell Biology</i> , 2018 , 149, 569-575	2.4	9
19	DNA methylome and transcriptome alterations and cancer prevention by curcumin in colitis-accelerated colon cancer in mice. <i>Carcinogenesis</i> , 2018 , 39, 669-680	4.6	68
18	An evolutionary perspective on field cancerization. <i>Nature Reviews Cancer</i> , 2018 , 18, 19-32	31.3	196
17	Low levels of ADAM23 expression in epithelial ovarian cancer are associated with poor survival. <i>Pathology Research and Practice</i> , 2018 , 214, 1115-1122	3.4	7
16	Establishment of permutation for cancer risk estimation in the urothelium based on genome-wide DNA methylation analysis. <i>Carcinogenesis</i> , 2019 , 40, 1308-1319	4.6	9
15	Altered DNA methylation is associated with aberrant stemness gene expression in early-stage HNSCC. <i>International Journal of Oncology</i> , 2019 , 55, 915-924	4.4	2
14	Analysis of the clinical significance of DNA methylation in gastric cancer based on a genome-wide high-resolution array. <i>Clinical Epigenetics</i> , 2019 , 11, 154	7.7	8
13	TiO nanoparticles generate superoxide and alter gene expression in human lung cells.. <i>RSC Advances</i> , 2019 , 9, 25039-25047	3.7	13
12	Type XXIII collagen. 2019 , 181-185		

11	Deficiency of Stomach-Type Claudin-18 in Mice Induces Gastric Tumor Formation Independent of H ₂ O ₂ Infection. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019 , 8, 119-142	7.9	16
10	Genome-wide DNA methylation profile of early-onset endometrial cancer: its correlation with genetic aberrations and comparison with late-onset endometrial cancer. <i>Carcinogenesis</i> , 2019 , 40, 611-623	4.6	28
9	Olfactomedin 4 downregulation is associated with tumor initiation, growth and progression in human prostate cancer. <i>International Journal of Cancer</i> , 2020 , 146, 1346-1358	7.5	5
8	Exploring the roles of MACIT and multiplexin collagens in stem cells and cancer. <i>Seminars in Cancer Biology</i> , 2020 , 62, 134-148	12.7	13
7	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. <i>Carcinogenesis</i> , 2020 , 41, 1473-1484	4.6	2
6	Establishment of diagnostic criteria for upper urinary tract urothelial carcinoma based on genome-wide DNA methylation analysis. <i>Epigenetics</i> , 2020 , 15, 1289-1301	5.7	3
5	DNA hypermethylation of the ZNF132 gene participates in the clinicopathological aggressiveness of pan-negative type lung adenocarcinomas. <i>Carcinogenesis</i> , 2021 , 42, 169-179	4.6	1
4	Clinicopathological impacts of DNA methylation alterations on pancreatic ductal adenocarcinoma: prediction of early recurrence based on genome-wide DNA methylation profiling. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021 , 147, 1341-1354	4.9	1
3	Epigenetic silencing of olfactomedin-4 enhances gastric cancer cell invasion via activation of focal adhesion kinase signaling. <i>BMB Reports</i> , 2015 , 48, 630-5	5.5	11
2	Feasibility and reproducibility of a plasma-based multiplex DNA methylation assay for early detection of gastric cancer. 2022 , 154086		
1	DNA methylation status of the SPHK1 and LTB genes underlies the clinicopathological diversity of non-alcoholic steatohepatitis-related hepatocellular carcinomas.		0