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Alterations of the spindle checkpoint pathway in clinicopathologically aggressive CpG island methylator phenotype clear cell renal cell carcinomas

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#	Paper	IF	Citations
38	The proteomic landscape of renal tumors. <i>Expert Review of Proteomics</i> , 2016 , 13, 1103-1120	4.2	11
37	The Potential Roles of Long Noncoding RNAs (lncRNA) in Glioblastoma Development. <i>Molecular Cancer Therapeutics</i> , 2016 , 15, 2977-2986	6.1	39
36	Methylation of tumor suppressor gene CDH13 and SHP1 promoters and their epigenetic regulation by the UHRF1/PRMT5 complex in endometrial carcinoma. <i>Gynecologic Oncology</i> , 2016 , 140, 145-51	4.9	34
35	Anti-SIRP antibodies as a potential new tool for cancer immunotherapy. <i>JCI Insight</i> , 2017 , 2, e89140	9.9	78
34	The Japanese Society of Pathology Guidelines on the handling of pathological tissue samples for genomic research: Standard operating procedures based on empirical analyses. <i>Pathology International</i> , 2018 , 68, 63-90	1.8	27
33	Novel method for DNA methylation analysis using high-performance liquid chromatography and its clinical application. <i>Cancer Science</i> , 2018 , 109, 1690-1700	6.9	13
32	The Role of DNA Methylation in Renal Cell Carcinoma. <i>Molecular Diagnosis and Therapy</i> , 2018 , 22, 431-442	4.5	29
31	Epigenome mapping of human normal purified hepatocytes: personal epigenome variation and genome-epigenome correlation. <i>Epigenomics</i> , 2018 , 10, 955-979	4.4	2
30	NEK2 Is an Effective Target for Cancer Therapy With Potential to Induce Regression of Multiple Human Malignancies. <i>Anticancer Research</i> , 2019 , 39, 2251-2258	2.3	19
29	Somatic mutation of DNAH genes implicated higher chemotherapy response rate in gastric adenocarcinoma patients. <i>Journal of Translational Medicine</i> , 2019 , 17, 109	8.5	6
28	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
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23	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
22	Identification of WHO II/III gliomas by 16 prognostic-related gene signatures using machine learning methods. <i>Current Medicinal Chemistry</i> , 2021 ,	4.3	0

21	Phenotypes and genotypes in non-consanguineous and consanguineous primary microcephaly: High incidence of epilepsy. <i>Molecular Genetics & Genomic Medicine</i> , 2021 , 9, e1768	2.3	1
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17	Reproductive history and blood cell DNA methylation later in life: the Young Finns Study.. <i>Clinical Epigenetics</i> , 2021 , 13, 227	7.7	0
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9	Impact of neoadjuvant chemotherapy on somatic mutation status in high-grade serous ovarian carcinoma.. <i>Journal of Ovarian Research</i> , 2022 , 15, 50	5.5	0
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