Toshihiro Tanaka

List of Publications by Year
in descending order

169	39,190	12330	5679
papers	citations	69 h-index	162 g-index

174	174	174	47099
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The International HapMap Project. Nature, 2003, 426, 789-796.	27.8	5,735
2	A haplotype map of the human genome. Nature, 2005, 437, 1299-1320.	27.8	5,440
3	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
4	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
5	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	27.8	1,788
6	p53AIP1, a Potential Mediator of p53-Dependent Apoptosis, and Its Regulation by Ser-46-Phosphorylated p53. Cell, 2000, 102, 849-862.	28.9	1,095
7	Functional SNPs in the lymphotoxin-Î± gene that are associated with susceptibility to myocardial infarction. Nature Genetics, 2002, 32, 650-654.	21.4	878
8	Complete sequencing and characterization of 21,243 full-length human cDNAs. Nature Genetics, 2004, 36, 40-45.	21.4	796
9	GWAS of 126,559 Individuals Identifies Genetic Variants Associated with Educational Attainment. Science, 2013, 340, 1467-1471.	12.6	750
10	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
11	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. Journal of Human Genetics, 2006, 51, 1087-1099.	2.3	597
12	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
13	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. Nature Genetics, 2012, 44, 670-675.	21.4	533
14	Hyperglycemia causes oxidative stress in pancreatic beta-cells of GK rats, a model of type 2 diabetes. Diabetes, 1999, 48, 927-932.	0.6	447
15	A functional polymorphism in the 5â€² UTR of GDF5 is associated with susceptibility to osteoarthritis. Nature Genetics, 2007, 39, 529-533.	21.4	435
16	A high-throughput SNP typing system for genome-wide association studies. Journal of Human Genetics, 2001, 46, 471-477.	2.3	421
17	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	21.4	372
18	p53DINP1, a p53-Inducible Gene, Regulates p53-Dependent Apoptosis. Molecular Cell, 2001, 8, 85-94.	9.7	314

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19	A genome-wide association study identifies three new risk loci for Kawasaki disease. Nature Genetics, 2012, 44, 517-521.	21.4	284
20	Gene-based SNP discovery as part of the Japanese Millennium Genome Project: identification of 190 562 genetic variations in the human genome. Journal of Human Genetics, 2002, 47, 0605-0610.	2.3	281
21	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
22	Large-scale genome-wide association studies in east Asians identify new genetic loci influencing metabolic traits. Nature Genetics, 2011, 43, 990-995.	21.4	270
23	Linkage of Familial Moyamoya Disease (Spontaneous Occlusion of the Circle of Willis) to Chromosome 17q25. Stroke, 2000, 31, 930-935.	2.0	261
24	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	21.4	254
25	JSNP: a database of common gene variations in the Japanese population. Nucleic Acids Research, 2002, 30, 158-162.	14.5	247
26	Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. Nature Genetics, 2012, 44, 302-306.	21.4	240
27	Functional variation in LGALS2 confers risk of myocardial infarction and regulates lymphotoxin-Î± secretion in vitro. Nature, 2004, 429, 72-75.	27.8	236
28	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. Molecular Psychiatry, 2015, 20, 647-656.	7.9	235
29	Identification by cDNA microarray of genes involved in ovarian carcinogenesis. Cancer Research, 2000, 60, 5007-11.	0.9	235
30	Identification and Characterization of the Potential Promoter Regions of 1031 Kinds of Human Genes. Genome Research, 2001, 11, 677-684.	5.5	201
31	Alterations of gene expression during colorectal carcinogenesis revealed by cDNA microarrays after laser-capture microdissection of tumor tissues and normal epithelia. Cancer Research, 2001, 61, 3544-9.	0.9	196
32	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.	2.9	192
33	Integrating Genetic, Transcriptional, and Functional Analyses to Identify 5 Novel Genes for Atrial Fibrillation. Circulation, 2014, 130, 1225-1235.	1.6	183
34	Homocysteine and Coronary Heart Disease: Meta-analysis of MTHFR Case-Control Studies, Avoiding Publication Bias. PLoS Medicine, 2012, 9, e1001177.	8.4	167
35	Novel Calmodulin Mutations Associated With Congenital Arrhythmia Susceptibility. Circulation: Cardiovascular Genetics, 2014, 7, 466-474.	5.1	165
36	Identification of the gene responsible for gelatinous drop-like corneal dystrophy. Nature Genetics, 1999, 21, 420-423.	21.4	164

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37	Diverse transcriptional initiation revealed by fine, largeâ€scale mapping of mRNA start sites. EMBO Reports, 2001, 2, 388-393.	4.5	154
38	The p53 Family Member Genes Are Involved in the Notch Signal Pathway. Journal of Biological Chemistry, 2002, 277, 719-724.	3.4	151
39	Small intestinal stem cell identity is maintained with functional Paneth cells in heterotopically grafted epithelium onto the colon. Genes and Development, 2014, 28, 1752-1757.	5.9	148
40	Osteopenia and male-specific sudden cardiac death in mice lacking a zinc transporter gene, Znt5. Human Molecular Genetics, 2002, 11, 1775-1784.	2.9	144
41	Genotype-Phenotype Correlation of SCN5A Mutation for the Clinical and Electrocardiographic Characteristics of Probands With Brugada Syndrome. Circulation, 2017, 135, 2255-2270.	1.6	142
42	Common variants in CASP3 confer susceptibility to Kawasaki disease. Human Molecular Genetics, 2010, 19, 2898-2906.	2.9	141
43	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. Nature Genetics, 2017, 49, 953-958.	21.4	136
44	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.	2.9	135
45	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. Nature Genetics, 2008, 40, 994-998.	21.4	134
46	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. Molecular Psychiatry, 2016, 21, 189-197.	7.9	134
47	Mutations in the NMMHC-A gene cause autosomal dominant macrothrombocytopenia with leukocyte inclusions (May-Hegglin anomaly/Sebastian syndrome). Blood, 2001, 97, 1147-1149.	1.4	130
48	Prediction of sensitivity of esophageal tumors to adjuvant chemotherapy by cDNA microarray analysis of gene-expression profiles. Cancer Research, 2001, 61, 6474-9.	0.9	129
49	Novel Genetic Markers Associate With Atrial Fibrillation Risk in Europeans and Japanese. Journal of the American College of Cardiology, 2014, 63, 1200-1210.	2.8	127
50	Multiple Loci Are Associated with White Blood Cell Phenotypes. PLoS Genetics, 2011, 7, e1002113.	3.5	106
51	Novel Mechanism of HERG Current Suppression in LQT2. Circulation Research, 1998, 83, 415-422.	4.5	105
52	ITPKC and CASP3 polymorphisms and risks for IVIG unresponsiveness and coronary artery lesion formation in Kawasaki disease. Pharmacogenomics Journal, 2013, 13, 52-59.	2.0	105
53	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
54	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. Nature Genetics, 2006, 38, 921-925.	21.4	102

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55	A Functional Polymorphism in THBS2 that Affects Alternative Splicing and MMP Binding Is Associated with Lumbar-Disc Herniation. American Journal of Human Genetics, 2008, 82, 1122-1129.	6.2	102
56	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. Nature Genetics, 2009, 41, 329-333.	21.4	102
57	Four Novel KVLQT1 and Four Novel HERG Mutations in Familial Long-QT Syndrome. Circulation, 1997, 95, 565-567.	1.6	100
58	The Id2 gene is a novel target of transcriptional activation by EWS-ETS fusion proteins in Ewing family tumors. Oncogene, 2002, 21, 8302-8309.	5.9	99
59	Expression of the gene for a membrane-bound fatty acid receptor in the pancreas and islet cell tumours in humans: evidence for GPR40 expression in pancreatic beta cells and implications for insulin secretion. Diabetologia, 2006, 49, 962-968.	6.3	91
60	Isolation of a Novel Human Gene, MARKLI, Homologous to MARK3 and Its Involvement in Hepatocellular Carcinogenesis. Neoplasia, 2001, 3, 4-9.	5.3	88
61	Identification of 187 single nucleotide polymorphisms (SNPs) among 41 candidate genes for ischemic heart disease in the Japanese population. Human Genetics, 2000, 106, 288-292.	3.8	86
62	Up-regulation of the ectodermal-neural cortex 1 (ENC1) gene, a downstream target of the beta-catenin/T-cell factor complex, in colorectal carcinomas. Cancer Research, 2001, 61, 7722-6.	0.9	83
63	Genome-wide association study for C-reactive protein levels identified pleiotropic associations in the IL6 locus. Human Molecular Genetics, 2011, 20, 1224-1231.	2.9	82
64	Genomic organization and mutational analysis of HERG , a gene responsible for familial long QT syndrome. Human Genetics, 1998, 102, 435-439.	3.8	80
65	Identification of 187 single nucleotide polymorphisms (SNPs) among 41 candidate genes for ischemic heart disease in the Japanese population. Human Genetics, 2000, 106, 288-292.	3.8	80
66	Association between Single-Nucleotide Polymorphisms in Selectin Genes and Immunoglobulin A Nephropathy. American Journal of Human Genetics, 2002, 70, 781-786.	6.2	78
67	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.	6.2	77
68	Unique activation status of peripheral blood mononuclear cells at acute phase of Kawasaki disease. Clinical and Experimental Immunology, 2010, 160, 246-255.	2.6	75
69	Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. Journal of Human Genetics, 2016, 61, 861-866.	2.3	75
70	Growth and gene expression profile analyses of endometrial cancer cells expressing exogenous PTEN. Cancer Research, 2001, 61, 3741-9.	0.9	71
71	Identification of Nine Novel Loci Associated with White Blood Cell Subtypes in a Japanese Population. PLoS Genetics, 2011, 7, e1002067.	3.5	69
72	Discovery and Fine Mapping of Serum Protein Loci through Transethnic Meta-analysis. American Journal of Human Genetics, 2012, 91, 744-753.	6.2	69

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73	Molecular genetics of coronary artery disease. Journal of Human Genetics, 2016, 61, 71-77.	2.3	69
74	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.	5.9	64
75	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.6	61
76	Trans-ethnic meta-analysis of white blood cell phenotypes. Human Molecular Genetics, 2014, 23, 6944-6960.	2.9	60
77	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.	2.3	59
78	Genomic organization and mutational analysis of KVLQT1, a gene responsible for familial long QT syndrome. Human Genetics, 1998, 103, 290-294.	3.8	57
79	Twenty single nucleotide polymorphisms (SNPs) and their allelic frequencies in four genes that are responsible for familial long QT syndrome in the Japanese population. Journal of Human Genetics, 2000, 45, 182-183.	2.3	57
80	Genome Wide Analysis of Drug-Induced Torsades de Pointes: Lack of Common Variants with Large Effect Sizes. PLoS ONE, 2013, 8, e78511.	2.5	57
81	A functional variant in ZNF512B is associated with susceptibility to amyotrophic lateral sclerosis in Japanese. Human Molecular Genetics, 2011, 20, 3684-3692.	2.9	53
82	Variation of gene-based SNPs and linkage disequilibrium patterns in the human genome. Human Molecular Genetics, 2004, 13, 1623-1632.	2.9	50
83	Prediction model for knee osteoarthritis based on genetic and clinical information. Arthritis Research and Therapy, 2010, 12, R187.	3.5	49
84	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.	2.8	48
85	Genome-wide association study to identify SNPs conferring risk of myocardial infarction and their functional analyses. Cellular and Molecular Life Sciences, 2005, 62, 1804-1813.	5.4	47
86	Overview of BioBank Japan follow-up data in 32 diseases. Journal of Epidemiology, 2017, 27, S22-S28.	2.4	47
87	Voltage-shift of the current activation in HERG S4 mutation (R534C) in LQT2. Cardiovascular Research, 1999, 44, 283-293.	3.8	46
88	Genomic structure and multiple single-nucleotide polymorphisms (SNPs) of the thiopurine S-methyltransferase (TPMT) gene. Journal of Human Genetics, 2000, 45, 299-302.	2.3	45
89	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
90	Haplotypes with Copy Number and Single Nucleotide Polymorphisms in CYP2A6 Locus Are Associated with Smoking Quantity in a Japanese Population. PLoS ONE, 2012, 7, e44507.	2.5	45

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91	Significant impact of miRNAâ€“target gene networks on genetics of human complex traits. Scientific Reports, 2016, 6, 22223.	3.3	44
92	Homozygosity Mapping of a Gene Responsible for Gelatinous Dropâ€“like Corneal Dystrophy to Chromosome 1p. American Journal of Human Genetics, 1998, 63, 1073-1077.	6.2	41
93	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. Journal of Human Genetics, 2011, 56, 47-51.	2.3	41
94	Variations in ORAI1 Gene Associated with Kawasaki Disease. PLoS ONE, 2016, 11, e0145486.	2.5	41
95	Mapping of a gene for May-Hegglin anomaly to chromosome 22q. Human Genetics, 1999, 105, 379-383.	3.8	40
96	A functional SNP in EDG2 increases susceptibility to knee osteoarthritis in Japanese. Human Molecular Genetics, 2008, 17, 1790-1797.	2.9	40
97	Induction of tenascin-C by tumor-specificEWS-ETS fusion genes. Genes Chromosomes and Cancer, 2003, 36, 224-232.	2.8	39
98	Inhibition of Experimental Intimal Thickening in Mice Lacking a Novel G-Proteinâ€“Coupled Receptor. Circulation, 2003, 107, 313-319.	1.6	39
99	Variants at HLA-A, HLA-C, and HLA-DQB1 Confer Risk of Psoriasis Vulgaris in Japanese. Journal of Investigative Dermatology, 2018, 138, 542-548.	0.7	39
100	A functional SNP in ITIH3 is associated with susceptibility to myocardial infarction. Journal of Human Genetics, 2007, 52, 220-229.	2.3	38
101	PTPRD gene associated with blood pressure response to atenolol and resistant hypertension. Journal of Hypertension, 2015, 33, 2278-2285.	0.5	38
102	Mapping of a gene for May-Hegglin anomaly to chromosome 22q. Human Genetics, 1999, 105, 379-383.	3.8	36
103	BRAP Activates Inflammatory Cascades and Increases the Risk for Carotid Atherosclerosis. Molecular Medicine, 2011, 17, 1065-1074.	4.4	36
104	Isolation and Chromosomal Mapping of the Human Homolog of Perilipin (PLIN), a Rat Adipose Tissue-Specific Gene, by Differential Display Method. Genomics, 1998, 48, 254-257.	2.9	35
105	Common Variants in a Novel Gene, FONG on Chromosome 2q33.1 Confer Risk of Osteoporosis in Japanese. PLoS ONE, 2011, 6, e19641.	2.5	35
106	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. PLoS ONE, 2015, 10, e0139262.	2.5	35
107	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.	2.3	34
108	Impact of atherosclerosis-related gene polymorphisms on mortality and recurrent events after myocardial infarction. Atherosclerosis, 2006, 185, 400-405.	0.8	33

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109	Identification of AF17 as a downstream gene of the beta-catenin/T-cell factor pathway and its involvement in colorectal carcinogenesis. Cancer Research, 2001, 61, 6345-9.	0.9	33
110	Isolation of HELAD1, a novel human helicase gene up-regulated in colorectal carcinomas. Oncogene, 2002, 21, 6387-6394.	5.9	32
111	Identification of 142 single nucleotide polymorphisms in 41 candidate genes for rheumatoid arthritis in the Japanese population. Human Genetics, 2000, 106, 293-297.	3.8	31
112	Inflammation as a risk factor for myocardial infarction. Journal of Human Genetics, 2006, 51, 595-604.	2.3	31
113	Regulatory polymorphism in transcription factor KLF5 at the MEF2 element alters the response to angiotensin II and is associated with human hypertension. FASEB Journal, 2010, 24, 1780-1788.	0.5	30
114	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. PLoS ONE, 2015, 10, e0130329.	2.5	30
115	Identification of 142 single nucleotide polymorphisms in 41 candidate genes for rheumatoid arthritis in the Japanese population. Human Genetics, 2000, 106, 293-297.	3.8	28
116	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.	2.3	27
117	Association of an IGHV3-66 gene variant with Kawasaki disease. Journal of Human Genetics, 2021, 66, 475-489.	2.3	27
118	Localization of the gene responsible for Peutz-Jeghers syndrome within a 6-cM region of chromosome 19p13.3. Human Genetics, 1998, 102, 203-206.	3.8	24
119	Regional evaluation of childhood acute lymphoblastic leukemia genetic susceptibility loci among Japanese. Scientific Reports, 2018, 8, 789.	3.3	23
120	Variants in the SCN5A Promoter Associated With Various Arrhythmia Phenotypes. Journal of the American Heart Association, 2016, 5, .	3.7	22
121	Genetic variations in five genes involved in the excitement of cardiomyocytes. Journal of Human Genetics, 2001, 46, 549-552.	2.3	21
122	Multiple single-nucleotide polymorphisms (SNPs) in the Japanese population in six candidate genes for long QT syndrome. Journal of Human Genetics, 2001, 46, 158-162.	2.3	21
123	Construction of a Normalized Directionally Cloned cDNA Library from Adult Heart and Analysis of 3040 Clones by Partial Sequencing. Genomics, 1996, 35, 231-235.	2.9	20
124	Identification of a Novel Gene (ECM2) Encoding a Putative Extracellular Matrix Protein Expressed Predominantly in Adipose and Female-Specific Tissues and Its Chromosomal Localization to 9q22.3. Genomics, 1998, 52, 378-381.	2.9	20
125	Characterization of S818L mutation in HERG C-terminus in LQT2. FEBS Letters, 2000, 481, 197-203.	2.8	19
126	Correlation of genetic etiology with response to Î²-adrenergic blockade among symptomatic patients with familial long-QT syndrome. Journal of Human Genetics, 2001, 46, 38-40.	2.3	19

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127	Molecular Cloning and Mapping of a Human cDNA for Cytosolic Malate Dehydrogenase (MDH1). Genomics, 1996, 32, 128-130.	2.9	18
128	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.	2.5	18
129	Association between maternal education and malocclusion in Mongolian adolescents: a cross-sectional study. BMJ Open, 2016, 6, e012283.	1.9	18
130	Phenotypic Variability of <i>ANK2</i> Mutations in Patients With Inherited Primary Arrhythmia Syndromes. Circulation Journal, 2016, 80, 2435-2442.	1.6	18
131	Genetic Variants Associated With Susceptibility to Atrial Fibrillation in a Japanese Population. Canadian Journal of Cardiology, 2017, 33, 443-449.	1.7	18
132	Genome-wide association analysis of common genetic variants of resistant hypertension. Pharmacogenomics Journal, 2019, 19, 295-304.	2.0	16
133	A Genome-Wide Association Study to Identify Genomic Modulators of Rate Control Therapy in Patients With Atrial Fibrillation. American Journal of Cardiology, 2014, 114, 593-600.	1.6	15
134	Submicroscopic Deletions at 13q32.1 Cause Congenital Microcoria. American Journal of Human Genetics, 2015, 96, 631-639.	6.2	13
135	Refined mapping of caltractin in human Xq28 and in the homologous region of the mouse X Chromosome places the gene within the bare patches (Bpa) and striated (Str) critical regions. Mammalian Genome, 1995, 6, 802-804.	2.2	12
136	Fine-scale SNP map of an 11-kb genomic region at 22q13.1 containing the galectin-1 gene. Journal of Human Genetics, 2005, 50, 42-45.	2.3	12
137	Reduced risk of recurrent myocardial infarction in homozygous carriers of the chromosome 9p21 rs1333049 C risk allele in the contemporary percutaneous coronary intervention era: a prospective observational study. BMJ Open, 2014, 4, e005438-e005438.	1.9	12
138	Molecular cloning of a human cDNA encoding putative cysteine protease (PRSC1) and its chromosome assignment to 14q32.1. Cytogenetic and Genome Research, 1996, 74, 120-123.	1.1	11
139	High-density SNP map of human ITR, a gene associated with vascular remodeling. Journal of Human Genetics, 2003, 48, 170-172.	2.3	10
140	A functional SNP in FLT1 increases risk of coronary artery disease in a Japanese population. Journal of Human Genetics, 2016, 61, 435-441.	2.3	10
141	Genetic linkage analyses of Romano-Ward syndrome (RWS) in 13 Japanese families. Human Genetics, 1994, 94, 380-4.	3.8	9
142	Identification of 46 novel SNPs in the 130-kb region containing a myocardial infarction susceptibility gene on chromosomal band 6p21. Journal of Human Genetics, 2003, 48, 476-479.	2.3	9
143	Linkage disequilibrium of evolutionarily conserved regions in the human genome. BMC Genomics, 2006, 7, 326.	2.8	9
144	Recombination rates of genes expressed in human tissues. Human Molecular Genetics, 2008, 17, 577-586.	2.9	9

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145	Renin-Angiotensin-Aldosterone System Polymorphisms and 5-Year Mortality in Survivors of Acute Myocardial Infarction. International Heart Journal, 2014, 55, 190-196.	1.0	9
146	Investigation of novel variations of ORAI1 gene and their association with Kawasaki disease. Journal of Human Genetics, 2019, 64, 511-519.	2.3	9
147	Identification by differential display of eight known genes induced during in vivo intimal hyperplasia. Journal of Human Genetics, 1998, 43, 9-13.	2.3	8
148	Lymphotoxin-Î±3 mediates monocyteâ€“endothelial interaction by TNFR I/NF-Î¹B signaling. Biochemical and Biophysical Research Communications, 2009, 379, 374-378.	2.1	8
149	High-density single-nucleotide polymorphism (SNP) map in the 96-kb region containing the entire human DiGeorge syndrome critical region 2 (DGCR2) gene at 22q11.2. Journal of Human Genetics, 2001, 46, 604-608.	2.3	7
150	Genome-wide association study identifies pharmacogenomic loci linked with specific antihypertensive drug treatment and new-onset diabetes. Pharmacogenomics Journal, 2018, 18, 106-112.	2.0	7
151	Heterozygosities and allelic frequencies of 358 dinucleotide-repeat marker loci in the Japanese population. Journal of Human Genetics, 1998, 43, 165-168.	2.3	6
152	Twenty single-nucleotide polymorphisms in four genes encoding cardiac ion channels. Journal of Human Genetics, 2002, 47, 208-212.	2.3	5
153	Pathway analysis with genome-wide association study (GWAS) data detected the association of atrial fibrillation with the mTOR signaling pathway. IJC Heart and Vasculature, 2019, 24, 100383.	1.1	5
154	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. Human Immunology, 2019, 80, 731-738.	2.4	5
155	Genome-Wide Association Study to Identify Single-Nucleotide Polymorphisms Conferring Risk of Myocardial Infarction. Methods in Molecular Medicine, 2006, 128, 173-180.	0.8	5
156	Decreased mortality associated with statin treatment in patients with acute myocardial infarction and lymphotoxin-alpha C804A polymorphism. Atherosclerosis, 2013, 227, 373-379.	0.8	4
157	Clinical utility and functional analysis of variants in atrial fibrillation-associated locus 4q25. Journal of Cardiology, 2017, 70, 366-373.	1.9	4
158	Identification of OPN3 as associated with non-syndromic oligodontia in a Japanese population. Journal of Human Genetics, 2021, 66, 769-775.	2.3	4
159	Assignment of the human caltractin gene (CALT) to Xq28 by fluorescence in situ hybridization. Genomics, 1994, 24, 609-10.	2.9	4
160	Cardiovascular genetics. Journal of Human Genetics, 2016, 61, 1-1.	2.3	2
161	Association between Smoking during Pregnancy and Short Root Anomaly in Offspring. International Journal of Environmental Research and Public Health, 2021, 18, 11662.	2.6	1
162	Chapter 7 Mutational Analysis of Familial Long QT Syndrome in Japan. Current Topics in Membranes, 1999, 46, 103-116.	0.9	0

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163	Genetic backgrounds of myocardial infarction. Current Cardiovascular Risk Reports, 2007, 1, 427-431.	2.0	0
164	Identification of myocardial infarction-susceptible genes and their functional analyses. , 0, , 79-88.		0
165	Genetic Background of Myocardial Infarction. , 2011, , 113-120.		0
166	Genetics of Coronary Disease. , 2019, , 21-36.		0
167	Squamous Cell Carcinoma at the Site of Cutaneous Lymphoid Hyperplasia. Annals of Dermatology, 2022, 34, 146.	0.9	0
168	JHG Young Scientist Award. Journal of Human Genetics, 2022, 67, 69-69.	2.3	0
169	Integrating biomedical and clinical data with BioBank Japan. , 2022, 1, 597-598.		0