Hiromu Suzuki

List of Publications by Year in descending order

103 papers	7,736 citations	94269 37 h-index	51492 86 g-index
105 all docs	105 docs citations	105 times ranked	10113 citing authors

#	Article	IF	Citations
1	Epigenetic inactivation of SFRP genes allows constitutive WNT signaling in colorectal cancer. Nature Genetics, 2004, 36, 417-422.	9.4	976
2	A genomic screen for genes upregulated by demethylation and histone deacetylase inhibition in human colorectal cancer. Nature Genetics, 2002, 31, 141-149.	9.4	820
3	Epigenetic Silencing of MicroRNA-34b/c and B-Cell Translocation Gene 4 Is Associated with CpG Island Methylation in Colorectal Cancer. Cancer Research, 2008, 68, 4123-4132.	0.4	593
4	Upregulation of miR-196a and HOTAIR Drive Malignant Character in Gastrointestinal Stromal Tumors. Cancer Research, 2012, 72, 1126-1136.	0.4	336
5	Comparing the DNA Hypermethylome with Gene Mutations in Human Colorectal Cancer. PLoS Genetics, 2007, 3, e157.	1.5	307
6	GATA-4 and GATA-5 Transcription Factor Genes and Potential Downstream Antitumor Target Genes Are Epigenetically Silenced in Colorectal and Gastric Cancer. Molecular and Cellular Biology, 2003, 23, 8429-8439.	1.1	234
7	DNA methylation and microRNA dysregulation in cancer. Molecular Oncology, 2012, 6, 567-578.	2.1	228
8	Frequent hypermethylation of CpG islands and loss of expression of the 14-3-3â€‰Ïƒ gene in human hepatocellular carcinoma. Oncogene, 2000, 19, 5298-5302.	2.6	227
9	Frequent epigenetic inactivation of DICKKOPF family genes in human gastrointestinal tumors. Carcinogenesis, 2007, 28, 2459-2466.	1.3	191
10	Methylation-associated silencing of microRNA-34b/c in gastric cancer and its involvement in an epigenetic field defect. Carcinogenesis, 2010, 31, 2066-2073.	1.3	188
11	Targeting of miR34aâ€“NOTCH1 Axis Reduced Breast Cancer Stemness and Chemoresistance. Cancer Research, 2014, 74, 7573-7582.	0.4	179
12	Genetic, epigenetic, and clinicopathologic features of gastric carcinomas with the CpG island methylator phenotype and an association with Epsteinâ€“Barr virus. Cancer, 2006, 106, 1467-1479.	2.0	178
13	Long noncoding RNA involvement in cancer. BMB Reports, 2012, 45, 604-611.	1.1	178
14	A Novel Pit Pattern Identifies the Precursor of Colorectal Cancer Derived From Sessile Serrated Adenoma. American Journal of Gastroenterology, 2012, 107, 460-469.	0.2	164
15	Genome-wide Profiling of Chromatin Signatures Reveals Epigenetic Regulation of MicroRNA Genes in Colorectal Cancer. Cancer Research, 2011, 71, 5646-5658.	0.4	156
16	Distinct methylation pattern and microsatellite instability in sporadic gastric cancer. , 1999, 83, 309-313.		149
17	Epigenetic alteration and microRNA dysregulation in cancer. Frontiers in Genetics, 2013, 4, 258.	1.1	144
18	The Ras Effector RASSF2 Is a Novel Tumor-Suppressor Gene in Human Colorectal Cancer. Gastroenterology, 2005, 129, 156-169.	0.6	132

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19	Frequent epigenetic inactivation of SFRP genes in hepatocellular carcinoma. Journal of Gastroenterology, 2008, 43, 378-389.	2.3	109
20	IGFBP7 is a p53-responsive gene specifically silenced in colorectal cancer with CpG island methylator phenotype. Carcinogenesis, 2010, 31, 342-349.	1.3	90
21	Biological significance of the CpG island methylator phenotype. Biochemical and Biophysical Research Communications, 2014, 455, 35-42.	1.0	86
22	A Novel Correlation between LINE-1 Hypomethylation and the Malignancy of Gastrointestinal Stromal Tumors. Clinical Cancer Research, 2010, 16, 5114-5123.	3.2	83
23	Methylation of a Panel of MicroRNA Genes Is a Novel Biomarker for Detection of Bladder Cancer. European Urology, 2013, 63, 1091-1100.	0.9	83
24	Colorectal Carcinomas With CpG Island Methylator Phenotype 1 Frequently Contain Mutations in Chromatin Regulators. Gastroenterology, 2014, 146, 530-538.e5.	0.6	76
25	Aberrant methylation and histone deacetylation of cyclooxygenase 2 in gastric cancer. International Journal of Cancer, 2002, 97, 272-277.	2.3	75
26	Molecular Dissection of Premalignant Colorectal Lesions Reveals Early Onset of the CpG Island Methylator Phenotype. American Journal of Pathology, 2012, 181, 1847-1861.	1.9	74
27	An updated review of gastric cancer in the next-generation sequencing era: Insights from bench to bedside andvice versa. World Journal of Gastroenterology, 2014, 20, 3927.	1.4	72
28	Genomic Screening for Genes Silenced by DNA Methylation Revealed an Association between RASD1 Inactivation and Dexamethasone Resistance in Multiple Myeloma. Clinical Cancer Research, 2009, 15, 4356-4364.	3.2	69
29	LINE-1 Hypomethylation Is Associated with Increased CpG Island Methylation in Helicobacter pyloriâ€“Related Enlarged-Fold Gastritis. Cancer Epidemiology Biomarkers and Prevention, 2008, 17, 2555-2564.	1.1	62
30	Role of DNA Methylation in the Development of Diffuse-Type Gastric Cancer. Digestion, 2011, 83, 241-249.	1.2	60
31	Stromal fibroblasts induce metastatic tumor cell clusters via epithelialâ€“mesenchymal plasticity. Life Science Alliance, 2019, 2, e201900425.	1.3	48
32	Aberrant TET1 Methylation Closely Associated with CpG Island Methylator Phenotype in Colorectal Cancer. Cancer Prevention Research, 2015, 8, 702-711.	0.7	47
33	A Requirement for DICER to Maintain Full Promoter CpG Island Hypermethylation in Human Cancer Cells. Cancer Research, 2008, 68, 2570-2575.	0.4	46
34	Screening for long noncoding RNAs associated with oral squamous cell carcinoma reveals the potentially oncogenic actions of DLEU1. Cell Death and Disease, 2018, 9, 826.	2.7	46
35	Hypermethylation of Sox17 gene is useful as a molecular diagnostic application in early gastric cancer. Tumor Biology, 2012, 33, 383-393.	0.8	45
36	Aberrant methylation of microRNA-34b/c is a predictive marker of metachronous gastric cancer risk. Journal of Gastroenterology, 2014, 49, 1135-1144.	2.3	45

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37	Clinical prognostic value of <scp>DNA</scp> methylation in hepatoblastoma: Four novel tumor suppressor candidates. Cancer Science, 2016, 107, 812-819.	1.7	44
38	DNA methylation and cancer pathways in gastrointestinal tumors. Pharmacogenomics, 2008, 9, 1917-1928.	0.6	43
39	Epigenetic inactivation of SFRP genes in oral squamous cell carcinoma. International Journal of Oncology, 1992, 32, 1253-1261.	1.4	42
40	Analysis of DNA Methylation in Bowel Lavage Fluid for Detection of Colorectal Cancer. Cancer Prevention Research, 2014, 7, 1002-1010.	0.7	38
41	Dual EZH2 and G9a inhibition suppresses multiple myeloma cell proliferation by regulating the interferon signal and IRF4-MYC axis. Cell Death Discovery, 2021, 7, 7.	2.0	37
42	Epigenetic Alteration of DNA in Mucosal Wash Fluid Predicts Invasiveness of Colorectal Tumors. Cancer Prevention Research, 2011, 4, 674-683.	0.7	35
43	Analysis of the DNA methylation level of cancer-related genes in colorectal cancer and the surrounding normal mucosa. Clinical Epigenetics, 2017, 9, 55.	1.8	35
44	A genomic screen for long noncoding RNA genes epigenetically silenced by aberrant DNA methylation in colorectal cancer. Scientific Reports, 2016, 6, 26699.	1.6	34
45	Clinicopathological and molecular alterations in early gastric cancers with the microsatellite instabilityâ€high phenotype. International Journal of Cancer, 2016, 138, 1689-1697.	2.3	34
46	Emerging links between epigenetic alterations and dysregulation of noncoding RNAs in cancer. Tumor Biology, 2012, 33, 277-285.	0.8	33
47	Aberrant Methylation of RASGRF1 Is Associated with an Epigenetic Field Defect and Increased Risk of Gastric Cancer. Cancer Prevention Research, 2012, 5, 1203-1212.	0.7	32
48	Epigenetic silencing ofNTSR1is associated with lateral and noninvasive growth of colorectal tumors. Oncotarget, 2015, 6, 29975-29990.	0.8	32
49	Molecular differences in the microsatellite stable phenotype between leftâ€sided and rightâ€sided colorectal cancer. International Journal of Cancer, 2016, 139, 2493-2501.	2.3	31
50	Epigenetic silencing of miR-200b is associated with cisplatin resistance in bladder cancer. Oncotarget, 2018, 9, 24457-24469.	0.8	31
51	Epigenetic silencing of diacylglycerol kinase gamma in colorectal cancer. Molecular Carcinogenesis, 2017, 56, 1743-1752.	1.3	27
52	UHRF1 depletion and HDAC inhibition reactivate epigenetically silenced genes in colorectal cancer cells. Clinical Epigenetics, 2019, 11, 70.	1.8	27
53	Endoscopic and molecular characterization of colorectal sessile serrated adenoma/polyps with cytologic dysplasia. Gastrointestinal Endoscopy, 2017, 86, 1131-1138.e4.	0.5	26
54	DOT1L inhibition blocks multiple myeloma cell proliferation by suppressing IRF4-MYC signaling. Haematologica, 2019, 104, 155-165.	1.7	26

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55	Inflammation-Related Aberrant Patterns of DNA Methylation: Detection and Role in Epigenetic Deregulation of Cancer Cell Transcriptome. Methods in Molecular Biology, 2009, 512, 55-69.	0.4	26
56	Upregulation of adipocyte enhancerâ€binding protein 1 in endothelial cells promotes tumor angiogenesis in colorectal cancer. Cancer Science, 2020, 111, 1631-1644.	1.7	26
57	Quantitative DNA methylation analysis by fluorescent polymerase chain reaction single-strand conformation polymorphism using an automated DNA sequencer. Electrophoresis, 2000, 21, 904-908.	1.3	23
58	Genomeâ€wide analysis of DNA copy number alterations in early and advanced gastric cancers. Molecular Carcinogenesis, 2017, 56, 527-537.	1.3	23
59	Epigenetic silencing ofSMOC1in traditional serrated adenoma and colorectal cancer. Oncotarget, 2018, 9, 4707-4721.	0.8	21
60	Association between genomic alterations and metastatic behavior of colorectal cancer identified by arrayâ€based comparative genomic hybridization. Genes Chromosomes and Cancer, 2013, 52, 140-149.	1.5	20
61	Relationship Between Noncoding RNA Dysregulation and Epigenetic Mechanisms in Cancer. Advances in Experimental Medicine and Biology, 2016, 927, 109-135.	0.8	18
62	Dysregulation of miRNA in chronic hepatitis B is associated with hepatocellular carcinoma risk after nucleos(t)ide analogue treatment. Cancer Letters, 2018, 434, 91-100.	3.2	18
63	Analysis of the expression of cancer-associated fibroblast- and EMT-related proteins in submucosal invasive colorectal cancer. Journal of Cancer, 2018, 9, 2702-2712.	1.2	18
64	Identification and characterization of a metastatic suppressor <scp>BRMS</scp>1L as a target gene of p53. Cancer Science, 2017, 108, 2413-2421.	1.7	17
65	Characterization of <scp>RNF43</scp> frameshift mutations that drive <scp>Wnt</scp> ligandâ€and <scp>R</scp>â€spondinâ€dependent colon cancer. Journal of Pathology, 2022, 257, 39-52.	2.1	17
66	Integrated genetic and epigenetic analysis of cancerâ€related genes in nonâ€ampullary duodenal adenomas and intramucosal adenocarcinomas. Journal of Pathology, 2020, 252, 330-342.	2.1	16
67	Molecular alterations in colorectal adenomas and intramucosal adenocarcinomas defined by high-density single-nucleotide polymorphism arrays. Journal of Gastroenterology, 2017, 52, 1158-1168.	2.3	14
68	Molecular Profiling Based on KRAS/BRAF Mutation, Methylation, and Microsatellite Statuses in Serrated Lesions. Digestive Diseases and Sciences, 2018, 63, 2626-2638.	1.1	14
69	A Screen for Epigenetically Silenced microRNA Genes in Gastrointestinal Stromal Tumors. PLoS ONE, 2015, 10, e0133754.	1.1	14
70	Increased expression of T-fimbrin gene after DNA damage in CHO cells and inactivation of T-fimbrin by CpG methylation in human colorectal cancer cells. International Journal of Cancer, 2002, 97, 211-216.	2.3	13
71	TET1 Depletion Induces Aberrant CpG Methylation in Colorectal Cancer Cells. PLoS ONE, 2016, 11, e0168281.	1.1	13
72	Molecular subtypes of colorectal cancers determined by <scp>PCR</scp>â€based analysis. Cancer Science, 2017, 108, 427-434.	1.7	13

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73	Molecular profiling and genomeâ€wide analysis based on somatic copy number alterations in advanced colorectal cancers. Molecular Carcinogenesis, 2018, 57, 451-461.	1.3	13
74	A genomeâ€wide study of the relationship between chromosomal abnormalities and gene expression in colorectal tumors. Genes Chromosomes and Cancer, 2021, 60, 250-262.	1.5	13
75	Roles and causes of abnormal DNA methylation in gastrointestinal cancers. Asian Pacific Journal of Cancer Prevention, 2006, 7, 177-85.	0.5	13
76	Molecular profiling and comprehensive genome-wide analysis of somatic copy number alterations in gastric intramucosal neoplasias based on microsatellite status. Gastric Cancer, 2018, 21, 765-775.	2.7	12
77	Evaluation of Urinary DNA Methylation as a Marker for Recurrent Bladder Cancer: A 2-Center Prospective Study. Urology, 2018, 113, 71-78.	0.5	12
78	Traditional serrated adenoma has two distinct genetic pathways for molecular tumorigenesis with potential neoplastic progression. Journal of Gastroenterology, 2020, 55, 846-857.	2.3	12
79	Epigenetic activation of LY6K predicts the presence of metastasis and poor prognosis in breast carcinoma. Oncotarget, 2016, 7, 55677-55689.	0.8	11
80	Sessile serrated adenoma/polyp showed rapid malignant transformation in the final 13Âmonths. Digestive Endoscopy, 2020, 32, 979-983.	1.3	10
81	DLEU1 promotes oral squamous cell carcinoma progression by activating interferon-stimulated genes. Scientific Reports, 2021, 11, 20438.	1.6	10
82	Analysis of molecular alterations in laterally spreading tumors of the colorectum. Journal of Gastroenterology, 2017, 52, 715-723.	2.3	9
83	Subtypes of the Type II Pit Pattern Reflect Distinct Molecular Subclasses in the Serrated Neoplastic Pathway. Digestive Diseases and Sciences, 2018, 63, 1920-1928.	1.1	9
84	Activated macrophages promote invasion by early colorectal cancer via an interleukin 1Î²â€serum amyloid A1 axis. Cancer Science, 2021, 112, 4151-4165.	1.7	9
85	Low-Frequency IL23R Coding Variant Associated with Crohnâ€™s Disease Susceptibility in Japanese Subjects Identified by Personal Genomics Analysis. PLoS ONE, 2015, 10, e0137801.	1.1	8
86	Frequent downregulation of LRRC26 by epigenetic alterations is involved in the malignant progression of triple-negative breast cancer. International Journal of Oncology, 2018, 52, 1539-1558.	1.4	8
87	The clinicopathological and molecular features of sporadic gastric foveolar type neoplasia. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2020, 477, 835-844.	1.4	8
88	Integrated Analysis of the Endoscopic, Pathological and Molecular Characteristics of Colorectal Tumorigenesis. Digestion, 2019, 99, 33-38.	1.2	6
89	Comprehensive molecular analysis based on somatic copy number alterations in intramucosal colorectal neoplasias and early invasive colorectal cancers. Oncotarget, 2018, 9, 22895-22906.	0.8	6
90	Molecular analysis of isolated tumor glands from endometrial endometrioid adenocarcinomas. Pathology International, 2015, 65, 240-249.	0.6	5

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91	Surface microstructures are associated with mutational intratumoral heterogeneity in colorectal tumors. Journal of Gastroenterology, 2018, 53, 1241-1252.	2.3	5
92	A genomeâ€wide analysis of the molecular alterations occurring in the adenomatous and carcinomatous components of the same tumor based on the adenomaâ€“carcinoma sequence. Pathology International, 2021, 71, 582-593.	0.6	5
93	Comparative analysis of methods to determine DNA methylation levels of a tumor-related microRNA gene. Analytical Biochemistry, 2015, 484, 66-71.	1.1	4
94	Dysregulation of microRNA expression during the progression of colorectal tumors. Pathology International, 2020, 70, 633-643.	0.6	4
95	Comprehensive analyses of microRNA and mRNA expression in colorectal serrated lesions and colorectal cancer with a MSI phenotype. Genes Chromosomes and Cancer, 2021, , .	1.5	3
96	Gastric cancers with microsatellite instability sharing clinical features, chemoresistance and germline MSH6 variants. Clinical Journal of Gastroenterology, 2013, 6, 122-126.	0.4	2
97	Cribriform type adenocarcinoma of the colorectum: comprehensive molecular analyses of a distinctive histologic subtype of colorectal cancer. Carcinogenesis, 2022, , .	1.3	2
98	Epigenetic Regulation of microRNA Genes in Colorectal Cancer. , 2014, , 199-211.		1
99	An Integrated Epigenome and Transcriptome Analysis to Clarify the Effect of Epigenetic Inhibitors on GIST. Anticancer Research, 2021, 41, 2817-2828.	0.5	1
100	Immunohistochemical Examination is Highly Sensitive and Specific for Detection of the V600E BRAF Mutation in Colorectal Serrated Lesions. Applied Immunohistochemistry and Molecular Morphology, 2021, 29, 446-453.	0.6	1
101	DNA and Histone Methylation in Colon Cancer. Cancer Drug Discovery and Development, 2017, , 461-487.	0.2	0
102	Aggressive variant of splenic marginal zone lymphoma characterized using a cancer panel test and treated with rituximab-containing chemotherapy. Medicine (United States), 2020, 99, e21938.	0.4	0
103	Genomeâ€wide analysis of <scp>mRNA</scp> and <scp>microRNA</scp> expression in colorectal cancer and adjacent normal mucosa. Journal of Pathology: Clinical Research, 2022, , .	1.3	0