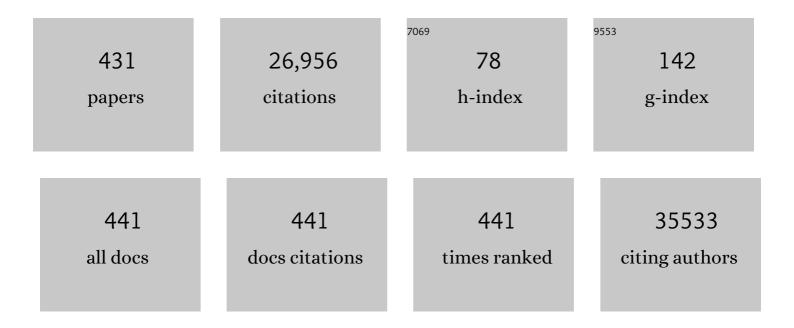
List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	p53AIP1, a Potential Mediator of p53-Dependent Apoptosis, and Its Regulation by Ser-46-Phosphorylated p53. Cell, 2000, 102, 849-862.	13.5	1,095
2	AXIN1 mutations in hepatocellular carcinomas, and growth suppression in cancer cells by virus-mediated transfer of AXIN1. Nature Genetics, 2000, 24, 245-250.	9.4	919
3	A ribonucleotide reductase gene involved in a p53-dependent cell-cycle checkpoint for DNA damage. Nature, 2000, 404, 42-49.	13.7	815
4	An ancient retrotransposal insertion causes Fukuyama-type congenital muscular dystrophy. Nature, 1998, 394, 388-392.	13.7	758
5	SMYD3 encodes a histone methyltransferase involved in the proliferation of cancer cells. Nature Cell Biology, 2004, 6, 731-740.	4.6	665
6	A cross-population atlas of genetic associations for 220 human phenotypes. Nature Genetics, 2021, 53, 1415-1424.	9.4	560
7	Genome-wide association study of hematological and biochemical traits in a Japanese population. Nature Genetics, 2010, 42, 210-215.	9.4	460
8	Overview of the BioBank Japan Project: Study design and profile. Journal of Epidemiology, 2017, 27, S2-S8.	1.1	451
9	Overexpression of LSD1 contributes to human carcinogenesis through chromatin regulation in various cancers. International Journal of Cancer, 2011, 128, 574-586.	2.3	420
10	Mutation in Npps in a mouse model of ossification of the posterior longitudinal ligament of the spine. Nature Genetics, 1998, 19, 271-273.	9.4	392
11	Growth-suppressive effects of BPOZ and EGR2, two genes involved in the PTEN signaling pathway. Oncogene, 2001, 20, 4457-4465.	2.6	335
12	Genome-wide association study identifies a susceptibility locus for HCV-induced hepatocellular carcinoma. Nature Genetics, 2011, 43, 455-458.	9.4	332
13	Japanese Population Structure, Based on SNP Genotypes from 7003 Individuals Compared to Other Ethnic Groups: Effects on Population-Based Association Studies. American Journal of Human Genetics, 2008, 83, 445-456.	2.6	327
14	SARS-CoV-2 genomic variations associated with mortality rate of COVID-19. Journal of Human Genetics, 2020, 65, 1075-1082.	1.1	316
15	Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. Nature Genetics, 2020, 52, 669-679.	9.4	304
16	Positional cloning of the gene for Nijmegen breakage syndrome. Nature Genetics, 1998, 19, 179-181.	9.4	302
17	Critical roles of non-histone protein lysine methylation in human tumorigenesis. Nature Reviews Cancer, 2015, 15, 110-124.	12.8	299
18	Genome-wide association study identifies multiple susceptibility loci for pancreatic cancer. Nature Genetics, 2014, 46, 994-1000.	9.4	294

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19	Functional Variants in ADH1B and ALDH2 Coupled With Alcohol and Smoking Synergistically Enhance Esophageal Cancer Risk. Gastroenterology, 2009, 137, 1768-1775.	0.6	277
20	A novel brain-specific p53-target gene, BAI1, containing thrombospondin type 1 repeats inhibits experimental angiogenesis. Oncogene, 1997, 15, 2145-2150.	2.6	270
21	Dysregulation of PRMT1 and PRMT6, Type I arginine methyltransferases, is involved in various types of human cancers. International Journal of Cancer, 2011, 128, 562-573.	2.3	260
22	Genome-wide association study identifies five new susceptibility loci for prostate cancer in the Japanese population. Nature Genetics, 2010, 42, 751-754.	9.4	258
23	Enhanced SMYD3 expression is essential for the growth of breast cancer cells. Cancer Science, 2006, 97, 113-118.	1.7	246
24	A radiation hybrid map of the rat genome containing 5,255 markers. Nature Genetics, 1999, 22, 27-36.	9.4	231
25	Variations in the FTO gene are associated with severe obesity in the Japanese. Journal of Human Genetics, 2008, 53, 546-553.	1.1	219
26	Identification of ALDH4 as a p53-inducible gene and its protective role in cellular stresses. Journal of Human Genetics, 2004, 49, 134-140.	1.1	202
27	Association analysis of genetic variants in IL23R, ATG16L1 and 5p13.1 loci with Crohn's disease in Japanese patients. Journal of Human Genetics, 2007, 52, 575-583.	1.1	191
28	Demethylation of RB Regulator MYPT1 by Histone Demethylase LSD1 Promotes Cell Cycle Progression in Cancer Cells. Cancer Research, 2011, 71, 655-660.	0.4	190
29	Overexpression of the JmjC histone demethylase KDM5B in human carcinogenesis: involvement in the proliferation of cancer cells through the E2F/RB pathway. Molecular Cancer, 2010, 9, 59.	7.9	183
30	Myasthenic crisis and polymyositis induced by one dose of nivolumab. Cancer Science, 2016, 107, 1055-1058.	1.7	176
31	Validation of the histone methyltransferase EZH2 as a therapeutic target for various types of human cancer and as a prognostic marker. Cancer Science, 2011, 102, 1298-1305.	1.7	170
32	RB1 Methylation by SMYD2 Enhances Cell Cycle Progression through an Increase of RB1 Phosphorylation. Neoplasia, 2012, 14, 476-IN8.	2.3	169
33	Variation in TP63 is associated with lung adenocarcinoma susceptibility in Japanese and Korean populations. Nature Genetics, 2010, 42, 893-896.	9.4	165
34	PDZ-Binding Kinase/T-LAK Cell-Originated Protein Kinase, a Putative Cancer/Testis Antigen with an Oncogenic Activity in Breast Cancer. Cancer Research, 2006, 66, 9186-9195.	0.4	164
35	Overexpressed P-Cadherin/CDH3 Promotes Motility of Pancreatic Cancer Cells by Interacting with p120ctn and Activating Rho-Family GTPases. Cancer Research, 2005, 65, 3092-3099.	0.4	163
36	Isolation of p53-target genes and their functional analysis. Cancer Science, 2004, 95, 7-11.	1.7	160

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37	Variation in the DEPDC5 locus is associated with progression to hepatocellular carcinoma in chronic hepatitis C virus carriers. Nature Genetics, 2011, 43, 797-800.	9.4	156
38	Histone Lysine Methyltransferase SETD8 Promotes Carcinogenesis by Deregulating PCNA Expression. Cancer Research, 2012, 72, 3217-3227.	0.4	155
39	Gains, losses, and amplifications of genomic materials in primary gastric cancers analyzed by comparative genomic hybridization. , 1999, 24, 299-305.		153
40	Bcl-2/E1B 19 kDa-interacting protein 3-like protein (Bnip3L) interacts with Bcl-2/Bcl-xL and induces apoptosis by altering mitochondrial membrane permeability. Oncogene, 1999, 18, 4523-4529.	2.6	151
41	p53RDL1 regulates p53-dependent apoptosis. Nature Cell Biology, 2003, 5, 216-223.	4.6	150
42	The Lysine 831 of Vascular Endothelial Growth Factor Receptor 1 Is a Novel Target of Methylation by SMYD3. Cancer Research, 2007, 67, 10759-10765.	0.4	150
43	Amplification and over-expression of theAIB1 nuclear receptor co-activator gene in primary gastric cancers. International Journal of Cancer, 2000, 89, 217-223.	2.3	146
44	Critical Roles of Mucin 1 Glycosylation by Transactivated Polypeptide <i>N</i> -Acetylgalactosaminyltransferase 6 in Mammary Carcinogenesis. Cancer Research, 2010, 70, 2759-2769.	0.4	146
45	Genome-wide association analysis in East Asians identifies breast cancer susceptibility loci at 1q32.1, 5q14.3 and 15q26.1. Nature Genetics, 2014, 46, 886-890.	9.4	135
46	Afatinib Activity in Platinum-Refractory Metastatic Urothelial Carcinoma in Patients With <i>ERBB</i> Alterations. Journal of Clinical Oncology, 2016, 34, 2165-2171.	0.8	134
47	Cross-sectional analysis of BioBank Japan clinical data: A large cohort of 200,000 patients with 47 common diseases. Journal of Epidemiology, 2017, 27, S9-S21.	1.1	133
48	Phase II Clinical Trial of Multiple Peptide Vaccination for Advanced Head and Neck Cancer Patients Revealed Induction of Immune Responses and Improved OS. Clinical Cancer Research, 2015, 21, 312-321.	3.2	126
49	Genome-Wide Association Study of Pancreatic Cancer in Japanese Population. PLoS ONE, 2010, 5, e11824.	1.1	126
50	The BioBank Japan Project. Clinical Advances in Hematology and Oncology, 2007, 5, 696-7.	0.3	125
51	Multicenter, phase II clinical trial of cancer vaccination for advanced esophageal cancer with three peptides derived from novel cancer-testis antigens. Journal of Translational Medicine, 2012, 10, 141.	1.8	124
52	Bioinformatic prediction of potential T cell epitopes for SARS-Cov-2. Journal of Human Genetics, 2020, 65, 569-575.	1.1	123
53	Localization of membrane-associated guanylate kinase (MAGI)-1/BAI-associated protein (BAP) 1 at tight junctions of epithelial cells. Oncogene, 1999, 18, 7810-7815.	2.6	114
54	A genome-wide association study identifies two susceptibility loci for duodenal ulcer in the Japanese population. Nature Genetics, 2012, 44, 430-434.	9.4	114

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55	A variable number of tandem repeats polymorphism in an E2F-1 binding element in the 5′ flanking region of SMYD3 is a risk factor for human cancers. Nature Genetics, 2005, 37, 1104-1107.	9.4	112
56	Enhanced Expression of EHMT2 Is Involved in the Proliferation of Cancer Cells through Negative Regulation of SIAH1. Neoplasia, 2011, 13, 676-IN10.	2.3	112
57	Association analysis of SLC22A4, SLC22A5 and DLG5 in Japanese patients with Crohn disease. Journal of Human Genetics, 2004, 49, 664-668.	1.1	107
58	Intratumoral expression levels of <i>PD-L1</i> , <i>GZMA</i> , and <i>HLA-A</i> along with oligoclonal T cell expansion associate with response to nivolumab in metastatic melanoma. Oncolmmunology, 2016, 5, e1204507.	2.1	107
59	Novel Mechanism of HERG Current Suppression in LQT2. Circulation Research, 1998, 83, 415-422.	2.0	105
60	Molecular features of triple negative breast cancer cells by genome-wide gene expression profiling analysis. International Journal of Oncology, 2013, 42, 478-506.	1.4	104
61	Cenome-wide association study for intracranial aneurysm in the Japanese population identifies three candidate susceptible loci and a functional genetic variant at EDNRA. Human Molecular Genetics, 2012, 21, 2102-2110.	1.4	102
62	Comparative genomic hybridization of squamous cell carcinoma of the esophagus: The possible involvement of theDP1 gene in the 13q34 amplicon. Genes Chromosomes and Cancer, 1999, 24, 337-344.	1.5	99
63	Common variants at 11q12, 10q26 and 3p11.2 are associated with prostate cancer susceptibility in Japanese. Nature Genetics, 2012, 44, 426-429.	9.4	98
64	Isolation, mapping, and functional analysis of a novel human cDNA (BNIP3L) encoding a protein homologous to human NIP3. , 1998, 21, 230-235.		97
65	Enhanced HSP70Âlysine methylation promotes proliferation of cancer cells through activation of Aurora kinase B. Nature Communications, 2012, 3, 1072.	5.8	96
66	TOPK inhibitor induces complete tumor regression in xenograft models of human cancer through inhibition of cytokinesis. Science Translational Medicine, 2014, 6, 259ra145.	5.8	95
67	Critical role of lysine 134 methylation on histone H2AX for Î ³ -H2AX production and DNA repair. Nature Communications, 2014, 5, 5691.	5.8	93
68	Histone Lysine Methyltransferase Wolf-Hirschhorn Syndrome Candidate 1 Is Involved in Human Carcinogenesis through Regulation of the Wnt Pathway. Neoplasia, 2011, 13, 887-IN11.	2.3	92
69	Breast cancer: The translation of big genomic data to cancer precision medicine. Cancer Science, 2018, 109, 497-506.	1.7	92
70	Microsatellite instability in endometrial carcinomas: Frequent replication errors in tumors of early onset and/or of poorly differentiated type. Genes Chromosomes and Cancer, 1995, 14, 128-132.	1.5	91
71	CSR, a scavenger receptor-like protein with a protective role against cellular damage causedby UV irradiation and oxidative stress. Human Molecular Genetics, 1998, 7, 1039-1046.	1.4	88
72	Polypeptide N-acetylgalactosaminyltransferase 6 Disrupts Mammary Acinar Morphogenesis through O-glycosylation of Fibronectin. Neoplasia, 2011, 13, 320-IN10.	2.3	88

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73	The Histone Methyltransferase SMYD2 Methylates PARP1 and Promotes Poly(ADP-ribosyl)ation Activity in Cancer Cells. Neoplasia, 2014, 16, 257-264.e2.	2.3	88
74	Dose-adjustment study of tamoxifen based on CYP2D6 genotypes in Japanese breast cancer patients. Breast Cancer Research and Treatment, 2012, 131, 137-145.	1.1	86
75	The JmjC domainâ€containing histone demethylase KDM3A is a positive regulator of the G ₁ /S transition in cancer cells <i>via</i> transcriptional regulation of the <i>HOXA1</i> gene. International Journal of Cancer, 2012, 131, E179-89.	2.3	85
76	Citrullination of RGG Motifs in FET Proteins by PAD4 Regulates Protein Aggregation and ALS Susceptibility. Cell Reports, 2018, 22, 1473-1483.	2.9	85
77	Association studies of 33 single nucleotide polymorphisms (SNPs) in 29 candidate genes for bronchial asthma: positive association of a T924C polymorphism in the thromboxane A2 receptor gene. Human Genetics, 2000, 106, 440-446.	1.8	83
78	Clonal Hematopoiesis in Liquid Biopsy: From Biological Noise to Valuable Clinical Implications. Cancers, 2020, 12, 2277.	1.7	83
79	A pilot study of durvalumab and tremelimumab and immunogenomic dynamics in metastatic breast cancer. Oncotarget, 2018, 9, 18985-18996.	0.8	83
80	WHSC1 Promotes Oncogenesis through Regulation of NIMA-Related Kinase-7 in Squamous Cell Carcinoma of the Head and Neck. Molecular Cancer Research, 2015, 13, 293-304.	1.5	82
81	Novel and recurrent COMP (cartilage oligomeric matrix protein) mutations in pseudoachondroplasia and multiple epiphyseal dysplasia. Human Genetics, 1998, 103, 633-638.	1.8	81
82	A Single Nucleotide Polymorphism in the Matrix Metalloproteinase-1 Promoter in Endometrial Carcinomas. Japanese Journal of Cancer Research, 2000, 91, 612-615.	1.7	81
83	Genomic organization and mutational analysis of HERG , a gene responsible for familial long QT syndrome. Human Genetics, 1998, 102, 435-439.	1.8	80
84	SMYD2-dependent HSP90 methylation promotes cancer cell proliferation by regulating the chaperone complex formation. Cancer Letters, 2014, 351, 126-133.	3.2	79
85	Mapping of a new target region of allelic loss to a 2-cM interval at 22q13.1 in primary breast cancer. Genes Chromosomes and Cancer, 1998, 21, 108-112.	1.5	78
86	Expression and chromosomal localization of KIAA0369, a putative kinase structurally related to Doublecortin. Journal of Human Genetics, 1998, 43, 169-177.	1.1	78
87	Genetic dissection of ``OLETF'', a rat model for non-insulin-dependent diabetes mellitus. Mammalian Genome, 1998, 9, 419-425.	1.0	78
88	Whole-Exome Sequencing of Muscle-Invasive Bladder Cancer Identifies Recurrent Mutations of <i>UNC5C</i> and Prognostic Importance of DNA Repair Gene Mutations on Survival. Clinical Cancer Research, 2014, 20, 6605-6617.	3.2	77
89	A phase I study of combination vaccine treatment of five therapeutic epitope-peptides for metastatic colorectal cancer; safety, immunological response, and clinical outcome. Journal of Translational Medicine, 2014, 12, 63.	1.8	76
90	The NSD family of protein methyltransferases in human cancer. Epigenomics, 2015, 7, 863-874.	1.0	76

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91	A phase ΙI study of five peptides combination with oxaliplatin-based chemotherapy as a first-line therapy for advanced colorectal cancer (FXV study). Journal of Translational Medicine, 2014, 12, 108.	1.8	75
92	Dysregulation of AKT Pathway by SMYD2-Mediated Lysine Methylation on PTEN. Neoplasia, 2015, 17, 367-373.	2.3	75
93	Association of ulcerative colitis with rare VNTR alleles of the human intestinal mucin gene, MUC3. Human Molecular Genetics, 1999, 8, 307-311.	1.4	74
94	Analysis of numerical aberrations in specific chromosomes by fluorescent in situ hybridization as a diagnostic tool in breast cancer. , 1996, 77, 2064-2069.		73
95	DNA variations in human and medical genetics: 25 years of my experience. Journal of Human Genetics, 2009, 54, 1-8.	1.1	73
96	A genomewide linkage analysis of Kawasaki disease: evidence for linkage to chromosome 12. Journal of Human Genetics, 2007, 52, 179-190.	1.1	72
97	Phase I clinical study of multiple epitope peptide vaccine combined with chemoradiation therapy in esophageal cancer patients. Journal of Translational Medicine, 2014, 12, 84.	1.8	70
98	Cancer Precision Medicine: From Cancer Screening to Drug Selection and Personalized Immunotherapy. Trends in Pharmacological Sciences, 2017, 38, 15-24.	4.0	70
99	Induction of Neoantigen-Specific Cytotoxic T Cells and Construction of T-cell Receptor–Engineered T Cells for Ovarian Cancer. Clinical Cancer Research, 2018, 24, 5357-5367.	3.2	70
100	Novel and recurrentEBP mutations in X-linked dominant chondrodysplasia punctata. American Journal of Medical Genetics Part A, 2000, 94, 300-305.	2.4	69
101	Nonrandom Chromosomal Imbalances in Esophageal Squamous Cell Carcinoma Cell Lines: Possible Involvement of theATF3andCENPFGenes in the 1q32 Amplicon. Japanese Journal of Cancer Research, 2000, 91, 1126-1133.	1.7	68
102	Critical roles of Tâ€LAK cellâ€originated protein kinase in cytokinesis. Cancer Science, 2010, 101, 403-411.	1.7	68
103	Quantitative T cell repertoire analysis by deep cDNA sequencing of T cell receptor α and β chains using next-generation sequencing (NGS). Oncolmmunology, 2014, 3, e968467.	2.1	68
104	Regulation of iron homeostasis by the p53-ISCU pathway. Scientific Reports, 2015, 5, 16497.	1.6	68
105	Eradication of Large Solid Tumors by Gene Therapy with a T-Cell Receptor Targeting a Single Cancer-Specific Point Mutation. Clinical Cancer Research, 2016, 22, 2734-2743.	3.2	68
106	Characterization of the human p57KIP2 gene: Alternative splicing, insertion/deletion polymorphisms in VNTR sequences in the coding region, and mutational analysis. Human Genetics, 1996, 97, 625-631.	1.8	67
107	Dysregulation of protein methyltransferases in human cancer: An emerging target class for anticancer therapy. Cancer Science, 2016, 107, 377-384.	1.7	67
108	Mutational Analysis of Mismatch Repair Genes,hMLH1andhMSH2, in Sporadic Endometrial Carcinomas with Microsatellite Instability. Japanese Journal of Cancer Research, 1996, 87, 141-145.	1.7	66

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109	A CAG/CTG expansion in the normal population. Nature Genetics, 1997, 17, 385-386.	9.4	64
110	Identification of AXUD1, a novel human gene induced by AXIN1 and its reduced expression in human carcinomas of the lung, liver, colon and kidney. Oncogene, 2001, 20, 5062-5066.	2.6	64
111	Isolation of a novel gene on 8p21.3–22 whose expression is reduced significantly in human colorectal cancers with liver metastasis. Genes Chromosomes and Cancer, 2000, 29, 9-15.	1.5	63
112	Association between single nucleotide polymorphisms within genes encoding sirtuin families and diabetic nephropathy in Japanese subjects with type 2 diabetes. Clinical and Experimental Nephrology, 2011, 15, 381-390.	0.7	63
113	Low T-cell Receptor Diversity, High Somatic Mutation Burden, and High Neoantigen Load as Predictors of Clinical Outcome in Muscle-invasive Bladder Cancer. European Urology Focus, 2016, 2, 445-452.	1.6	63
114	T-LAK Cell-Originated Protein Kinase (TOPK) as a Prognostic Factor and a Potential Therapeutic Target in Ovarian Cancer. Clinical Cancer Research, 2016, 22, 6110-6117.	3.2	63
115	The Histone Demethylase JMJD2B Plays an Essential Role in Human Carcinogenesis through Positive Regulation of Cyclin-Dependent Kinase 6. Cancer Prevention Research, 2011, 4, 2051-2061.	0.7	62
116	Clinical significance of clonal hematopoiesis in the interpretation of blood liquid biopsy. Molecular Oncology, 2020, 14, 1719-1730.	2.1	62
117	Localization of a tumor suppressor gene associated with the progression of human breast carcinoma within a 1-cm interval of 8p22-p23.1. , 1999, 85, 447-452.		60
118	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	1.4	60
119	Association of single-nucleotide polymorphisms in the polymeric immunoglobulin receptor gene with immunoglobulinÂA nephropathy (IgAN) in Japanese patients. Journal of Human Genetics, 2003, 48, 293-299.	1.1	59
120	Deregulation of the histone demethylase JMJD2A is involved in human carcinogenesis through regulation of the G1/S transition. Cancer Letters, 2013, 336, 76-84.	3.2	59
121	Beta-defensin 1, aryl hydrocarbon receptor and plasma kynurenine in major depressive disorder: metabolomics-informed genomics. Translational Psychiatry, 2018, 8, 10.	2.4	59
122	Frequent β-Catenin Abnormalities in Bone and Soft-tissue Tumors. Japanese Journal of Cancer Research, 1999, 90, 205-209.	1.7	58
123	Genomic organization and mutational analysis of KVLQT1, a gene responsible for familial long QT syndrome. Human Genetics, 1998, 103, 290-294.	1.8	57
124	Immune profiles in primary squamous cell carcinoma of the head and neck. Oral Oncology, 2019, 96, 77-88.	0.8	57
125	Preclinical efficacy of maternal embryonic leucine-zipper kinase (MELK) inhibition in acute myeloid leukemia. Oncotarget, 2014, 5, 12371-12382.	0.8	56
126	Comparison of exome-based HLA class I genotyping tools: identification of platform-specific genotyping errors. Journal of Human Genetics, 2017, 62, 397-405.	1.1	55

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127	Allelic loss on chromosome 1p is Associated with progression and lymph node metastasis of primary breast carcinoma. , 1998, 82, 317-322.		54
128	Activation of an estrogen/estrogen receptor signaling by BIG3 through its inhibitory effect on nuclear transport of PHB2/REA in breast cancer. Cancer Science, 2009, 100, 1468-1478.	1.7	54
129	Phase II clinical trial of peptide cocktail therapy for patients with advanced pancreatic cancer: <scp>VENUS</scp> â€ <scp>PC</scp> study. Cancer Science, 2017, 108, 73-80.	1.7	54
130	Integrated analysis of somatic mutations and immune microenvironment in malignant pleural mesothelioma. Oncolmmunology, 2017, 6, e1278330.	2.1	54
131	Isolation of a novel TP53 target gene from a colon cancer cell line carrying a highly regulated wild-type TP53 expression system. , 1998, 23, 1-9.		53
132	Mutations in the N-terminal globular domain of the type X collagen gene (COL10A1) in patients with Schmid metaphyseal chondrodysplasia. Human Mutation, 1997, 9, 131-135.	1.1	52
133	Detailed deletion mapping of chromosome arm 3p in breast cancers: A 2-cM region on 3p14.3-21.1 and a 5-cM region on 3p24.3-25.1 commonly deleted in tumors. Genes Chromosomes and Cancer, 1997, 20, 268-274.	1.5	52
134	Characterization of T cell repertoire of blood, tumor, and ascites in ovarian cancer patients using next generation sequencing. Oncolmmunology, 2015, 4, e1030561.	2.1	52
135	GWAS identifies two novel colorectal cancer loci at 16q24.1 and 20q13.12. Carcinogenesis, 2018, 39, 652-660.	1.3	52
136	IL-28B predicts response to chronic hepatitis C therapy – fine-mapping and replication study in Asian populations. Journal of General Virology, 2011, 92, 1071-1081.	1.3	50
137	Association of variations in HLA class II and other loci with susceptibility to EGFR-mutated lung adenocarcinoma. Nature Communications, 2016, 7, 12451.	5.8	49
138	A genome-wide association study identifies PLCL2 and AP3D1-DOT1L-SF3A2 as new susceptibility loci for myocardial infarction in Japanese. European Journal of Human Genetics, 2015, 23, 374-380.	1.4	48
139	Mutations in the BRCA1 gene in Japanese breast cancer patients. Human Mutation, 1996, 7, 334-339.	1.1	47
140	Infrequent Mutations in thePTEN/MMAC1Gene among Primary Breast Cancers. Japanese Journal of Cancer Research, 1998, 89, 17-21.	1.7	47
141	Critical roles of LGN/GPSM2 phosphorylation by PBK/TOPK in cell division of breast cancer cells. Genes Chromosomes and Cancer, 2010, 49, 861-872.	1.5	47
142	The Transcriptional Landscape of p53 Signalling Pathway. EBioMedicine, 2017, 20, 109-119.	2.7	47
143	Overview of BioBank Japan follow-up data in 32 diseases. Journal of Epidemiology, 2017, 27, S22-S28.	1.1	47
144	Pharmacogenetic Discovery in CALGB (Alliance) 90401 and Mechanistic Validation of a <i>VAC14</i> Polymorphism that Increases Risk of Docetaxel-Induced Neuropathy. Clinical Cancer Research, 2016, 22, 4890-4900.	3.2	46

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145	Genomic structure and multiple single-nucleotide polymorphisms (SNPs) of the thiopurine S-methyltransferase (TPMT) gene. Journal of Human Genetics, 2000, 45, 299-302.	1.1	45
146	Phase I clinical trial of a five-peptide cancer vaccine combined with cyclophosphamide in advanced solid tumors. Clinical Immunology, 2016, 166-167, 48-58.	1.4	45
147	Shared Genetic Risk Factors of Intracranial, Abdominal, and Thoracic Aneurysms. Journal of the American Heart Association, 2016, 5, .	1.6	45
148	Immunopharmacogenomics towards personalized cancer immunotherapy targeting neoantigens. Cancer Science, 2018, 109, 542-549.	1.7	45
149	Genetic mechanisms in esophageal carcinogenesis: Frequent deletion of 3p and 17p in premalignant lesions. , 1996, 15, 165-169.		44
150	Amplification on double-minute chromosomes and partial-tandem duplication of theMILL gene in leukemic cells of a patient with acute myelogenous leukemia. Genes Chromosomes and Cancer, 1998, 23, 267-272.	1.5	44
151	CD44 is a potential target of amplification within the 11p13 amplicon detected in gastric cancer cell lines. Genes Chromosomes and Cancer, 2000, 29, 315-324.	1.5	44
152	Effective screening of T cells recognizing neoantigens and construction of T-cell receptor-engineered T cells. Oncotarget, 2018, 9, 11009-11019.	0.8	44
153	SUV39H2 methylates and stabilizes LSD1 by inhibiting polyubiquitination in human cancer cells. Oncotarget, 2015, 6, 16939-16950.	0.8	44
154	Oncogenic roles of TOPK and MELK, and effective growth suppression by small molecular inhibitors in kidney cancer cells. Oncotarget, 2016, 7, 17652-17664.	0.8	44
155	INSIC2 gene rs7566605 polymorphism is associated with severe obesity in Japanese. Journal of Human Genetics, 2008, 53, 857-862.	1.1	43
156	Mutational analysis of the RET proto-oncogene in 71 Japanese patients with medullary thyroid carcinoma. Journal of Human Genetics, 1998, 43, 101-106.	1.1	42
157	Genomeâ€wide association study of chemotherapeutic agentâ€induced severe neutropenia/leucopenia for patients in Biobank Japan. Cancer Science, 2013, 104, 1074-1082.	1.7	42
158	A first-in-human study investigating biodistribution, safety and recommended dose of a new radiolabeled MAb targeting FZD10 in metastatic synovial sarcoma patients. BMC Cancer, 2018, 18, 646.	1.1	42
159	Effective growth-suppressive activity of maternal embryonic leucine-zipper kinase (MELK) inhibitor against small cell lung cancer. Oncotarget, 2016, 7, 13621-13633.	0.8	41
160	Characterization of T-cell Receptor Repertoire in Inflamed Tissues of Patients with Crohn's Disease Through Deep Sequencing. Inflammatory Bowel Diseases, 2016, 22, 1275-1285.	0.9	40
161	Plasma or Serum: Which Is Preferable for Mutation Detection in Liquid Biopsy?. Clinical Chemistry, 2020, 66, 946-957.	1.5	40
162	Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591.	9.0	40

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163	Mutations in Zinc-binding Domains of p53 as a Prognostic Marker of Esophageal-cancer Patients. Japanese Journal of Cancer Research, 2000, 91, 190-198.	1.7	39
164	Structural organization, complete genomic sequences and mutational analyses of the Fukuyama-type congenital muscular dystrophy gene, fukutin. FEBS Letters, 2001, 489, 192-196.	1.3	39
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