Tatushiko Tsunoda

List of Publications by Citations

345 papers	45,677 citations	96 h-index	211 g-index
366 ext. papers	53,413 ext. citations	11.1 avg, IF	8.07 L-index

#	Paper	IF	Citations
345	The International HapMap Project. *Nature*, **2003**, 426, 789-96	50.4	5039
344	A haplotype map of the human genome. *Nature*, **2005**, 437, 1299-320	50.4	4818
343	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
342	International network of cancer genome projects. *Nature*, **2010**, 464, 993-8	50.4	1613
341	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
340	Genome-wide association study identifies common variants at four loci as genetic risk factors for Parkinson's disease. *Nature Genetics*, **2009**, 41, 1303-7	36.3	1045
339	Functional haplotypes of PADI4, encoding citrullinating enzyme peptidylarginine deiminase 4, are associated with rheumatoid arthritis. *Nature Genetics*, **2003**, 34, 395-402	36.3	966
338	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
337	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
336	Functional SNPs in the lymphotoxin-alpha gene that are associated with susceptibility to myocardial infarction. *Nature Genetics*, **2002**, 32, 650-4	36.3	755
335	Integrated molecular analysis of clear-cell renal cell carcinoma. *Nature Genetics*, **2013**, 45, 860-7	36.3	723
334	Whole-genome sequencing of liver cancers identifies etiological influences on mutation patterns and recurrent mutations in chromatin regulators. *Nature Genetics*, **2012**, 44, 760-4	36.3	671
333	SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations. *Nature Genetics*, **2008**, 40, 1098-102	36.3	555
332	An intronic SNP in a RUNX1 binding site of SLC22A4, encoding an organic cation transporter, is associated with rheumatoid arthritis. *Nature Genetics*, **2003**, 35, 341-8	36.3	494
331	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
330	A genome-wide association study identifies variants in the HLA-DP locus associated with chronic hepatitis B in Asians. *Nature Genetics*, **2009**, 41, 591-5	36.3	428
329	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423

328	Single nucleotide polymorphisms in TNFSF15 confer susceptibility to Crohn's disease. *Human Molecular Genetics*, **2005**, 14, 3499-506	5.6	376
327	Overexpression of LSD1 contributes to human carcinogenesis through chromatin regulation in various cancers. *International Journal of Cancer*, **2011**, 128, 574-86	7.5	353
326	ITPKC functional polymorphism associated with Kawasaki disease susceptibility and formation of coronary artery aneurysms. *Nature Genetics*, **2008**, 40, 35-42	36.3	339
325	Integrating ethics and science in the International HapMap Project. *Nature Reviews Genetics*, **2004**, 5, 467-75	30.1	334
324	A functional variant in FCRL3, encoding Fc receptor-like 3, is associated with rheumatoid arthritis and several autoimmunities. *Nature Genetics*, **2005**, 37, 478-85	36.3	310
323	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
322	Meta-analysis identifies common variants associated with body mass index in east Asians. *Nature Genetics*, **2012**, 44, 307-11	36.3	301
321	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, 2192-205	9.2	277
320	Genome-wide association study identifies three new susceptibility loci for adult asthma in the Japanese population. *Nature Genetics*, **2011**, 43, 893-6	36.3	252
319	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
318	Estimating transcription factor bindability on DNA. *Bioinformatics*, **1999**, 15, 622-30	7.2	242
317	Genome-wide association study identifies eight new susceptibility loci for atopic dermatitis in the Japanese population. *Nature Genetics*, **2012**, 44, 1222-6	36.3	241
316	Association of a novel long non-coding RNA in 8q24 with prostate cancer susceptibility. *Cancer Science*, **2011**, 102, 245-52	6.9	236
315	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
314	Functional variants in ADH1B and ALDH2 coupled with alcohol and smoking synergistically enhance esophageal cancer risk. *Gastroenterology*, **2009**, 137, 1768-75	13.3	232
313	Genome-wide association study identifies five new susceptibility loci for prostate cancer in the Japanese population. *Nature Genetics*, **2010**, 42, 751-4	36.3	230
312	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
311	Identification of membrane-type matrix metalloproteinase-1 as a target of the beta-catenin/Tcf4 complex in human colorectal cancers. *Oncogene*, **2002**, 21, 5861-7	9.2	220

310	A genome-wide association study identifies three new risk loci for Kawasaki disease. *Nature Genetics*, **2012**, 44, 517-21	36.3	217
309	Dysregulation of PRMT1 and PRMT6, Type I arginine methyltransferases, is involved in various types of human cancers. *International Journal of Cancer*, **2011**, 128, 562-73	7.5	214
308	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, 864-8	36.3	214
307	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, 2385-400	9.2	210
306	A regulatory variant in CCR6 is associated with rheumatoid arthritis susceptibility. *Nature Genetics*, **2010**, 42, 515-9	36.3	209
305	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. *Nature Genetics*, **2012**, 44, 904-9	36.3	201
304	A genome-wide association study identifies three new susceptibility loci for ulcerative colitis in the Japanese population. *Nature Genetics*, **2009**, 41, 1325-9	36.3	199
303	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, 1287-93	2.2	197
302	Prepublication data sharing. *Nature*, **2009**, 461, 168-70	50.4	197
301	Predicting response to methotrexate, vinblastine, doxorubicin, and cisplatin neoadjuvant chemotherapy for bladder cancers through genome-wide gene expression profiling. *Clinical Cancer Research*, **2005**, 11, 2625-36	12.9	197
300	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. *Nature Genetics*, **2012**, 44, 302-6	36.3	192
299	Molecular features of the transition from prostatic intraepithelial neoplasia (PIN) to prostate cancer: genome-wide gene-expression profiles of prostate cancers and PINs. *Cancer Research*, **2004**, 64, 5963-72	10.1	185
298	Identification and characterization of the potential promoter regions of 1031 kinds of human genes. *Genome Research*, **2001**, 11, 677-84	9.7	184
297	A functional SNP in CILP, encoding cartilage intermediate layer protein, is associated with susceptibility to lumbar disc disease. *Nature Genetics*, **2005**, 37, 607-12	36.3	182
296	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, 218-25	6.9	181
295	A genome-wide association study identifies common variants near LBX1 associated with adolescent idiopathic scoliosis. *Nature Genetics*, **2011**, 43, 1237-40	36.3	175
294	A genome-wide association study of chronic hepatitis B identified novel risk locus in a Japanese population. *Human Molecular Genetics*, **2011**, 20, 3884-92	5.6	174
293	Genetic variants in GPR126 are associated with adolescent idiopathic scoliosis. *Nature Genetics*, **2013**, 45, 676-9	36.3	172

292	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
291	Genetic variations in the gene encoding ELMO1 are associated with susceptibility to diabetic nephropathy. *Diabetes*, **2005**, 54, 1171-8	0.9	163
290	Thymic stromal lymphopoietin gene promoter polymorphisms are associated with susceptibility to bronchial asthma. *American Journal of Respiratory Cell and Molecular Biology*, **2011**, 44, 787-93	5.7	161
289	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	10.1	158
288	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	42.1	154
287	Genomic basis for RNA alterations in cancer. *Nature*, **2020**, 578, 129-136	50.4	148
286	Molecular features of hormone-refractory prostate cancer cells by genome-wide gene expression profiles. *Cancer Research*, **2007**, 67, 5117-25	10.1	147
285	Variation in TP63 is associated with lung adenocarcinoma susceptibility in Japanese and Korean populations. *Nature Genetics*, **2010**, 42, 893-6	36.3	145
284	ITPA polymorphism affects ribavirin-induced anemia and outcomes of therapy--a genome-wide study of Japanese HCV virus patients. *Gastroenterology*, **2010**, 139, 1190-7	13.3	145
283	Molecular diagnosis of colorectal tumors by expression profiles of 50 genes expressed differentially in adenomas and carcinomas. *Oncogene*, **2002**, 21, 4120-8	9.2	145
282	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. *Circulation*, **2014**, 130, 1225-35	16.7	143
281	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, 5492-504	5.6	141
280	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites. *EMBO Reports*, **2001**, 2, 388-93	6.5	141
279	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. *Nature Communications*, **2015**, 6, 6120	17.4	139
278	Prediction of sensitivity of advanced non-small cell lung cancers to gefitinib (Iressa, ZD1839). *Human Molecular Genetics*, **2004**, 13, 3029-43	5.6	139
277	Genome-wide association study identifies three novel loci for type 2 diabetes. *Human Molecular Genetics*, **2014**, 23, 239-46	5.6	138
276	Variation in the DEPDC5 locus is associated with progression to hepatocellular carcinoma in chronic hepatitis C virus carriers. *Nature Genetics*, **2011**, 43, 797-800	36.3	137
275	Novel calmodulin mutations associated with congenital arrhythmia susceptibility. *Circulation: Cardiovascular Genetics*, **2014**, 7, 466-74		133

274	A genome-wide association study identifies four susceptibility loci for keloid in the Japanese population. *Nature Genetics*, **2010**, 42, 768-71	36.3	133
273	High-risk ovarian cancer based on 126-gene expression signature is uniquely characterized by downregulation of antigen presentation pathway. *Clinical Cancer Research*, **2012**, 18, 1374-85	12.9	131
272	Histone lysine methyltransferase SETD8 promotes carcinogenesis by deregulating PCNA expression. *Cancer Research*, **2012**, 72, 3217-27	10.1	131
271	Common variant in 6q26-q27 is associated with distal colon cancer in an Asian population. *Gut*, **2011**, 60, 799-805	19.2	128
270	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, 832-43	11	127
269	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
268	c-MYC overexpression with loss of Ink4a/Arf transforms bone marrow stromal cells into osteosarcoma accompanied by loss of adipogenesis. *Oncogene*, **2010**, 29, 5687-99	9.2	121
267	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications*, **2019**, 10, 2674	17.4	119
266	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	10.1	117
265	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. *Nature Genetics*, **2008**, 40, 994-8	36.3	116
264	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	10.1	116
263	Common variants in CASP3 confer susceptibility to Kawasaki disease. *Human Molecular Genetics*, **2010**, 19, 2898-906	5.6	114
262	The landscape of viral associations in human cancers. *Nature Genetics*, **2020**, 52, 320-330	36.3	113
261	Genome-wide analysis of gene expression in human intrahepatic cholangiocarcinoma. *Hepatology*, **2005**, 41, 1339-48	11.2	113
260	Identification of CRYM as a candidate responsible for nonsyndromic deafness, through cDNA microarray analysis of human cochlear and vestibular tissues. *American Journal of Human Genetics*, **2003**, 72, 73-82	11	107
259	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	6.4	107
258	Novel genetic markers associate with atrial fibrillation risk in Europeans and Japanese. *Journal of the American College of Cardiology*, **2014**, 63, 1200-1210	15.1	102
257	A genome-wide association study identifies 2 susceptibility Loci for Crohn's disease in a Japanese population. *Gastroenterology*, **2013**, 144, 781-8	13.3	101

256	Comparison of gene expression profiles between Opisthorchis viverrini and non-Opisthorchis viverrini associated human intrahepatic cholangiocarcinoma. *Hepatology*, **2006**, 44, 1025-38	11.2	101
255	Comparison of gene-expression profiles between diffuse- and intestinal-type gastric cancers using a genome-wide cDNA microarray. *Oncogene*, **2004**, 23, 6830-44	9.2	101
254	Prevalence of allergic rhinitis and sensitization to common aeroallergens in a Japanese population. *International Archives of Allergy and Immunology*, **2010**, 151, 255-61	3.7	100
253	Genome-wide analysis of gene expression in synovial sarcomas using a cDNA microarray. *Cancer Research*, **2002**, 62, 5859-66	10.1	100
252	Whole-genome sequencing and comprehensive variant analysis of a Japanese individual using massively parallel sequencing. *Nature Genetics*, **2010**, 42, 931-6	36.3	98
251	Enhanced expression of EHMT2 is involved in the proliferation of cancer cells through negative regulation of SIAH1. *Neoplasia*, **2011**, 13, 676-84	6.4	97
250	A functional single nucleotide polymorphism in the core promoter region of CALM1 is associated with hip osteoarthritis in Japanese. *Human Molecular Genetics*, **2005**, 14, 1009-17	5.6	96
249	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
248	Functional SNPs in CD244 increase the risk of rheumatoid arthritis in a Japanese population. *Nature Genetics*, **2008**, 40, 1224-9	36.3	92
247	Assessment of network module identification across complex diseases. *Nature Methods*, **2019**, 16, 843-852	25.6	91
246	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. *Nature Genetics*, **2006**, 38, 921-5	36.3	91
245	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	5.6	90
244	Photosynthesis nuclear genes generally lack TATA-boxes: a tobacco photosystem I gene responds to light through an initiator. *Plant Journal*, **2002**, 29, 1-10	6.9	90
243	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, 2848-53	0.9	90
242	A genome-wide association study identified AFF1 as a susceptibility locus for systemic lupus eyrthematosus in Japanese. *PLoS Genetics*, **2012**, 8, e1002455	6	89
241	A single-nucleotide polymorphism in ANK1 is associated with susceptibility to type 2 diabetes in Japanese populations. *Human Molecular Genetics*, **2012**, 21, 3042-9	5.6	86
240	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. *Nature Genetics*, **2017**, 49, 1120-1125	36.3	83
239	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. *Nature Genetics*, **2009**, 41, 329-33	36.3	83

238	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. *Journal of Clinical Investigation*, **2013**, 123, 4909-17	15.9	81
237	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	3.7	79
236	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Communications Biology*, **2020**, 3, 56	6.7	77
235	Genome-wide profiling of gene expression in 29 normal human tissues with a cDNA microarray. *DNA Research*, **2002**, 9, 35-45	4.5	77
234	Histone lysine methyltransferase Wolf-Hirschhorn syndrome candidate 1 is involved in human carcinogenesis through regulation of the Wnt pathway. *Neoplasia*, **2011**, 13, 887-98	6.4	75
233	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	6	73
232	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, 179-85	6.3	73
231	Association between single-nucleotide polymorphisms in selectin genes and immunoglobulin A nephropathy. *American Journal of Human Genetics*, **2002**, 70, 781-6	11	73
230	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, 674-85	11	72
229	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. *Human Molecular Genetics*, **2015**, 24, 1791-800	5.6	71
228	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, 408-14	13.4	70
227	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		70
226	The JmjC domain-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	7.5	69
225	Genome-wide screening of genes showing altered expression in liver metastases of human colorectal cancers by cDNA microarray. *Neoplasia*, **2001**, 3, 395-401	6.4	69
224	Isolation of a novel human gene, MARKL1, homologous to MARK3 and its involvement in hepatocellular carcinogenesis. *Neoplasia*, **2001**, 3, 4-9	6.4	69
223	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. *Human Molecular Genetics*, **2011**, 20, 1224-31	5.6	68
222	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, 915-26	3.4	66
221	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	6	64

220	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, 237-48	4	64
219	An improved discriminative filter bank selection approach for motor imagery EEG signal classification using mutual information. *BMC Bioinformatics*, **2017**, 18, 545	3.6	63
218	CYP2D6 genotyping for functional-gene dosage analysis by allele copy number detection. *Clinical Chemistry*, **2009**, 55, 1546-54	5.5	63
217	Single nucleotide polymorphisms in the gene encoding Krüppel-like factor 7 are associated with type 2 diabetes. *Diabetologia*, **2005**, 48, 1315-22	10.3	63
216	Genetic variations in the gene encoding TFAP2B are associated with type 2 diabetes mellitus. *Journal of Human Genetics*, **2005**, 50, 283-292	4.3	63
215	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62
214	A genomewide linkage analysis of Kawasaki disease: evidence for linkage to chromosome 12. *Journal of Human Genetics*, **2007**, 52, 179-190	4.3	62
213	Identification of nine novel loci associated with white blood cell subtypes in a Japanese population. *PLoS Genetics*, **2011**, 7, e1002067	6	61
212	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	6.6	60
211	Validation study of the prediction system for clinical response of M-VAC neoadjuvant chemotherapy. *Cancer Science*, **2007**, 98, 113-7	6.9	60
210	Radioimmunotherapy of human synovial sarcoma using a monoclonal antibody against FZD10. *Cancer Science*, **2008**, 99, 432-40	6.9	59
209	DeepInsight: A methodology to transform a non-image data to an image for convolution neural network architecture. *Scientific Reports*, **2019**, 9, 11399	4.9	58
208	A meta-analysis identifies adolescent idiopathic scoliosis association with LBX1 locus in multiple ethnic groups. *Journal of Medical Genetics*, **2014**, 51, 401-6	5.8	58
207	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	3.7	58
206	The histone demethylase JMJD2B plays an essential role in human carcinogenesis through positive regulation of cyclin-dependent kinase 6. *Cancer Prevention Research*, **2011**, 4, 2051-61	3.2	58
205	Gene expression profiles of small-cell lung cancers: molecular signatures of lung cancer. *International Journal of Oncology*, **2006**, 29, 567-75	1	58
204	Performance comparison of four commercial human whole-exome capture platforms. *Scientific Reports*, **2015**, 5, 12742	4.9	56
203	Association study of COL9A2 with lumbar disc disease in the Japanese population. *Journal of Human Genetics*, **2006**, 51, 1063-1067	4.3	56

202	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	6	54
201	Polymorphisms in the 3RUTR in the neurocalcin delta gene affect mRNA stability, and confer susceptibility to diabetic nephropathy. *Human Genetics*, **2007**, 122, 397-407	6.3	54
200	Comprehensive gene expression profiling of anaplastic thyroid cancers with cDNA microarray of 25 344 genes. *Endocrine-Related Cancer*, **2004**, 11, 843-54	5.7	54
199	Integrative pathway enrichment analysis of multivariate omics data. *Nature Communications*, **2020**, 11, 735	17.4	53
198	Deregulation of the histone demethylase JMJD2A is involved in human carcinogenesis through regulation of the G(1)/S transition. *Cancer Letters*, **2013**, 336, 76-84	9.9	53
197	Activation of the non-canonical Dvl-Rac1-JNK pathway by Frizzled homologue 10 in human synovial sarcoma. *Oncogene*, **2009**, 28, 1110-20	9.2	53
196	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, 5062-6	9.2	52
195	Association of single-nucleotide polymorphisms in the polymeric immunoglobulin receptor gene with immunoglobulin A nephropathy (IgAN) in Japanese patients. *Journal of Human Genetics*, **2003**, 48, 293-299	4.3	51
194	Identification of a Human Clonogenic Progenitor with Strict Monocyte Differentiation Potential: A Counterpart of Mouse cMoPs. *Immunity*, **2017**, 46, 835-848.e4	32.3	50
193	A Deep Learning Approach for Motor Imagery EEG Signal Classification **2016**,		50
192	Circulating Tumor DNA Analysis for Liver Cancers and Its Usefulness as a Liquid Biopsy. *Cellular and Molecular Gastroenterology and Hepatology*, **2015**, 1, 516-534	7.9	48
191	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, 1665-72	5.6	47
190	Morphological and microarray analyses of human hepatocytes from xenogeneic host livers. *Laboratory Investigation*, **2013**, 93, 54-71	5.9	47
189	Analysis of gene-expression profiles after gamma irradiation of normal human fibroblasts. *International Journal of Radiation Oncology Biology Physics*, **2006**, 64, 272-9	4	47
188	Prediction of sensitivity to STI571 among chronic myeloid leukemia patients by genome-wide cDNA microarray analysis. *Japanese Journal of Cancer Research*, **2002**, 93, 849-56		47
187	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. *Analytical Biochemistry*, **2017**, 527, 24-32	3.1	46
186	KIF1A mutation in a patient with progressive neurodegeneration. *Journal of Human Genetics*, **2014**, 59, 639-41	4.3	46
185	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	4.9	46

184	Association of single-nucleotide polymorphisms in MTMR9 gene with obesity. *Human Molecular Genetics*, **2007**, 16, 3017-26	5.6	46
183	The histone methyltransferase Wolf-Hirschhorn syndrome candidate 1-like 1 (WHSC1L1) is involved in human carcinogenesis. *Genes Chromosomes and Cancer*, **2013**, 52, 126-39	5	45
182	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. *Journal of Theoretical Biology*, **2017**, 425, 97-102	2.3	44
181	Calbindin 1, fibroblast growth factor 20, and alpha-synuclein in sporadic Parkinson's disease. *Human Genetics*, **2008**, 124, 89-94	6.3	44
180	Variation of gene-based SNPs and linkage disequilibrium patterns in the human genome. *Human Molecular Genetics*, **2004**, 13, 1623-32	5.6	44
179	Identification of histological markers for malignant glioma by genome-wide expression analysis: dynein, alpha-PIX and sorcin. *Acta Neuropathologica*, **2006**, 111, 29-38	14.3	43
178	Identification of a susceptibility locus for severe adolescent idiopathic scoliosis on chromosome 17q24.3. *PLoS ONE*, **2013**, 8, e72802	3.7	42
177	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, 1468-78	6.9	42
176	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. *Human Molecular Genetics*, **2011**, 20, 3684-92	5.6	42
175	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. *Bioinformatics*, **2018**, 34, 1850-1858	7.2	41
174	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. *BMC Genomics*, **2018**, 19, 923	4.5	40
173	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, 374-80	5.3	39
172	Coding SNP in tenascin-C Fn-III-D domain associates with adult asthma. *Human Molecular Genetics*, **2005**, 14, 2779-86	5.6	39
171	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
170	FGFR2 is associated with hair thickness in Asian populations. *Journal of Human Genetics*, **2009**, 54, 461-5	4.3	38
169	Functional variants in NFKBIE and RTKN2 involved in activation of the NF-B pathway are associated with rheumatoid arthritis in Japanese. *PLoS Genetics*, **2012**, 8, e1002949	6	38
168	Lessons for pharmacogenomics studies: association study between CYP2D6 genotype and tamoxifen response. *Pharmacogenetics and Genomics*, **2010**, 20, 565-8	1.9	38
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