Tatushiko Tsunoda

List of Publications by Year in Descending Order

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	Immune subtypes and neoantigen-related immune evasion in advanced colorectal cancer.. *IScience*, **2022**, 25, 103740	6.1	0
344	Association between high immune activity and worse prognosis in uveal melanoma and low-grade glioma in TCGA transcriptomic data.. *BMC Genomics*, **2022**, 23, 351	4.5	1
343	Hemorrhagic shock and encephalopathy syndrome in a patient with a de novo heterozygous variant in KIF1A.. *Brain and Development*, **2021**,	2.2	0
342	Landscape of prognostic signatures and immunogenomics of the AXL/GAS6 axis in renal cell carcinoma. *British Journal of Cancer*, **2021**, 125, 1533-1543	8.7	3
341	Homozygous ADCY5 mutation causes early-onset movement disorder with severe intellectual disability. *Neurological Sciences*, **2021**, 42, 2975-2978	3.5	2
340	De novo ATP1A3 variants cause polymicrogyria. *Science Advances*, **2021**, 7,	14.3	3
339	Forecasting the spread of COVID-19 using LSTM network. *BMC Bioinformatics*, **2021**, 22, 316	3.6	5
338	Genotype-Structure-Phenotype Correlations of Disease-Associated IGF1R Variants and Similarities to Those of INSR Variants. *Diabetes*, **2021**, 70, 1874-1884	0.9	
337	SPECTRA: a tool for enhanced brain wave signal recognition. *BMC Bioinformatics*, **2021**, 22, 195	3.6	0
336	Structural basis of ethnic-specific variants of PAX4 associated with type 2 diabetes. *Human Genome Variation*, **2021**, 8, 25	1.8	0
335	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	7.4	5
334	Single-stranded and double-stranded DNA-binding protein prediction using HMM profiles. *Analytical Biochemistry*, **2021**, 612, 113954	3.1	3
333	Association of an IGHV3-66 gene variant with Kawasaki disease. *Journal of Human Genetics*, **2021**, 66, 475-489	4.3	9
332	A hypomorphic variant in EYS detected by genome-wide association study contributes toward retinitis pigmentosa. *Communications Biology*, **2021**, 4, 140	6.7	1
331	Effects of clovamide and its related compounds on the aggregations of amyloid polypeptides. *Journal of Natural Medicines*, **2021**, 75, 299-307	3.3	4
330	ELF3 Overexpression as Prognostic Biomarker for Recurrence of Stage II Colorectal Cancer. *In Vivo*, **2021**, 35, 191-201	2.3	2
329	Deep Learning Approach for Automated Detection of Myopic Maculopathy and Pathologic Myopia in Fundus Images. *Ophthalmology Retina*, **2021**, 5, 1235-1244	3.8	6

328	DeepFeature: feature selection in nonimage data using convolutional neural network. *Briefings in Bioinformatics*, **2021**, 22,	13.4	1
327	Profiling the inhibitory receptors LAG-3, TIM-3, and TIGIT in renal cell carcinoma reveals malignancy. *Nature Communications*, **2021**, 12, 5547	17.4	5
326	Four pedigrees with aminoacyl-tRNA synthetase abnormalities. *Neurological Sciences*, **2021**, 1	3.5	1
325	Quantification of multicellular colonization in tumor metastasis using exome-sequencing data. *International Journal of Cancer*, **2020**, 146, 2488-2497	7.5	2
324	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	4.5	10
323	Combined burden and functional impact tests for cancer driver discovery using DriverPower. *Nature Communications*, **2020**, 11, 734	17.4	16
322	Integrative pathway enrichment analysis of multivariate omics data. *Nature Communications*, **2020**, 11, 735	17.4	53
321	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
320	The evolutionary history of 2,658 cancers. *Nature*, **2020**, 578, 122-128	50.4	307
319	Patterns of somatic structural variation in human cancer genomes. *Nature*, **2020**, 578, 112-121	50.4	232
318	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
317	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
316	Pan-cancer analysis of whole genomes. *Nature*, **2020**, 578, 82-93	50.4	840
315	Genomic basis for RNA alterations in cancer. *Nature*, **2020**, 578, 129-136	50.4	148
314	The landscape of viral associations in human cancers. *Nature Genetics*, **2020**, 52, 320-330	36.3	113
313	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. *Nature Genetics*, **2020**, 52, 306-319	36.3	122
312	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. *Nature Genetics*, **2020**, 52, 331-341	36.3	168
311	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Communications Biology*, **2020**, 3, 56	6.7	77

310	Predicting protein-peptide binding sites with a deep convolutional neural network. *Journal of Theoretical Biology*, **2020**, 496, 110278	2.3	7
309	DeepInsight: Methodology to Handle Non-image Data, such as Genomics Data, with Deep Learning. *Seibutsu Butsuri*, **2020**, 60, 149-152	0	
308	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	7.4	1
307	PupStruct: Prediction of Pupylated Lysine Residues Using Structural Properties of Amino Acids. *Genes*, **2020**, 11,	4.2	3
306	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimer's disease created by integrative analysis of multi-omics data. *Alzheimer's Research and Therapy*, **2020**, 12, 145	9	9
305	Integrative immunogenomic analysis of gastric cancer dictates novel immunological classification and the functional status of tumor-infiltrating cells. *Clinical and Translational Immunology*, **2020**, 9, e1194	6.8	6
304	RAM-PGK: Prediction of Lysine Phosphoglycerylation Based on Residue Adjacency Matrix. *Genes*, **2020**, 11,	4.2	2
303	Variants encoding a restricted carboxy-terminal domain of SLC12A2 cause hereditary hearing loss in humans. *PLoS Genetics*, **2020**, 16, e1008643	6	19
302	Assessment of network module identification across complex diseases. *Nature Methods*, **2019**, 16, 843-852	12.6	91
301	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. *Nature Communications*, **2019**, 10, 2674	17.4	119
300	Brain wave classification using long short-term memory network based OPTICAL predictor. *Scientific Reports*, **2019**, 9, 9153	4.9	34
299	EvolStruct-Phogly: incorporating structural properties and evolutionary information from profile bigrams for the phosphoglycerylation prediction. *BMC Genomics*, **2019**, 19, 984	4.5	11
298	Navigating the disease landscape: knowledge representations for contextualizing molecular signatures. *Briefings in Bioinformatics*, **2019**, 20, 609-623	13.4	12
297	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. *BMC Genomics*, **2019**, 19, 982	4.5	6
296	GlyStruct: glycation prediction using structural properties of amino acid residues. *BMC Bioinformatics*, **2019**, 19, 547	3.6	17
295	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. *Communications Biology*, **2019**, 2, 77	6.7	27
294	Computational Pipelines and Workflows in Bioinformatics **2019**, 113-134		
293	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

292	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data. *BMC Medical Genomics*, **2019**, 12, 150	3.7	13
291	The Future of and Beyond GWAS **2019**, 193-209		
290	Genotyping and Statistical Analysis **2019**, 1-20		
289	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	0.9	0
288	Clustering of Small-Sample Single-Cell RNA-Seq Data via Feature Clustering and Selection. *Lecture Notes in Computer Science*, **2019**, 445-456	0.9	1
287	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	0.9	1
286	Subject-Specific-Frequency-Band for Motor Imagery EEG Signal Recognition Based on Common Spatial Spectral Pattern. *Lecture Notes in Computer Science*, **2019**, 712-722	0.9	4
285	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. *BMC Bioinformatics*, **2019**, 19, 378	3.6	7
284	Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix. *BMC Molecular and Cell Biology*, **2019**, 20, 57	2.7	6
283	Exploring predictive biomarkers from clinical genome-wide association studies via multidimensional hierarchical mixture models. *European Journal of Human Genetics*, **2019**, 27, 140-149	5.3	3
282	de novo gain-of-function mutation in a patient with a novel megalencephaly syndrome. *Journal of Medical Genetics*, **2019**, 56, 388-395	5.8	6
281	OPAL+: Length-Specific MoRF Prediction in Intrinsically Disordered Protein Sequences. *Proteomics*, **2019**, 19, e1800058	4.8	20
280	Structure-activity relationship of clovamide and its related compounds for the inhibition of amyloid aggregation. *Bioorganic and Medicinal Chemistry*, **2018**, 26, 3202-3209	3.4	14
279	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	4.9	15
278	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. *Bioinformatics*, **2018**, 34, 1850-1858	7.2	41
277	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
276	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. *Pharmacogenomics Journal*, **2018**, 18, 106-112	3.5	3
275	MoRFPred-plus: Computational Identification of MoRFs in Protein Sequences using Physicochemical Properties and HMM profiles. *Journal of Theoretical Biology*, **2018**, 437, 9-16	2.3	30

274	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	4.3	6
273	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. *BMC Genomics*, **2018**, 19, 923	4.5	40
272	Empirical Bayes Estimation of Semi-parametric Hierarchical Mixture Models for Unbiased Characterization of Polygenic Disease Architectures. *Frontiers in Genetics*, **2018**, 9, 115	4.5	8
271	Sample Size for Successful Genome-Wide Association Study of Major Depressive Disorder. *Frontiers in Genetics*, **2018**, 9, 227	4.5	19
270	Integrated analysis of human genetic association study and mouse transcriptome suggests LBH and SHF genes as novel susceptible genes for amyloid-β accumulation in Alzheimer's disease. *Human Genetics*, **2018**, 137, 521-533	6.3	11
269	Discovery of a Cynomolgus Monkey Family With Retinitis Pigmentosa **2018**, 59, 826-830		13
268	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	4.3	5
267	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	3.7	35
266	An integrative machine learning approach for prediction of toxicity-related drug safety. *Life Science Alliance*, **2018**, 1, e201800098	5.8	16
265	Genotype–Phenotype Correlations and Structural Basis of INSR and IGF1R Mutations Causing Severe Insulin/IGF-1 Resistance. *Diabetes*, **2018**, 67, 1349-P	0.9	
264	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. *Scientific Reports*, **2018**, 8, 17923	4.9	24
263	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. *Molecules*, **2018**, 23,	4.8	6
262	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,	4.6	3
261	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	2.6	11
260	Gene expression dataset for whole cochlea of Macaca fascicularis. *Scientific Reports*, **2018**, 8, 15554	4.9	3
259	Whole genome sequencing and mutation rate analysis of trios with paternal dioxin exposure. *Human Mutation*, **2018**, 39, 1384-1392	4.7	11
258	Hierarchical Maximum Likelihood Clustering Approach. *IEEE Transactions on Biomedical Engineering*, **2017**, 64, 112-122	5	23
257	Novel MCA/ID syndrome with ASH1L mutation. *American Journal of Medical Genetics, Part A*, **2017**, 173, 1644-1648	2.5	16

256	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
255	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
254	Role of a heterotrimeric G-protein, Gi2, in the corticogenesis: possible involvement in periventricular nodular heterotopia and intellectual disability. *Journal of Neurochemistry*, **2017**, 140, 82-95	5	10
253	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	4.3	17
252	Defects in autophagosome-lysosome fusion underlie Vici syndrome, a neurodevelopmental disorder with multisystem involvement. *Scientific Reports*, **2017**, 7, 3552	4.9	35
251	The prediction models for postoperative overall survival and disease-free survival in patients with breast cancer. *Cancer Medicine*, **2017**, 6, 1627-1638	4.8	8
250	Polygenic burdens on cell-specific pathways underlie the risk of rheumatoid arthritis. *Nature Genetics*, **2017**, 49, 1120-1125	36.3	83
249	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. *Analytical Biochemistry*, **2017**, 527, 24-32	3.1	46
248	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
247	Divisive hierarchical maximum likelihood clustering. *BMC Bioinformatics*, **2017**, 18, 546	3.6	17
246	Arete - candidate gene prioritization using biological network topology with additional evidence types. *BioData Mining*, **2017**, 10, 22	4.3	6
245	An improved discriminative filter bank selection approach for motor imagery EEG signal classification using mutual information. *BMC Bioinformatics*, **2017**, 18, 545	3.6	63
244	A genome-wide association analysis identifies NMNAT2 and HCP5 as susceptibility loci for Kawasaki disease. *Journal of Human Genetics*, **2017**, 62, 1023-1029	4.3	29
243	Structural Basis and Genotype-Phenotype Correlations of INSR Mutations Causing Severe Insulin Resistance. *Diabetes*, **2017**, 66, 2713-2723	0.9	14
242	A novel genetic syndrome with STARD9 mutation and abnormal spindle morphology. *American Journal of Medical Genetics, Part A*, **2017**, 173, 2690-2696	2.5	5
241	Siblings with optic neuropathy and RTN4IP1 mutation. *Journal of Human Genetics*, **2017**, 62, 927-929	4.3	6
240	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	14
239	Whole genome sequencing discriminates hepatocellular carcinoma with intrahepatic metastasis from multi-centric tumors. *Journal of Hepatology*, **2017**, 66, 363-373	13.4	62

238	2D-EM clustering approach for high-dimensional data through folding feature vectors. *BMC Bioinformatics*, **2017**, 18, 547	3.6	6
237	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		33
236	Phenotypic Variability of ANK2 Mutations in Patients With Inherited Primary Arrhythmia Syndromes. *Circulation Journal*, **2016**, 80, 2435-2442	2.9	12
235	Variants in the SCN5A Promoter Associated With Various Arrhythmia Phenotypes. *Journal of the American Heart Association*, **2016**, 5,	6	18
234	Decimation filter with Common Spatial Pattern and Fishers Discriminant Analysis for motor imagery classification **2016**,		14
233	Systematic analysis of mutation distribution in three dimensional protein structures identifies cancer driver genes. *Scientific Reports*, **2016**, 6, 26483	4.9	15
232	Stepwise iterative maximum likelihood clustering approach. *BMC Bioinformatics*, **2016**, 17, 319	3.6	11
231	Gene masking - a technique to improve accuracy for cancer classification with high dimensionality in microarray data. *BMC Medical Genomics*, **2016**, 9, 74	3.7	5
230	A functional SNP in FLT1 increases risk of coronary artery disease in a Japanese population. *Journal of Human Genetics*, **2016**, 61, 435-41	4.3	8
229	Protein fold recognition using HMM-HMM alignment and dynamic programming. *Journal of Theoretical Biology*, **2016**, 393, 67-74	2.3	27
228	ALDH18A1-related cutis laxa syndrome with cyclic vomiting. *Brain and Development*, **2016**, 38, 678-84	2.2	13
227	Chromothripsis-like chromosomal rearrangements induced by ionizing radiation using proton microbeam irradiation system. *Oncotarget*, **2016**, 7, 10182-92	3.3	35
226	Novel splicing mutation in the ASXL3 gene causing Bainbridge-Ropers syndrome. *American Journal of Medical Genetics, Part A*, **2016**, 170, 1863-7	2.5	25
225	Predicting MoRFs in protein sequences using HMM profiles. *BMC Bioinformatics*, **2016**, 17, 504	3.6	18
224	A Deep Learning Approach for Motor Imagery EEG Signal Classification **2016**,		50
223	Whole-genome mutational landscape and characterization of noncoding and structural mutations in liver cancer. *Nature Genetics*, **2016**, 48, 500-9	36.3	423
222	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	5.3	7
221	Gene expression profiling of DBA/2J mice cochleae treated with l-methionine and valproic acid. *Genomics Data*, **2015**, 5, 323-5		1

220	A deletion mutation in myosin heavy chain 11 causing familial thoracic aortic dissection in two Japanese pedigrees. *International Journal of Cardiology*, **2015**, 195, 290-2	3.2	6
219	Performance comparison of four commercial human whole-exome capture platforms. *Scientific Reports*, **2015**, 5, 12742	4.9	56
218	Primary microcephaly with anterior predominant pachygyria caused by novel compound heterozygous mutations in ASPM. *Pediatric Neurology*, **2015**, 52, e7-8	2.9	5
217	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
216	Sudden death in a case of megalencephaly capillary malformation associated with a de novo mutation in AKT3. *Childs Nervous System*, **2015**, 31, 465-71	1.7	7
215	Genome-wide association study of warfarin maintenance dose in a Brazilian sample. *Pharmacogenomics*, **2015**, 16, 1253-63	2.6	23
214	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
213	The subcellular localization and activity of cortactin is regulated by acetylation and interaction with Keap1. *Science Signaling*, **2015**, 8, ra120	8.8	36
212	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
211	Targeted next-generation sequencing in the diagnosis of neurodevelopmental disorders. *Clinical Genetics*, **2015**, 88, 288-92	4	26
210	TUBA1A mutation can cause a hydranencephaly-like severe form of cortical dysgenesis. *Scientific Reports*, **2015**, 5, 15165	4.9	15
209	Importance of dimensionality reduction in protein fold recognition **2015**,		1
208	Truncating mutation in NFIA causes brain malformation and urinary tract defects. *Human Genome Variation*, **2015**, 2, 15007	1.8	13
207	A combination of targeted enrichment methodologies for whole-exome sequencing reveals novel pathogenic mutations. *Scientific Reports*, **2015**, 5, 9331	4.9	13
206	Application of cepstrum analysis and linear predictive coding for motor imaginary task classification **2015**,		2
205	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	3.7	9
204	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
203	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

202	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
201	Whole-genome mutational landscape of liver cancers displaying biliary phenotype reveals hepatitis impact and molecular diversity. *Nature Communications*, **2015**, 6, 6120	17.4	139
200	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. *PLoS ONE*, **2015**, 10, e0130329	3.7	20
199	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. *PLoS ONE*, **2015**, 10, e0139262	3.7	24
198	Genome-wide association study identifies three novel loci for type 2 diabetes. *Human Molecular Genetics*, **2014**, 23, 239-46	5.6	138
197	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
196	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. *Circulation*, **2014**, 130, 1225-35	16.7	143
195	KIF1A mutation in a patient with progressive neurodegeneration. *Journal of Human Genetics*, **2014**, 59, 639-41	4.3	46
194	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
193	Novel calmodulin mutations associated with congenital arrhythmia susceptibility. *Circulation: Cardiovascular Genetics*, **2014**, 7, 466-74		133
192	The construction of risk prediction models using GWAS data and its application to a type 2 diabetes prospective cohort. *PLoS ONE*, **2014**, 9, e92549	3.7	26
191	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
190	Transcriptome analysis of distinct mouse strains reveals kinesin light chain-1 splicing as an amyloid-β accumulation modifier. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 2638-43	11.5	25
189	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
188	Pathway analysis of genome-wide data improves warfarin dose prediction. *BMC Genomics*, **2013**, 14 Suppl 3, S11	4.5	11
187	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
186	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, E1667-73	5.6	29
185	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	4.9	9

184	The oncogenic polycomb histone methyltransferase EZH2 methylates lysine 120 on histone H2B and competes ubiquitination. *Neoplasia*, **2013**, 15, 1251-61	6.4	34
183	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
182	Integrated molecular analysis of clear-cell renal cell carcinoma. *Nature Genetics*, **2013**, 45, 860-7	36.3	723
181	Genetic variants in GPR126 are associated with adolescent idiopathic scoliosis. *Nature Genetics*, **2013**, 45, 676-9	36.3	172
180	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
179	Morphological and microarray analyses of human hepatocytes from xenogeneic host livers. *Laboratory Investigation*, **2013**, 93, 54-71	5.9	47
178	A practical method to detect SNVs and indels from whole genome and exome sequencing data. *Scientific Reports*, **2013**, 3, 2161	4.9	30
177	Identification of a susceptibility locus for severe adolescent idiopathic scoliosis on chromosome 17q24.3. *PLoS ONE*, **2013**, 8, e72802	3.7	42
176	HLA-DQB1*03 confers susceptibility to chronic hepatitis C in Japanese: a genome-wide association study. *PLoS ONE*, **2013**, 8, e84226	3.7	27
175	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. *Journal of Clinical Investigation*, **2013**, 123, 4909-17	15.9	81
174	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
173	A genome-wide association study identifies three new risk loci for Kawasaki disease. *Nature Genetics*, **2012**, 44, 517-21	36.3	217
172	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
171	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
170	Meta-analysis identifies common variants associated with body mass index in east Asians. *Nature Genetics*, **2012**, 44, 307-11	36.3	301
169	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
168	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. *Nature Genetics*, **2012**, 44, 904-9	36.3	201
167	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

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, 1665-72	5.6	47
165	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
164	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
163	A genome-wide association study identified AFF1 as a susceptibility locus for systemic lupus eyrthematosus in Japanese. *PLoS Genetics*, **2012**, 8, e1002455	6	89
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