Tatushiko Tsunoda

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5000143/publications.pdf

Version: 2024-02-01

354 papers	58,895 citations	1798 103 h-index	1136 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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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

#	Article	IF	Citations
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
173	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. PLoS ONE, 2018, 13, e0191900.	1.1	51
174	Variation of gene-based SNPs and linkage disequilibrium patterns in the human genome. Human Molecular Genetics, 2004, 13, 1623-1632.	1.4	50
175	IL-28B predicts response to chronic hepatitis C therapy â€“ fine-mapping and replication study in Asian populations. Journal of General Virology, 2011, 92, 1071-1081.	1.3	50
176	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. BMC Genomics, 2018, 19, 923.	1.2	50
177	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. Communications Biology, 2019, 2, 77.	2.0	50
178	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
179	The subcellular localization and activity of cortactin is regulated by acetylation and interaction with Keap1. Science Signaling, 2015, 8, ra120.	1.6	48
180	Functional Variants in NFKBIE and RTKN2 Involved in Activation of the NF-Îºß Pathway Are Associated with Rheumatoid Arthritis in Japanese. PLoS Genetics, 2012, 8, e1002949.	1.5	46

#	Article	IF	Citations
181	Defects in autophagosome-lysosome fusion underlie Vici syndrome, a neurodevelopmental disorder with multisystem involvement. Scientific Reports, 2017, 7, 3552.	1.6	46
182	Coding SNP in tenascin-C Fn-III-D domain associates with adult asthma. Human Molecular Genetics, 2005, 14, 2779-2786.	1.4	45
183	Gene expression profiles of small-cell lung cancers: Molecular signatures of lung cancer. International Journal of Oncology, 2006, 29, 567.	1.4	45
184	FGFR2 is associated with hair thickness in Asian populations. Journal of Human Genetics, 2009, 54, 461-465.	1.1	45
185	Genetic Variation in the SLC8A1 Calcium Signaling Pathway Is Associated With Susceptibility to Kawasaki Disease and Coronary Artery Abnormalities. Circulation: Cardiovascular Genetics, 2016, 9, 559-568.	5.1	45
186	Chromothripsis-like chromosomal rearrangements induced by ionizing radiation using proton microbeam irradiation system. Oncotarget, 2016, 7, 10182-10192.	0.8	44
187	An integrative machine learning approach for prediction of toxicity-related drug safety. Life Science Alliance, 2018, 1, e201800098.	1.3	44
188	Microarray Analysis of Gene-expression Profiles in Diffuse Large B-cell Lymphoma: Identification of Genes Related to Disease Progression. Japanese Journal of Cancer Research, 2002, 93, 894-901.	1.7	43
189	MoRFPred-plus: Computational Identification of MoRFs in Protein Sequences using Physicochemical Properties and HMM profiles. Journal of Theoretical Biology, 2018, 437, 9-16.	0.8	43
190	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. Journal of Human Genetics, 2011, 56, 47-51.	1.1	41
191	Functional Single-Nucleotide Polymorphisms in the Secretogranin III (SCG3) Gene that Form Secretory Granules with Appetite-Related Neuropeptides Are Associated with Obesity. Journal of Clinical Endocrinology and Metabolism, 2007, 92, 1145-1154.	1.8	40
192	A functional SNP in EDG2 increases susceptibility to knee osteoarthritis in Japanese. Human Molecular Genetics, 2008, 17, 1790-1797.	1.4	40
193	Lessons for pharmacogenomics studies: association study between CYP2D6 genotype and tamoxifen response. Pharmacogenetics and Genomics, 2010, 20, 565-568.	0.7	40
194	Growth Hormone-Dependent Pathogenesis of Human Hepatic Steatosis in a Novel Mouse Model Bearing a Human Hepatocyte-Repopulated Liver. Endocrinology, 2011, 152, 1479-1491.	1.4	40
195	A genome-wide association analysis identifies NMNAT2 and HCP5 as susceptibility loci for Kawasaki disease. Journal of Human Genetics, 2017, 62, 1023-1029.	1.1	40
196	Deep Learning Approach for Automated Detection of Myopic Maculopathy and Pathologic Myopia in Fundus Images. Ophthalmology Retina, 2021, 5, 1235-1244.	1.2	40
197	Population-genetic nature of copy number variations in the human genome. Human Molecular Genetics, 2010, 19, 761-773.	1.4	39
198	A practical method to detect SNVs and indels from whole genome and exome sequencing data. Scientific Reports, 2013, 3, 2161.	1.6	39

#	Article	IF	Citations
199	Combined burden and functional impact tests for cancer driver discovery using DriverPower. Nature Communications, 2020, 11, 734.	5.8	39
200	Expression Profile Analysis of Colon Cancer Cells in Response to Sulindac or Aspirin. Biochemical and Biophysical Research Communications, 2002, 292, 498-512.	1.0	37
201	Genes associated with liver metastasis of colon cancer, identified by genome-wide cDNA microarray. International Journal of Oncology, 2004, 24, 305.	1.4	37
202	IRX4 at 5p15 suppresses prostate cancer growth through the interaction with vitamin D receptor, conferring prostate cancer susceptibility. Human Molecular Genetics, 2012, 21, 2076-2085.	1.4	37
203	Assessing the Clinical Utility of a Genetic Risk Score Constructed Using 49 Susceptibility Alleles for Type 2 Diabetes in a Japanese Population. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E1667-E1673.	1.8	37
204	Expression profiles of two types of human knee-joint cartilage. Journal of Human Genetics, 2003, 48, 177-182.	1.1	36
205	The Oncogenic Polycomb Histone Methyltransferase EZH2Methylates Lysine 120 on Histone H2B and Competes Ubiquitination. Neoplasia, 2013, 15, 1251-IN10.	2.3	36
206	Variants encoding a restricted carboxy-terminal domain of SLC12A2 cause hereditary hearing loss in humans. PLoS Genetics, 2020, 16, e1008643.	1.5	36
207	Genome-wide gene-expression profiles of breast-cancer cells purified with laser microbeam microdissection: identification of genes associated with progression and metastasis. International Journal of Oncology, 2004, 25, 797-819.	1.4	36
208	Combinational effect of genes for the reninâ€“angiotensin system in conferring susceptibility to diabetic nephropathy. Journal of Human Genetics, 2007, 52, 143-151.	1.1	35
209	HLA-DQB1*03 Confers Susceptibility to Chronic Hepatitis C in Japanese: A Genome-Wide Association Study. PLoS ONE, 2013, 8, e84226.	1.1	35
210	Targeted nextâ€generation sequencing in the diagnosis of neurodevelopmental disorders. Clinical Genetics, 2015, 88, 288-292.	1.0	35
211	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. PLoS ONE, 2015, 10, e0139262.	1.1	35
212	Single-nucleotide polymorphisms in the class II region of the major histocompatibility complex in Japanese patients with immunoglobulin A nephropathy. Journal of Human Genetics, 2002, 47, 0532-0538.	1.1	34
213	Protein fold recognition using HMMâ€“HMM alignment and dynamic programming. Journal of Theoretical Biology, 2016, 393, 67-74.	0.8	33
214	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimerâ€™s disease created by integrative analysis of multi-omics data. Alzheimer's Research and Therapy, 2020, 12, 145.	3.0	33
215	Isolation of HELAD1, a novel human helicase gene up-regulated in colorectal carcinomas. Oncogene, 2002, 21, 6387-6394.	2.6	32
216	The Construction of Risk Prediction Models Using GWAS Data and Its Application to a Type 2 Diabetes Prospective Cohort. PLoS ONE, 2014, 9, e92549.	1.1	31

#	Article	IF	Citations
217	Transcriptome analysis of distinct mouse strains reveals kinesin light chain-1 splicing as an amyloid-Î² accumulation modifier. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 2638-2643.	3.3	31
218	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. Scientific Reports, 2018, 8, 17923.	1.6	31
219	Sample Size for Successful Genome-Wide Association Study of Major Depressive Disorder. Frontiers in Genetics, 2018, 9, 227.	1.1	31
220	GlyStruct: glycation prediction using structural properties of amino acid residues. BMC Bioinformatics, 2019, 19, 547.	1.2	31
221	DeepFeature: feature selection in nonimage data using convolutional neural network. Briefings in Bioinformatics, 2021, 22, .	3.2	31
222	Profiling the inhibitory receptors LAG-3, TIM-3, and TIGIT in renal cell carcinoma reveals malignancy. Nature Communications, 2021, 12, 5547.	5.8	31
223	OPAL+: Lengthâ€Specific MoRF Prediction in Intrinsically Disordered Protein Sequences. Proteomics, 2019, 19, e1800058.	1.3	30
224	Reproducibility, Performance, and Clinical Utility of a Genetic Risk Prediction Model for Prostate Cancer in Japanese. PLoS ONE, 2012, 7, e46454.	1.1	30
225	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. PLoS ONE, 2015, 10, e0130329.	1.1	30
226	Genome-wide association study of warfarin maintenance dose in a Brazilian sample. Pharmacogenomics, 2015, 16, 1253-1263.	0.6	29
227	Novel splicing mutation in the ASXL3 gene causing Bainbridgeâ€“Ropers syndrome. American Journal of Medical Genetics, Part A, 2016, 170, 1863-1867.	0.7	28
228	Hierarchical Maximum Likelihood Clustering Approach. IEEE Transactions on Biomedical Engineering, 2017, 64, 112-122.	2.5	28
229	Structural Basis and Genotypeâ€“Phenotype Correlations of INSR Mutations Causing Severe Insulin Resistance. Diabetes, 2017, 66, 2713-2723.	0.3	28
230	Association of a single-nucleotide polymorphism in the immunoglobulinÂÎ¼-binding protein 2 gene with immunoglobulin A nephropathy. Journal of Human Genetics, 2005, 50, 30-35.	1.1	27
231	Identification of independent risk loci for Gravesâ€™ disease within the MHC in the Japanese population. Journal of Human Genetics, 2011, 56, 772-778.	1.1	27
232	Novel MCA/ID syndrome with ASH1L mutation. American Journal of Medical Genetics, Part A, 2017, 173, 1644-1648.	0.7	27
233	Association of an IGHV3-66 gene variant with Kawasaki disease. Journal of Human Genetics, 2021, 66, 475-489.	1.1	27
234	CUL1, a component of E3 ubiquitin ligase, alters lymphocyte signal transduction with possible effect on rheumatoid arthritis. Genes and Immunity, 2005, 6, 194-202.	2.2	26

#	Article	IF	Citations
235	Expression profiles of metastatic brain tumor from lung adenocarcinomas on cDNA microarray. International Journal of Oncology, 2006, 28, 799.	1.4	25
236	Genome-wide gene expression profile analysis of esophageal squamous cell carcinomas. International Journal of Oncology, 2006, 28, 1375.	1.4	25
237	Common variants on 14q32 and 13q12 are associated with DLBCL susceptibility. Journal of Human Genetics, 2011, 56, 436-439.	1.1	25
238	Discovery of a Cynomolgus Monkey Family With Retinitis Pigmentosa. , 2018, 59, 826.		25
239	Predicting protein-peptide binding sites with a deep convolutional neural network. Journal of Theoretical Biology, 2020, 496, 110278.	0.8	25
240	Prediction of response to neoadjuvant chemotherapy for osteosarcoma by gene-expression profiles. International Journal of Oncology, 2004, 24, 647.	1.4	24
241	Truncating mutation in NFIA causes brain malformation and urinary tract defects. Human Genome Variation, 2015, 2, 15007.	0.4	24
242	Predicting MoRFs in protein sequences using HMM profiles. BMC Bioinformatics, 2016, 17, 504.	1.2	24
243	TUBA1A mutation can cause a hydranencephaly-like severe form of cortical dysgenesis. Scientific Reports, 2015, 5, 15165.	1.6	23
244	Divisive hierarchical maximum likelihood clustering. BMC Bioinformatics, 2017, 18, 546.	1.2	23
245	Structure-activity relationship of clovamide and its related compounds for the inhibition of amyloid Î² aggregation. Bioorganic and Medicinal Chemistry, 2018, 26, 3202-3209.	1.4	23
246	Variants in the SCN5A Promoter Associated With Various Arrhythmia Phenotypes. Journal of the American Heart Association, 2016, 5, .	1.6	22
247	A novel missense mutation in the HECT domain of NEDD4L identified in a girl with periventricular nodular heterotopia, polymicrogyria and cleft palate. Journal of Human Genetics, 2017, 62, 861-863.	1.1	22
248	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid-Î² accumulation in Alzheimerâ€™s disease. Human Genetics, 2018, 137, 521-533.	1.8	22
249	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data. BMC Medical Genomics, 2019, 12, 150.	0.7	22
250	Predicting response of bladder cancers to gemcitabine and carboplatin neoadjuvant chemotherapy through genome-wide gene expression profiling. Experimental and Therapeutic Medicine, 2011, 2, 47-56.	0.8	21
251	A combination of genetic and biochemical analyses for the diagnosis of PI3K-AKT-mTOR pathway-associated megalencephaly. BMC Medical Genetics, 2017, 18, 4.	2.1	21
252	Genome-wide gene expression profiles of clear cell renal cell carcinoma: Identification of molecular targets for treatment of renal cell carcinoma. International Journal of Oncology, 2006, 29, 799.	1.4	20

#	Article	IF	Citations
253	An Algorithm for Inferring Complex Haplotypes in a Region of Copy-Number Variation. American Journal of Human Genetics, 2008, 83, 157-169.	2.6	20
254	Systematic analysis of mutation distribution in three dimensional protein structures identifies cancer driver genes. Scientific Reports, 2016, 6, 26483.	1.6	20
255	IMSindel: An accurate intermediate-size indel detection tool incorporating de novo assembly and gapped global-local alignment with split read analysis. Scientific Reports, 2018, 8, 5608.	1.6	20
256	Decimation filter with Common Spatial Pattern and Fishers Discriminant Analysis for motor imagery classification. , 2016, , .		19
257	Unveiling synapse pathology in spinal bulbar muscular atrophy by genome-wide transcriptome analysis of purified motor neurons derived from disease specific iPSCs. Molecular Brain, 2020, 13, 18.	1.3	19
258	Analysis of gene-expression profiles in testicular seminomas using a genome-wide cDNA microarray. International Journal of Oncology, 2003, 23, 1615.	1.4	18
259	Gene expression patterns as marker for 5-year postoperative prognosis of primary breast cancers. Journal of Cancer Research and Clinical Oncology, 2004, 130, 537-45.	1.2	18
260	Phenotypic Variability of <i>ANK2</i> Mutations in Patients With Inherited Primary Arrhythmia Syndromes. Circulation Journal, 2016, 80, 2435-2442.	0.7	18
261	EvolStruct-Phogly: incorporating structural properties and evolutionary information from profile bigrams for the phosphoglycerylation prediction. BMC Genomics, 2019, 19, 984.	1.2	17
262	Multiplexed single-cell pathology reveals the association of CD8 T-cell heterogeneity with prognostic outcomes in renal cell carcinoma. Cancer Immunology, Immunotherapy, 2021, 70, 3001-3013.	2.0	17
263	Hepatitis C Virus Infection Suppresses the Interferon Response in the Liver of the Human Hepatocyte Chimeric Mouse. PLoS ONE, 2011, 6, e23856.	1.1	16
264	Navigating the disease landscape: knowledge representations for contextualizing molecular signatures. Briefings in Bioinformatics, 2019, 20, 609-623.	3.2	16
265	Genome-wide analysis of gene-expression profiles in chronic myeloid leukemia cells using a cDNA microarray. International Journal of Oncology, 2003, 23, 681.	1.4	15
266	MOCSphaser: a haplotype inference tool from a mixture of copy number variation and single nucleotide polymorphism data. Bioinformatics, 2008, 24, 1645-1646.	1.8	15
267	ALDH18A1-related cutis laxa syndrome with cyclic vomiting. Brain and Development, 2016, 38, 678-684.	0.6	15
268	Forecasting the spread of COVID-19 using LSTM network. BMC Bioinformatics, 2021, 22, 316.	1.2	15
269	Identification of biomarkers associated with migraine with aura. Neuroscience Research, 2009, 64, 104-110.	1.0	14
270	Pathway analysis of genome-wide data improves warfarin dose prediction. BMC Genomics, 2013, 14, S11.	1.2	14

#	Article	IF	Citations
271	A combination of targeted enrichment methodologies for whole-exome sequencing reveals novel pathogenic mutations. Scientific Reports, 2015, 5, 9331.	1.6	14
272	Stepwise iterative maximum likelihood clustering approach. BMC Bioinformatics, 2016, 17, 319.	1.2	14
273	A case report of reversible generalized seizures in a patient with Waardenburg syndrome associated with a novel nonsense mutation in the penultimate exon of SOX10. BMC Pediatrics, 2018, 18, 171.	0.7	14
274	Whole genome sequencing and mutation rate analysis of trios with paternal dioxin exposure. Human Mutation, 2018, 39, 1384-1392.	1.1	14
275	Role of a heterotrimeric Gâ€protein, Gi2, in the corticogenesis: possible involvement in periventricular nodular heterotopia and intellectual disability. Journal of Neurochemistry, 2017, 140, 82-95.	2.1	13
276	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. Molecules, 2018, 23, 3260.	1.7	13
277	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. BMC Bioinformatics, 2019, 19, 378.	1.2	13
278	De novo ATP1A3 variants cause polymicrogyria. Science Advances, 2021, 7, .	4.7	13
279	Landscape of prognostic signatures and immunogenomics of the AXL/GAS6 axis in renal cell carcinoma. British Journal of Cancer, 2021, 125, 1533-1543.	2.9	13
280	Unique characteristics of tertiary lymphoid structures in kidney clear cell carcinoma: prognostic outcome and comparison with bladder cancer. , 2022, 10, e003883.		13
281	Novel compound heterozygous variants in PLK4 identified in a patient with autosomal recessive microcephaly and chorioretinopathy. European Journal of Human Genetics, 2016, 24, 1702-1706.	1.4	12
282	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. BMC Genomics, 2019, 19, 982.	1.2	12
283	MYCNde novo gain-of-function mutation in a patient with a novel megalencephaly syndrome. Journal of Medical Genetics, 2019, 56, 388-395.	1.5	12
284	Attenuation of Progressive Hearing Loss in DBA/2J Mice by Reagents that Affect Epigenetic Modifications Is Associated with Up-Regulation of the Zinc Importer Zip4. PLoS ONE, 2015, 10, e0124301.	1.1	11
285	Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix. BMC Molecular and Cell Biology, 2019, 20, 57.	1.0	11
286	Integrative immunogenomic analysis of gastric cancer dictates novel immunological classification and the functional status of tumorâ€infiltrating cells. Clinical and Translational Immunology, 2020, 9, e1194.	1.7	11
287	Prediction of response to peginterferonâ€alfaâ€2b plus ribavirin therapy in Japanese patients infected with hepatitis C virus genotype 1b. Journal of Medical Virology, 2011, 83, 981-988.	2.5	10
288	Sudden death in a case of megalencephaly capillary malformation associated with a de novo mutation in AKT3. Child's Nervous System, 2015, 31, 465-471.	0.6	10

#	Article	IF	Citations
289	A functional SNP in FLT1 increases risk of coronary artery disease in a Japanese population. Journal of Human Genetics, 2016, 61, 435-441.	1.1	10
290	The prediction models for postoperative overall survival and diseaseâ€free survival in patients with breast cancer. Cancer Medicine, 2017, 6, 1627-1638.	1.3	10
291	Arete â€“ candidate gene prioritization using biological network topology with additional evidence types. BioData Mining, 2017, 10, 22.	2.2	10
292	Empirical Bayes Estimation of Semi-parametric Hierarchical Mixture Models for Unbiased Characterization of Polygenic Disease Architectures. Frontiers in Genetics, 2018, 9, 115.	1.1	10
293	A novel homozygous missense mutation in the SH3-binding motif of STAMBP causing microcephaly-capillary malformation syndrome. Journal of Human Genetics, 2018, 63, 957-963.	1.1	10
294	Predicting response to docetaxel neoadjuvant chemotherapy for advanced breast cancers through genome-wide gene expression profiling. International Journal of Oncology, 2009, 34, 361-70.	1.4	10
295	Linkage disequilibrium of evolutionarily conserved regions in the human genome. BMC Genomics, 2006, 7, 326.	1.2	9
296	Recombination rates of genes expressed in human tissues. Human Molecular Genetics, 2008, 17, 577-586.	1.4	9
297	Genetic differences in the two main groups of the Japanese population based on autosomal SNPs and haplotypes. Journal of Human Genetics, 2012, 57, 326-334.	1.1	9
298	Single-nucleotide polymorphisms in GALNT8 are associated with the response to interferon therapy for chronic hepatitis C. Journal of General Virology, 2013, 94, 81-89.	1.3	9
299	A deletion mutation in myosin heavy chain 11 causing familial thoracic aortic dissection in two Japanese pedigrees. International Journal of Cardiology, 2015, 195, 290-292.	0.8	9
300	Subject-Specific-Frequency-Band for Motor Imagery EEG Signal Recognition Based on Common Spatial Spectral Pattern. Lecture Notes in Computer Science, 2019, , 712-722.	1.0	9
301	Siblings with optic neuropathy and RTN4IP1 mutation. Journal of Human Genetics, 2017, 62, 927-929.	1.1	8
302	Genome-wide association study suggests four variants influencing outcomes with ranibizumab therapy in exudative age-related macular degeneration. Journal of Human Genetics, 2018, 63, 1083-1091.	1.1	8
303	Single-stranded and double-stranded DNA-binding protein prediction using HMM profiles. Analytical Biochemistry, 2021, 612, 113954.	1.1	8
304	Effects of clovamide and its related compounds on the aggregations of amyloid polypeptides. Journal of Natural Medicines, 2021, 75, 299-307.	1.1	8
305	Gene masking - a technique to improve accuracy for cancer classification with high dimensionality in microarray data. BMC Medical Genomics, 2016, 9, 74.	0.7	7
306	A novel genetic syndrome with STARD9 mutation and abnormal spindle morphology. American Journal of Medical Genetics, Part A, 2017, 173, 2690-2696.	0.7	7

#	Article	IF	Citations
307	2Dâ€“EM clustering approach for high-dimensional data through folding feature vectors. BMC Bioinformatics, 2017, 18, 547.	1.2	7
308	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. Pharmacogenomics Journal, 2018, 18, 106-112.	0.9	7
309	Four pedigrees with aminoacyl-tRNA synthetase abnormalities. Neurological Sciences, 2022, 43, 2765-2774.	0.9	7
310	Identification of a set of genes associated with response to interleukin-2 and interferon-Î± combination therapy for renal cell carcinoma through genome-wide gene expression profiling. Experimental and Therapeutic Medicine, 2010, 1, 955-961.	0.8	6
311	Primary Microcephaly With Anterior Predominant Pachygyria Caused by Novel Compound Heterozygous Mutations in ASPM. Pediatric Neurology, 2015, 52, e7-e8.	1.0	6
312	PupStruct: Prediction of Pupylated Lysine Residues Using Structural Properties of Amino Acids. Genes, 2020, 11, 1431.	1.0	6
313	A hypomorphic variant in EYS detected by genome-wide association study contributes toward retinitis pigmentosa. Communications Biology, 2021, 4, 140.	2.0	6
314	ELF3 Overexpression as Prognostic Biomarker for Recurrence of Stage II Colorectal Cancer. In Vivo, 2021, 35, 191-201.	0.6	6
315	MotifCombinator: a web-based tool to search for combinations of cis-regulatory motifs. BMC Bioinformatics, 2007, 8, 100.	1.2	5
316	Gene expression dataset for whole cochlea of Macaca fascicularis. Scientific Reports, 2018, 8, 15554.	1.6	5
317	RAM-PGK: Prediction of Lysine Phosphoglycerylation Based on Residue Adjacency Matrix. Genes, 2020, 11, 1524.	1.0	5
318	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. Human Genome Variation, 2021, 8, 25.	0.4	5
319	Association between high immune activity and worse prognosis in uveal melanoma and low-grade glioma in TCGA transcriptomic data. BMC Genomics, 2022, 23, 351.	1.2	5
320	Predicting response to docetaxel neoadjuvant chemotherapy for advanced breast cancers through genome-wide gene expression profiling. International Journal of Oncology, 1992, 34, 361.	1.4	4
321	Inferring Haplotypes of Copy Number Variations From High-Throughput Data With Uncertainty. G3: Genes, Genomes, Genetics, 2011, 1, 35-42.	0.8	4
322	Whole Genome Sequencing of a Vietnamese Family from a Dioxin Contamination Hotspot Reveals Novel Variants in the Son with Undiagnosed Intellectual Disability. International Journal of Environmental Research and Public Health, 2018, 15, 2629.	1.2	4
323	Exploring predictive biomarkers from clinical genome-wide association studies via multidimensional hierarchical mixture models. European Journal of Human Genetics, 2019, 27, 140-149.	1.4	4
324	SPECTRA: a tool for enhanced brain wave signal recognition. BMC Bioinformatics, 2021, 22, 195.	1.2	4

#	Article	IF	Citations
325	Clustering of Small-Sample Single-Cell RNA-Seq Data via Feature Clustering and Selection. Lecture Notes in Computer Science, 2019, , 445-456.	1.0	4
326	Immune subtypes and neoantigen-related immune evasion in advanced colorectal cancer. IScience, 2022, 25, 103740.	1.9	4
327	hzAnalyzer: detection, quantification, and visualization of contiguous homozygosity in high-density genotyping datasets. Genome Biology, 2011, 12, R21.	13.9	3
328	Clinical usefulness of multigene screening with phenotype-driven bioinformatics analysis for the diagnosis of patients with monogenic diabetes or severe insulin resistance. Diabetes Research and Clinical Practice, 2020, 169, 108461.	1.1	3
329	Homozygous ADCY5 mutation causes early-onset movement disorder with severe intellectual disability. Neurological Sciences, 2021, 42, 2975-2978.	0.9	3
330	Making a haplotype catalog with estimated frequencies based on SNP homozygotes. Journal of Human Genetics, 2010, 55, 500-506.	1.1	2
331	Application of cepstrum analysis and linear predictive coding for motor imaginary task classification. , 2015, , .		2
332	Quantification of multicellular colonization in tumor metastasis using exomeâ€sequencing data. International Journal of Cancer, 2020, 146, 2488-2497.	2.3	2
333	Time and Memory Efficient Algorithm for Extracting Palindromic and Repetitive Subsequences in Nucleic Acid Sequences. , 1998, , 202-13.		2
334	Abstract 1179: Combined genetic and genealogic studies uncover a large BAP1 cancer syndrome kindred, tracing back nine generations to a common ancestor from the 1700s. Cancer Research, 2016, 76, 1179-1179.	0.4	2
335	Activation of an Estrogen/ Estrogen Receptor Signaling by BIG3 Through Its Inhibitory Effect on Nuclear Transport of PHB2/REA in Breast Cancer. Nature Precedings, 2009, , .	0.1	1
336	Importance of dimensionality reduction in protein fold recognition. , 2015, , .		1
337	Gene expression profiling of DBA/2J mice cochleae treated with l-methionine and valproic acid. Genomics Data, 2015, 5, 323-325.	1.3	1
338	Genotype-Structure-Phenotype Correlations of Disease-Associated IGF1R Variants and Similarities to Those of INSR Variants. Diabetes, 2021, 70, 1874-1884.	0.3	1
339	Computational Prediction of Lysine Pupylation Sites in Prokaryotic Proteins Using Position Specific Scoring Matrix into Bigram for Feature Extraction. Lecture Notes in Computer Science, 2019, , 488-500.	1.0	1
340	Abstract 5177: Genome-wide profiling of somatic mutations in liver cancers revealed significantly mutated genes and non-coding regions in liver cancers. , 2014, , .		1
341	1325-P: Effectiveness of Comprehensive Gene Panel-Based Next-Generation Sequencing with Phenotype-Driven Bioinformatics Analysis for Diagnosis of Atypical Diabetes. Diabetes, 2019, 68, 1325-P.	0.3	1
342	Hemorrhagic shock and encephalopathy syndrome in a patient with a de novo heterozygous variant in KIF1A. Brain and Development, 2022, 44, 249-253.	0.6	1

#	Article	IF	Citations
343	144 GENOME-WIDE ASSOCIATION STUDY IDENTIFIES MULTIPLE NEW SUSCEPTIBILITY LOCI FOR PROSTATE CANCER IN JAPANESE POPULATION. Journal of Urology, 2011, 185, .	0.2	0
344	Computational Pipelines and Workflows in Bioinformatics. , 2019, , 113-134.		0
345	Abstract 5200: Genome-wide integrative analysis for the determination of the consequence of AT-rich interacting domain 2 (ARID2) depletion in hepatocellular carcinoma.. , 2013, , .		0
346	Abstract 33: A Meta-analysis Of Three Genome-wide Association Studies Identifies A Novel Susceptibility Locus For Kawasaki Disease.. Circulation, 2015, 131, .	1.6	0
347	Abstract 2970: Whole genome sequencing analysis of multiple liver cancer nodules for determination of causal events for multi-occurrence. , 2015, , .		0
348	Abstract 3890: Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. , 2015, , .		0
349	Abstract 4796: A founder mutation in the BAP1 gene among four caucasian families with high incidences of malignant peritoneal mesothelioma and uveal melanoma: a molecular and genealogical study in a 10-generation BAP1 cancer syndrome kindred. , 2015, , .		0
350	Abstract 12257: Calmodulin Interacting Genes as a Novel Candidate for Pathogenesis of Long-QT Syndrome. Circulation, 2015, 132, .	1.6	0
351	Genotypeâ€“Phenotype Correlations and Structural Basis of INSR and IGF1R Mutations Causing Severe Insulin/IGF-1 Resistance. Diabetes, 2018, 67, 1349-P.	0.3	0
352	The Future of and Beyond GWAS. , 2019, , 193-209.		0
353	Genotyping and Statistical Analysis. , 2019, , 1-20.		0
354	DeepInsight: Methodology to Handle Non-image Data, such as Genomics Data, with Deep Learning. Seibutsu Butsuri, 2020, 60, 149-152.	0.0	0