Tatushiko Tsunoda

List of Publications by Year in descending order

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354 papers	58,895 citations	1792 103 h-index	1131 230 g-index
366 all docs	366 docs citations	366 times ranked	69935 citing authors

#	Article	IF	Citations
1	The International HapMap Project. Nature, 2003, 426, 789-796.	13.7	5,735
2	A haplotype map of the human genome. Nature, 2005, 437, 1299-1320.	13.7	5,440
3	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
4	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
5	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
6	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
7	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
8	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease. Nature Genetics, 2009, 41, 1303-1307.	9.4	1,217
9	Functional haplotypes of PADI4, encoding citrullinating enzyme peptidylarginine deiminase 4, are associated with rheumatoid arthritis. Nature Genetics, 2003, 34, 395-402.	9.4	1,111
10	Integrated molecular analysis of clear-cell renal cell carcinoma. Nature Genetics, 2013, 45, 860-867.	9.4	955
11	Functional SNPs in the lymphotoxin-Î± gene that are associated with susceptibility to myocardial infarction. Nature Genetics, 2002, 32, 650-654.	9.4	878
12	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. Nature Genetics, 2012, 44, 760-764.	9.4	781
13	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
14	SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations. Nature Genetics, 2008, 40, 1098-1102.	9.4	641
15	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. Nature Genetics, 2016, 48, 500-509.	9.4	596
16	An intronic SNP in a RUNX1 binding site of SLC22A4, encoding an organic cation transporter, is associated with rheumatoid arthritis. Nature Genetics, 2003, 35, 341-348.	9.4	565
17	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
18	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	9.4	533

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19	A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians. Nature Genetics, 2009, 41, 591-595.	9.4	491
20	Single nucleotide polymorphisms in TNFSF15 confer susceptibility to Crohn's disease. Human Molecular Genetics, 2005, 14, 3499-3506.	1.4	438
21	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
22	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
23	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
24	ITPKC functional polymorphism associated with Kawasaki disease susceptibility and formation of coronary artery aneurysms. Nature Genetics, 2008, 40, 35-42.	9.4	423
25	Overexpression of LSD1 contributes to human carcinogenesis through chromatin regulation in various cancers. International Journal of Cancer, 2011, 128, 574-586.	2.3	420
26	Integrating ethics and science in the International HapMap Project. Nature Reviews Genetics, 2004, 5, 467-475.	7.7	378
27	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	9.4	372
28	A functional variant in FCRL3, encoding Fc receptor-like 3, is associated with rheumatoid arthritis and several autoimmunities. Nature Genetics, 2005, 37, 478-485.	9.4	356
29	Estimating transcription factor bindability on DNA. Bioinformatics, 1999, 15, 622-630.	1.8	324
30	Genome-wide association study identifies eight new susceptibility loci for atopic dermatitis in the Japanese population. Nature Genetics, 2012, 44, 1222-1226.	9.4	310
31	Expression profiles of non-small cell lung cancers on cDNA microarrays: Identification of genes for prediction of lymph-node metastasis and sensitivity to anti-cancer drugs. Oncogene, 2003, 22, 2192-2205.	2.6	297
32	Genome-wide association study identifies three new susceptibility loci for adult asthma in the Japanese population. Nature Genetics, 2011, 43, 893-896.	9.4	296
33	A genome-wide association study identifies three new risk loci for Kawasaki disease. Nature Genetics, 2012, 44, 517-521.	9.4	284
34	Genomic basis for RNA alterations in cancer. Nature, 2020, 578, 129-136.	13.7	280
35	Functional Variants in ADH1B and ALDH2 Coupled With Alcohol and Smoking Synergistically Enhance Esophageal Cancer Risk. Gastroenterology, 2009, 137, 1768-1775.	0.6	277
36	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275

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37	Association of a novel long nonâ€coding RNA in 8q24 with prostate cancer susceptibility. Cancer Science, 2011, 102, 245-252.	1.7	263
38	The landscape of viral associations in human cancers. Nature Genetics, 2020, 52, 320-330.	9.4	261
39	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
40	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
41	Meta-analysis identifies multiple loci associated with kidney functionâ€related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	9.4	254
42	A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B. Nature Genetics, 2010, 42, 864-868.	9.4	245
43	Prepublication data sharing. Nature, 2009, 461, 168-170.	13.7	243
44	A genome-wide association study identifies three new susceptibility loci for ulcerative colitis in the Japanese population. Nature Genetics, 2009, 41, 1325-1329.	9.4	241
45	A regulatory variant in CCR6 is associated with rheumatoid arthritis susceptibility. Nature Genetics, 2010, 42, 515-519.	9.4	241
46	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. Nature Genetics, 2012, 44, 302-306.	9.4	240
47	Genetic variants in GPR126 are associated with adolescent idiopathic scoliosis. Nature Genetics, 2013, 45, 676-679.	9.4	240
48	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	5.8	240
49	Genome-wide cDNA microarray analysis of gene expression profiles in pancreatic cancers using populations of tumor cells and normal ductal epithelial cells selected for purity by laser microdissection. Oncogene, 2004, 23, 2385-2400.	2.6	235
50	A genome-wide association study identifies common variants near LBX1 associated with adolescent idiopathic scoliosis. Nature Genetics, 2011, 43, 1237-1240.	9.4	233
51	Identification of membrane-type matrix metalloproteinase-1 as a target of the Î²-catenin/Tcf4 complex in human colorectal cancers. Oncogene, 2002, 21, 5861-5867.	2.6	231
52	Predicting Response to Methotrexate, Vinblastine, Doxorubicin, and Cisplatin Neoadjuvant Chemotherapy for Bladder Cancers through Genome-Wide Gene Expression Profiling. Clinical Cancer Research, 2005, 11, 2625-2636.	3.2	228
53	Molecular Features of the Transition from Prostatic Intraepithelial Neoplasia (PIN) to Prostate Cancer. Cancer Research, 2004, 64, 5963-5972.	0.4	223
54	A functional SNP in CILP, encoding cartilage intermediate layer protein, is associated with susceptibility to lumbar disc disease. Nature Genetics, 2005, 37, 607-612.	9.4	223

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55	Significant Effect of Polymorphisms in CYP2D6 and ABCC2 on Clinical Outcomes of Adjuvant Tamoxifen Therapy for Breast Cancer Patients. Journal of Clinical Oncology, 2010, 28, 1287-1293.	0.8	214
56	Assessment of network module identification across complex diseases. Nature Methods, 2019, 16, 843-852.	9.0	213
57	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population. Human Molecular Genetics, 2011, 20, 3884-3892.	1.4	205
58	Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. Genome Research, 2001, 11, 677-684.	2.4	201
59	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	1.4	192
60	Expression profiling to predict postoperative prognosis for estrogen receptor-negative breast cancers by analysis of 25,344 genes on a cDNA microarray. Cancer Science, 2004, 95, 218-225.	1.7	190
61	An integrated database of chemosensitivity to 55 anticancer drugs and gene expression profiles of 39 human cancer cell lines. Cancer Research, 2002, 62, 1139-47.	0.4	190
62	Genetic Variations in the Gene Encoding ELMO1 Are Associated With Susceptibility to Diabetic Nephropathy. Diabetes, 2005, 54, 1171-1178.	0.3	189
63	Thymic Stromal Lymphopoietin Gene Promoter Polymorphisms Are Associated with Susceptibility to Bronchial Asthma. American Journal of Respiratory Cell and Molecular Biology, 2011, 44, 787-793.	1.4	187
64	A genome-wide association study identifies four susceptibility loci for keloid in the Japanese population. Nature Genetics, 2010, 42, 768-771.	9.4	186
65	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
66	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. Circulation, 2014, 130, 1225-1235.	1.6	183
67	Molecular diagnosis of colorectal tumors by expression profiles of 50 genes expressed differentially in adenomas and carcinomas. Oncogene, 2002, 21, 4120-4128.	2.6	178
68	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. Nature Communications, 2015, 6, 6120.	5.8	178
69	Molecular Features of Hormone-Refractory Prostate Cancer Cells by Genome-Wide Gene Expression Profiles. Cancer Research, 2007, 67, 5117-5125.	0.4	169
70	Variation in TP63 is associated with lung adenocarcinoma susceptibility in Japanese and Korean populations. Nature Genetics, 2010, 42, 893-896.	9.4	165
71	High-Risk Ovarian Cancer Based on 126-Gene Expression Signature Is Uniquely Characterized by Downregulation of Antigen Presentation Pathway. Clinical Cancer Research, 2012, 18, 1374-1385.	3.2	165
72	Novel Calmodulin Mutations Associated With Congenital Arrhythmia Susceptibility. Circulation: Cardiovascular Genetics, 2014, 7, 466-474.	5.1	165

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73	DeepInsight: A methodology to transform a non-image data to an image for convolution neural network architecture. Scientific Reports, 2019, 9, 11399.	1.6	162
74	Association of the Gene Encoding Wingless-Type Mammary Tumor Virus Integration-Site Family Member 5B (WNT5B) with Type 2 Diabetes. American Journal of Human Genetics, 2004, 75, 832-843.	2.6	160
75	Genome-wide association study identifies three novel loci for type 2 diabetes. Human Molecular Genetics, 2014, 23, 239-246.	1.4	158
76	Prediction of sensitivity of advanced non-small cell lung cancers to gefitinib (Iressa, ZD1839). Human Molecular Genetics, 2004, 13, 3029-3043.	1.4	156
77	ITPA Polymorphism Affects Ribavirin-Induced Anemia and Outcomes of Therapyâ€"A Genome-Wide Study of Japanese HCV Virus Patients. Gastroenterology, 2010, 139, 1190-1197.e3.	0.6	156
78	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
79	Histone Lysine Methyltransferase SETD8 Promotes Carcinogenesis by Deregulating PCNA Expression. Cancer Research, 2012, 72, 3217-3227.	0.4	155
80	Diverse transcriptional initiation revealed by fine, largeâ€scale mapping of mRNA start sites. EMBO Reports, 2001, 2, 388-393.	2.0	154
81	c-MYC overexpression with loss of Ink4a/Arf transforms bone marrow stromal cells into osteosarcoma accompanied by loss of adipogenesis. Oncogene, 2010, 29, 5687-5699.	2.6	146
82	Common variant in 6q26-q27 is associated with distal colon cancer in an Asian population. Gut, 2011, 60, 799-805.	6.1	145
83	Common variants in CASP3 confer susceptibility to Kawasaki disease. Human Molecular Genetics, 2010, 19, 2898-2906.	1.4	141
84	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. Communications Biology, 2020, 3, 56.	2.0	140
85	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. Human Molecular Genetics, 2017, 26, 1770-1784.	1.4	135
86	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. Nature Genetics, 2008, 40, 994-998.	9.4	134
87	Genome-wide cDNA microarray screening to correlate gene expression profiles with sensitivity of 85 human cancer xenografts to anticancer drugs. Cancer Research, 2002, 62, 518-27.	0.4	133
88	Genome-wide analysis of gene expression in intestinal-type gastric cancers using a complementary DNA microarray representing 23,040 genes. Cancer Research, 2002, 62, 7012-7.	0.4	133
89	Classification of Sensitivity or Resistance of Cervical Cancers to Ionizing Radiation According to Expression Profiles of 62 Genes Selected by cDNA Microarray Analysis. Neoplasia, 2002, 4, 295-303.	2.3	130
90	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. Nature Genetics, 2017, 49, 1120-1125.	9.4	130

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91	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	1.2	127
92	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. Journal of Clinical Investigation, 2013, 123, 4909-4917.	3.9	126
93	A Genome-Wide Association Study Identifies 2 Susceptibility Loci for Crohn's Disease in a Japanese Population. Gastroenterology, 2013, 144, 781-788.	0.6	125
94	Integrative pathway enrichment analysis of multivariate omics data. Nature Communications, 2020, 11, 735.	5.8	125
95	Genome-wide analysis of gene expression in human intrahepatic cholangiocarcinoma. Hepatology, 2005, 41, 1339-1348.	3.6	124
96	Identification of CRYM as a Candidate Responsible for Nonsyndromic Deafness, through cDNA Microarray Analysis of Human Cochlear and Vestibular Tissues**Nucleotide sequence data reported herein are available in the DDBJ/EMBL/GenBank databases; for details, see the Electronic-Database Information section of this article.. American Journal of Human Genetics, 2003, 72, 73-82.	2.6	122
97	Comparison of gene-expression profiles between diffuse- and intestinal-type gastric cancers using a genome-wide cDNA microarray. Oncogene, 2004, 23, 6830-6844.	2.6	115
98	A Genome-Wide Association Study Identified AFF1 as a Susceptibility Locus for Systemic Lupus Eyrthematosus in Japanese. PLoS Genetics, 2012, 8, e1002455.	1.5	115
99	Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. Genome Research, 2001, 11, 677-684.	2.4	115
100	Comparison of gene expression profiles betweenOpisthorchis viverriniandnon-Opisthorchis viverriniassociated human intrahepatic cholangiocarcinoma. Hepatology, 2006, 44, 1025-1038.	3.6	114
101	Genome-wide analysis of gene expression in synovial sarcomas using a cDNA microarray. Cancer Research, 2002, 62, 5859-66.	0.4	114
102	Prevalence of Allergic Rhinitis and Sensitization to Common Aeroallergens in a Japanese Population. International Archives of Allergy and Immunology, 2010, 151, 255-261.	0.9	113
103	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
104	Association of Solute Carrier Family 12 (Sodium/Chloride) Member 3 With Diabetic Nephropathy, Identified by Genome-Wide Analyses of Single Nucleotide Polymorphisms. Diabetes, 2003, 52, 2848-2853.	0.3	107
105	A functional single nucleotide polymorphism in the core promoter region of CALM1 is associated with hip osteoarthritis in Japanese. Human Molecular Genetics, 2005, 14, 1009-1017.	1.4	106
106	Functional SNPs in CD244 increase the risk of rheumatoid arthritis in a Japanese population. Nature Genetics, 2008, 40, 1224-1229.	9.4	106
107	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. Nature Genetics, 2010, 42, 931-936.	9.4	106
108	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	1.5	106

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109	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
110	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. Nature Genetics, 2006, 38, 921-925.	9.4	102
111	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. Nature Genetics, 2009, 41, 329-333.	9.4	102
112	Photosynthesis nuclear genes generally lack TATA-boxes: a tobacco photosystem I gene responds to light through an initiator. Plant Journal, 2002, 29, 1-10.	2.8	99
113	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. Human Molecular Genetics, 2012, 21, 3042-3049.	1.4	99
114	New Sequence Variants in HLA Class II/III Region Associated with Susceptibility to Knee Osteoarthritis Identified by Genome-Wide Association Study. PLoS ONE, 2010, 5, e9723.	1.1	96
115	An improved discriminative filter bank selection approach for motor imagery EEG signal classification using mutual information. BMC Bioinformatics, 2017, 18, 545.	1.2	94
116	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
117	A replication study confirmed the EDAR gene to be a major contributor to population differentiation regarding head hair thickness in Asia. Human Genetics, 2008, 124, 179-185.	1.8	89
118	Isolation of a Novel Human Gene, MARKLI, Homologous to MARK3 and Its Involvement in Hepatocellular Carcinogenesis. Neoplasia, 2001, 3, 4-9.	2.3	88
119	The JmjC domainâ€ containing histone demethylase KDM3A is a positive regulator of the G₁/S transition in cancer cells via transcriptional regulation of the HOXA1 gene. International Journal of Cancer, 2012, 131, E179-89.	2.3	85
120	Genome-Wide Profiling of Gene Expression in 29 Normal Human Tissues with a cDNA Microarray. DNA Research, 2002, 9, 35-45.	1.5	82
121	Single nucleotide polymorphisms in the gene encoding KrÃ¼ppel-like factor 7 are associated with type 2 diabetes. Diabetologia, 2005, 48, 1315-1322.	2.9	82
122	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. Human Molecular Genetics, 2011, 20, 1224-1231.	1.4	82
123	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
124	A Deep Learning Approach for Motor Imagery EEG Signal Classification. , 2016, , .		82
125	Genome-Wide Screening of Genes Showing Altered Expression in Liver Metastases of Human Colorectal Cancers by cDNA Microarray. Neoplasia, 2001, 3, 395-401.	2.3	81
126	A Single Nucleotide Polymorphism within the Acetyl-Coenzyme A Carboxylase Beta Gene Is Associated with Proteinuria in Patients with Type 2 Diabetes. PLoS Genetics, 2010, 6, e1000842.	1.5	81

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127	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. Journal of Hepatology, 2017, 66, 363-373.	1.8	81
128	Integrated Analysis of Whole Genome and Transcriptome Sequencing Reveals Diverse Transcriptomic Aberrations Driven by Somatic Genomic Changes in Liver Cancers. PLoS ONE, 2014, 9, e114263.	1.1	79
129	A meta-analysis identifies adolescent idiopathic scoliosis association withLBX1locus in multiple ethnic groups. Journal of Medical Genetics, 2014, 51, 401-406.	1.5	79
130	Association between Single-Nucleotide Polymorphisms in Selectin Genes and Immunoglobulin A Nephropathy. American Journal of Human Genetics, 2002, 70, 781-786.	2.6	78
131	Association between a Single-Nucleotide Polymorphism in the Promoter of the Human Interleukin-3 Gene and Rheumatoid Arthritis in Japanese Patients, and Maximum-Likelihood Estimation of Combinatorial Effect That Two Genetic Loci Have on Susceptibility to the Disease. American Journal of Human Genetics, 2001, 68, 674-685.	2.6	77
132	Combined Genetic and Genealogic Studies Uncover a Large BAP1 Cancer Syndrome Kindred Tracing Back Nine Generations to a Common Ancestor from the 1700s. PLoS Genetics, 2015, 11, e1005633.	1.5	76
133	CYP2D6 Genotyping for Functional-Gene Dosage Analysis by Allele Copy Number Detection. Clinical Chemistry, 2009, 55, 1546-1554.	1.5	75
134	Analysis of single-nucleotide polymorphisms in Japanese rheumatoid arthritis patients shows additional susceptibility markers besides the classic shared epitope susceptibility sequences. Arthritis and Rheumatism, 2004, 50, 63-71.	6.7	74
135	Identification of a Human Clonogenic Progenitor with Strict Monocyte Differentiation Potential: A Counterpart of Mouse cMoPs. Immunity, 2017, 46, 835-848.e4.	6.6	74
136	Prediction of outcome of advanced cervical cancer to thermoradiotherapy according to expression profiles of 35 genes selected by cDNA microarray analysis. International Journal of Radiation Oncology Biology Physics, 2004, 60, 237-248.	0.4	73
137	Pathway and network analysis of more than 2500 whole cancer genomes. Nature Communications, 2020, 11, 729.	5.8	73
138	A genomewide linkage analysis of Kawasaki disease: evidence for linkage to chromosome 12. Journal of Human Genetics, 2007, 52, 179-190.	1.1	72
139	Predictive value of the IL28B polymorphism on the effect of interferon therapy in chronic hepatitis C patients with genotypes 2a and 2b. Journal of Hepatology, 2011, 54, 408-414.	1.8	72
140	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. IEEE Transactions on Nanobioscience, 2015, 14, 915-926.	2.2	72
141	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 2011, 7, e1002067.	1.5	69
142	Genetic variations in the gene encoding TFAP2B are associated with type 2 diabetes mellitus. Journal of Human Genetics, 2005, 50, 283-292.	1.1	68
143	Validation study of the prediction system for clinical response of M-VAC neoadjuvant chemotherapy. Cancer Science, 2007, 98, 113-117.	1.7	68
144	Radioimmunotherapy of human synovial sarcoma using a monoclonal antibody against FZD10. Cancer Science, 2008, 99, 432-440.	1.7	68

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145	Performance comparison of four commercial human whole-exome capture platforms. Scientific Reports, 2015, 5, 12742.	1.6	68
146	Circulating Tumor DNA Analysis for Liver Cancers and Its Usefulness as a Liquid Biopsy. Cellular and Molecular Gastroenterology and Hepatology, 2015, 1, 516-534.	2.3	67
147	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. Journal of Theoretical Biology, 2017, 425, 97-102.	0.8	65
148	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
149	The histone methyltransferase Wolfâ€“Hirschhorn syndrome candidate 1â€like 1 (WHSC1L1) is involved in human carcinogenesis. Genes Chromosomes and Cancer, 2013, 52, 126-139.	1.5	64
150	Brain wave classification using long short-term memory network based OPTICAL predictor. Scientific Reports, 2019, 9, 9153.	1.6	64
151	A Genome-Wide Association Study of Nephrolithiasis in the Japanese Population Identifies Novel Susceptible Loci at 5q35.3, 7p14.3, and 13q14.1. PLoS Genetics, 2012, 8, e1002541.	1.5	63
152	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
153	Gene expression profiles of small-cell lung cancers: molecular signatures of lung cancer. International Journal of Oncology, 2006, 29, 567-75.	1.4	60
154	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
155	Comprehensive gene expression profiling of anaplastic thyroid cancers with cDNA microarray of 25 344 genes. Endocrine-Related Cancer, 2004, 11, 843-854.	1.6	59
156	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
157	Morphological and microarray analyses of human hepatocytes from xenogeneic host livers. Laboratory Investigation, 2013, 93, 54-71.	1.7	59
158	Identification of a Susceptibility Locus for Severe Adolescent Idiopathic Scoliosis on Chromosome 17q24.3. PLoS ONE, 2013, 8, e72802.	1.1	59
159	Association study of COL9A2 with lumbar disc disease in the Japanese population. Journal of Human Genetics, 2006, 51, 1063-1067.	1.1	58
160	Activation of the non-canonical Dvlâ€“Rac1â€“JNK pathway by Frizzled homologue 10 in human synovial sarcoma. Oncogene, 2009, 28, 1110-1120.	2.6	58
161	Polymorphisms in the 3â€² UTR in the neurocalcin Î´ gene affect mRNA stability, and confer susceptibility to diabetic nephropathy. Human Genetics, 2007, 122, 397-407.	1.8	57
162	Calbindin 1, fibroblast growth factor 20, and Î±-synuclein in sporadic Parkinsonâ€™s disease. Human Genetics, 2008, 124, 89-94.	1.8	56

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163	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. Analytical Biochemistry, 2017, 527, 24-32.	1.1	55
164	Prediction of Sensitivity to STI571 among Chronic Myeloid Leukemia Patients by Genome-wide cDNA Microarray Analysis. Japanese Journal of Cancer Research, 2002, 93, 849-856.	1.7	54
165	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
166	A genome-wide association study identifies locus at 10q22 associated with clinical outcomes of adjuvant tamoxifen therapy for breast cancer patients in Japanese. Human Molecular Genetics, 2012, 21, 1665-1672.	1.4	54
167	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. Human Molecular Genetics, 2011, 20, 3684-3692.	1.4	53
168	KIF1A mutation in a patient with progressive neurodegeneration. Journal of Human Genetics, 2014, 59, 639-641.	1.1	53
169	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. Bioinformatics, 2018, 34, 1850-1858.	1.8	53
170	Analysis of gene-expression profiles after gamma irradiation of normal human fibroblasts. International Journal of Radiation Oncology Biology Physics, 2006, 64, 272-279.	0.4	52
171	Identification of histological markers for malignant glioma by genome-wide expression analysis: dynein, Î±-PIX and sorcin. Acta Neuropathologica, 2006, 111, 29-38.	3.9	52
172	Association of single-nucleotide polymorphisms in MTMR9 gene with obesity. Human Molecular Genetics, 2007, 16, 3017-3026.	1.4	51
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