Toshihiro Tanaka

List of Publications by Year in Descending Order

165 papers	32,385 citations	66 h-index	174 g-index
174 ext. papers	36,333 ext. citations	10.9 avg, IF	7.43 L-index

#	Paper	IF	Citations
165	Squamous Cell Carcinoma at the Site of Cutaneous Lymphoid Hyperplasia.. *Annals of Dermatology*, **2022**, 34, 146-148	0.4	
164	Association of an IGHV3-66 gene variant with Kawasaki disease. *Journal of Human Genetics*, **2021**, 66, 475-489	4.3	9
163	Identification of OPN3 as associated with non-syndromic oligodontia in a Japanese population. *Journal of Human Genetics*, **2021**, 66, 769-775	4.3	0
162	HLA-C variants associated with amino acid substitutions in the peptide binding groove influence susceptibility to Kawasaki disease. *Human Immunology*, **2019**, 80, 731-738	2.3	4
161	Investigation of novel variations of ORAI1 gene and their association with Kawasaki disease. *Journal of Human Genetics*, **2019**, 64, 511-519	4.3	6
160	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	2.4	2
159	Genetics of Coronary Disease **2019**, 21-36		
158	Genome-wide association analysis of common genetic variants of resistant hypertension. *Pharmacogenomics Journal*, **2019**, 19, 295-304	3.5	7
157	Regional evaluation of childhood acute lymphoblastic leukemia genetic susceptibility loci among Japanese. *Scientific Reports*, **2018**, 8, 789	4.9	14
156	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
155	Variants at HLA-A, HLA-C, and HLA-DQB1 Confer Risk of Psoriasis Vulgaris in Japanese. *Journal of Investigative Dermatology*, **2018**, 138, 542-548	4.3	29
154	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
153	Genetic Variants Associated With Susceptibility to Atrial Fibrillation in a Japanese Population. *Canadian Journal of Cardiology*, **2017**, 33, 443-449	3.8	10
152	Clinical utility and functional analysis of variants in atrial fibrillation-associated locus 4q25. *Journal of Cardiology*, **2017**, 70, 366-373	3	3
151	Identification of six new genetic loci associated with atrial fibrillation in the Japanese population. *Nature Genetics*, **2017**, 49, 953-958	36.3	89
150	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
149	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

148	Overview of BioBank Japan follow-up data in 32 diseases. *Journal of Epidemiology*, **2017**, 27, S22-S28	3.4	41
147	Genotype-Phenotype Correlation of Mutation for the Clinical and Electrocardiographic Characteristics of Probands With Brugada Syndrome: A Japanese Multicenter Registry. *Circulation*, **2017**, 135, 2255-2270	16.7	88
146	Molecular genetics of coronary artery disease. *Journal of Human Genetics*, **2016**, 61, 71-7	4.3	47
145	GWAS for executive function and processing speed suggests involvement of the CADM2 gene. *Molecular Psychiatry*, **2016**, 21, 189-197	15.1	85
144	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
143	Phenotypic Variability of ANK2 Mutations in Patients With Inherited Primary Arrhythmia Syndromes. *Circulation Journal*, **2016**, 80, 2435-2442	2.9	12
142	Variants in the SCN5A Promoter Associated With Various Arrhythmia Phenotypes. *Journal of the American Heart Association*, **2016**, 5,	6	18
141	Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. *Journal of Human Genetics*, **2016**, 61, 861-866	4.3	49
140	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
139	Variations in ORAI1 Gene Associated with Kawasaki Disease. *PLoS ONE*, **2016**, 11, e0145486	3.7	30
138	Significant impact of miRNA-target gene networks on genetics of human complex traits. *Scientific Reports*, **2016**, 6, 22223	4.9	36
137	Association between maternal education and malocclusion in Mongolian adolescents: a cross-sectional study. *BMJ Open*, **2016**, 6, e012283	3	10
136	Submicroscopic deletions at 13q32.1 cause congenital microcoria. *American Journal of Human Genetics*, **2015**, 96, 631-9	11	9
135	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
134	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. *Molecular Psychiatry*, **2015**, 20, 647-656	15.1	167
133	PTPRD gene associated with blood pressure response to atenolol and resistant hypertension. *Journal of Hypertension*, **2015**, 33, 2278-85	1.9	29
132	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
131	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687

130	Exome Analyses of Long QT Syndrome Reveal Candidate Pathogenic Mutations in Calmodulin-Interacting Genes. *PLoS ONE*, **2015**, 10, e0130329	3.7	20
129	Genome-Wide Association Study of Peripheral Arterial Disease in a Japanese Population. *PLoS ONE*, **2015**, 10, e0139262	3.7	24
128	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
127	Integrating genetic, transcriptional, and functional analyses to identify 5 novel genes for atrial fibrillation. *Circulation*, **2014**, 130, 1225-35	16.7	143
126	Small intestinal stem cell identity is maintained with functional Paneth cells in heterotopically grafted epithelium onto the colon. *Genes and Development*, **2014**, 28, 1752-7	12.6	113
125	Trans-ethnic meta-analysis of white blood cell phenotypes. *Human Molecular Genetics*, **2014**, 23, 6944-60	5.6	45
124	Novel calmodulin mutations associated with congenital arrhythmia susceptibility. *Circulation: Cardiovascular Genetics*, **2014**, 7, 466-74		133
123	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	3	11
122	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	3	8
121	Renin-angiotensin-aldosterone system polymorphisms and 5-year mortality in survivors of acute myocardial infarction: a report from the Osaka Acute Coronary Insufficiency Study. *International Heart Journal*, **2014**, 55, 190-6	1.8	7
120	Multiple nonglycemic genomic loci are newly associated with blood level of glycated hemoglobin in East Asians. *Diabetes*, **2014**, 63, 2551-62	0.9	46
119	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
118	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
117	Decreased mortality associated with statin treatment in patients with acute myocardial infarction and lymphotoxin-alpha C804A polymorphism. *Atherosclerosis*, **2013**, 227, 373-9	3.1	3
116	GWAS of 126,559 individuals identifies genetic variants associated with educational attainment. *Science*, **2013**, 340, 1467-71	33.3	563
115	ITPKC and CASP3 polymorphisms and risks for IVIG unresponsiveness and coronary artery lesion formation in Kawasaki disease. *Pharmacogenomics Journal*, **2013**, 13, 52-9	3.5	68
114	Genome wide analysis of drug-induced torsades de pointes: lack of common variants with large effect sizes. *PLoS ONE*, **2013**, 8, e78511	3.7	48
113	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

112	A genome-wide association study identifies three new risk loci for Kawasaki disease. *Nature Genetics*, **2012**, 44, 517-21	36.3	217
111	Discovery and fine mapping of serum protein loci through transethnic meta-analysis. *American Journal of Human Genetics*, **2012**, 91, 744-53	11	58
110	Meta-analysis identifies common variants associated with body mass index in east Asians. *Nature Genetics*, **2012**, 44, 307-11	36.3	301
109	Meta-analysis identifies six new susceptibility loci for atrial fibrillation. *Nature Genetics*, **2012**, 44, 670-5	36.3	429
108	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. *Nature Genetics*, **2012**, 44, 904-9	36.3	201
107	Homocysteine and coronary heart disease: meta-analysis of MTHFR case-control studies, avoiding publication bias. *PLoS Medicine*, **2012**, 9, e1001177	11.6	135
106	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	3.7	42
105	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
104	SNPs on chromosome 5p15.3 associated with myocardial infarction in Japanese population. *Journal of Human Genetics*, **2011**, 56, 47-51	4.3	26
103	Large-scale genome-wide association studies in East Asians identify new genetic loci influencing metabolic traits. *Nature Genetics*, **2011**, 43, 990-5	36.3	229
102	BRAP Activates Inflammatory Cascades and Increases the Risk for Carotid Atherosclerosis. *Molecular Medicine*, **2011**, 17, 1065-74	6.2	33
101	Common variants in a novel gene, FONG on chromosome 2q33.1 confer risk of osteoporosis in Japanese. *PLoS ONE*, **2011**, 6, e19641	3.7	27
100	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
99	Multiple loci are associated with white blood cell phenotypes. *PLoS Genetics*, **2011**, 7, e1002113	6	92
98	Identification of nine novel loci associated with white blood cell subtypes in a Japanese population. *PLoS Genetics*, **2011**, 7, e1002067	6	61
97	Genetic Background of Myocardial Infarction **2011**, 113-120		
96	Common variants in CASP3 confer susceptibility to Kawasaki disease. *Human Molecular Genetics*, **2010**, 19, 2898-906	5.6	114
95	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, 1780-8	0.9	24

94	Prediction model for knee osteoarthritis based on genetic and clinical information. *Arthritis Research and Therapy*, **2010**, 12, R187	5.7	40
93	Unique activation status of peripheral blood mononuclear cells at acute phase of Kawasaki disease. *Clinical and Experimental Immunology*, **2010**, 160, 246-55	6.2	59
92	SNPs in BRAP associated with risk of myocardial infarction in Asian populations. *Nature Genetics*, **2009**, 41, 329-33	36.3	83
91	Lymphotoxin-alpha3 mediates monocyte-endothelial interaction by TNFR I/NF-kappaB signaling. *Biochemical and Biophysical Research Communications*, **2009**, 379, 374-8	3.4	5
90	Common variants in DVWA on chromosome 3p24.3 are associated with susceptibility to knee osteoarthritis. *Nature Genetics*, **2008**, 40, 994-8	36.3	116
89	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, 1122-9	11	82
88	A functional SNP in EDG2 increases susceptibility to knee osteoarthritis in Japanese. *Human Molecular Genetics*, **2008**, 17, 1790-7	5.6	37
87	Recombination rates of genes expressed in human tissues. *Human Molecular Genetics*, **2008**, 17, 577-86	5.6	9
86	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
85	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
84	A functional polymorphism in the 5TUTR of GDF5 is associated with susceptibility to osteoarthritis. *Nature Genetics*, **2007**, 39, 529-33	36.3	370
83	Genetic backgrounds of myocardial infarction. *Current Cardiovascular Risk Reports*, **2007**, 1, 427-431	0.9	
82	A functional SNP in ITIH3 is associated with susceptibility to myocardial infarction. *Journal of Human Genetics*, **2007**, 52, 220-229	4.3	27
81	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, 962-8	10.3	77
80	Linkage disequilibrium of evolutionarily conserved regions in the human genome. *BMC Genomics*, **2006**, 7, 326	4.5	7
79	Impact of atherosclerosis-related gene polymorphisms on mortality and recurrent events after myocardial infarction. *Atherosclerosis*, **2006**, 185, 400-5	3.1	30
78	A functional SNP in PSMA6 confers risk of myocardial infarction in the Japanese population. *Nature Genetics*, **2006**, 38, 921-5	36.3	91
77	Identification of a novel non-coding RNA, MIAT, that confers risk of myocardial infarction. *Journal of Human Genetics*, **2006**, 51, 1087-1099	4.3	491

76	Inflammation as a risk factor for myocardial infarction. *Journal of Human Genetics*, **2006**, 51, 595-604	4.3	27
75	Genome-wide association study to identify single-nucleotide polymorphisms conferring risk of myocardial infarction. *Methods in Molecular Medicine*, **2006**, 128, 173-80		5
74	A haplotype map of the human genome. *Nature*, **2005**, 437, 1299-320	50.4	4818
73	Genome-wide association study to identify SNPs conferring risk of myocardial infarction and their functional analyses. *Cellular and Molecular Life Sciences*, **2005**, 62, 1804-13	10.3	41
72	Association of a single-nucleotide polymorphism in the immunoglobulin mu-binding protein 2 gene with immunoglobulin A nephropathy. *Journal of Human Genetics*, **2005**, 50, 30-35	4.3	23
71	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	4.3	10
70	Variation of gene-based SNPs and linkage disequilibrium patterns in the human genome. *Human Molecular Genetics*, **2004**, 13, 1623-32	5.6	44
69	Complete sequencing and characterization of 21,243 full-length human cDNAs. *Nature Genetics*, **2004**, 36, 40-5	36.3	695
68	Functional variation in LGALS2 confers risk of myocardial infarction and regulates lymphotoxin-alpha secretion in vitro. *Nature*, **2004**, 429, 72-5	50.4	206
67	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	4.9	14
66	High-density SNP map of human ITR, a gene associated with vascular remodeling. *Journal of Human Genetics*, **2003**, 48, 170-2	4.3	9
65	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
64	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	4.3	8
63	Induction of tenascin-C by tumor-specific EWS-ETS fusion genes. *Genes Chromosomes and Cancer*, **2003**, 36, 224-32	5	33
62	The International HapMap Project. *Nature*, **2003**, 426, 789-96	50.4	5039
61	Inhibition of experimental intimal thickening in mice lacking a novel G-protein-coupled receptor. *Circulation*, **2003**, 107, 313-9	16.7	31
60	Twenty single-nucleotide polymorphisms in four genes encoding cardiac ion channels. *Journal of Human Genetics*, **2002**, 47, 208-12	4.3	5
59	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, 532-8	4.3	30

58	Gene-based SNP discovery as part of the Japanese Millennium Genome Project: identification of 190,562 genetic variations in the human genome. Single-nucleotide polymorphism. *Journal of Human Genetics*, **2002**, 47, 605-10	4.3	253
57	Isolation of HELAD1, a novel human helicase gene up-regulated in colorectal carcinomas. *Oncogene*, **2002**, 21, 6387-94	9.2	29
56	The Id2 gene is a novel target of transcriptional activation by EWS-ETS fusion proteins in Ewing family tumors. *Oncogene*, **2002**, 21, 8302-9	9.2	92
55	Functional SNPs in the lymphotoxin-alpha gene that are associated with susceptibility to myocardial infarction. *Nature Genetics*, **2002**, 32, 650-4	36.3	755
54	Osteopenia and male-specific sudden cardiac death in mice lacking a zinc transporter gene, Znt5. *Human Molecular Genetics*, **2002**, 11, 1775-84	5.6	120
53	JSNP: a database of common gene variations in the Japanese population. *Nucleic Acids Research*, **2002**, 30, 158-62	20.1	211
52	The p53 family member genes are involved in the Notch signal pathway. *Journal of Biological Chemistry*, **2002**, 277, 719-24	5.4	137
51	Association between single-nucleotide polymorphisms in selectin genes and immunoglobulin A nephropathy. *American Journal of Human Genetics*, **2002**, 70, 781-6	11	73
50	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, 604-8	4.3	7
49	Genetic variations in five genes involved in the excitement of cardiomyocytes. *Journal of Human Genetics*, **2001**, 46, 549-52	4.3	20
48	A high-throughput SNP typing system for genome-wide association studies. *Journal of Human Genetics*, **2001**, 46, 471-7	4.3	405
47	Multiple single-nucleotide polymorphisms (SNPs) in the Japanese population in six candidate genes for long QT syndrome. *Journal of Human Genetics*, **2001**, 46, 158-62	4.3	16
46	Correlation of genetic etiology with response to beta-adrenergic blockade among symptomatic patients with familial long-QT syndrome. *Journal of Human Genetics*, **2001**, 46, 38-40	4.3	19
45	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
44	Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites. *EMBO Reports*, **2001**, 2, 388-93	6.5	141
43	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
42	p53DINP1, a p53-inducible gene, regulates p53-dependent apoptosis. *Molecular Cell*, **2001**, 8, 85-94	17.6	283
41	Isolation of a novel human gene, MARKL1, homologous to MARK3 and its involvement in hepatocellular carcinogenesis. *Neoplasia*, **2001**, 3, 4-9	6.4	69

40	Mutations in the NMMHC-A gene cause autosomal dominant macrothrombocytopenia with leukocyte inclusions (May-Hegglin anomaly/Sebastian syndrome). *Blood*, **2001**, 97, 1147-9	2.2	118
39	Identification and characterization of the potential promoter regions of 1031 kinds of human genes. *Genome Research*, **2001**, 11, 677-84	9.7	184
38	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	10.1	160
37	Growth and gene expression profile analyses of endometrial cancer cells expressing exogenous PTEN. *Cancer Research*, **2001**, 61, 3741-9	10.1	61
36	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	10.1	30
35	Prediction of sensitivity of esophageal tumors to adjuvant chemotherapy by cDNA microarray analysis of gene-expression profiles. *Cancer Research*, **2001**, 61, 6474-9	10.1	109
34	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	10.1	71
33	Linkage of familial moyamoya disease (spontaneous occlusion of the circle of Willis) to chromosome 17q25. *Stroke*, **2000**, 31, 930-5	6.7	230
32	Identification of 187 single nucleotide polymorphisms (SNPs) among 41 candidate genes for ischemic heart disease in the Japanese population. *Human Genetics*, **2000**, 106, 288-92	6.3	59
31	Identification of 142 single nucleotide polymorphisms in 41 candidate genes for rheumatoid arthritis in the Japanese population. *Human Genetics*, **2000**, 106, 293-7	6.3	20
30	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, 182-3	4.3	56
29	Genomic structure and multiple single-nucleotide polymorphisms (SNPs) of the thiopurine S-methyltransferase (TPMT) gene. *Journal of Human Genetics*, **2000**, 45, 299-302	4.3	44
28	p53AIP1, a potential mediator of p53-dependent apoptosis, and its regulation by Ser-46-phosphorylated p53. *Cell*, **2000**, 102, 849-62	56.2	1005
27	Characterization of S818L mutation in HERG C-terminus in LQT2. Modification of activation-deactivation gating properties. *FEBS Letters*, **2000**, 481, 197-203	3.8	15
26	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	6.3	81
25	Identification of 142 single nucleotide polymorphisms in 41 candidate genes for rheumatoid arthritis in the Japanese population. *Human Genetics*, **2000**, 106, 293-297	6.3	27
24	Identification by cDNA microarray of genes involved in ovarian carcinogenesis. *Cancer Research*, **2000**, 60, 5007-11	10.1	187
23	Voltage-shift of the current activation in HERG S4 mutation (R534C) in LQT2. *Cardiovascular Research*, **1999**, 44, 283-93	9.9	36

22	Mapping of a gene for May-Hegglin anomaly to chromosome 22q. *Human Genetics*, **1999**, 105, 379-83	6.3	29
21	Mapping of a gene for May-Hegglin anomaly to chromosome 22q. *Human Genetics*, **1999**, 105, 379-383	6.3	35
20	Identification of the gene responsible for gelatinous drop-like corneal dystrophy. *Nature Genetics*, **1999**, 21, 420-3	36.3	137
19	Chapter 7 Mutational Analysis of Familial Long QT Syndrome in Japan. *Current Topics in Membranes*, **1999**, 46, 103-116	2.2	
18	Hyperglycemia causes oxidative stress in pancreatic beta-cells of GK rats, a model of type 2 diabetes. *Diabetes*, **1999**, 48, 927-32	0.9	376
17	Localization of the gene responsible for Peutz-Jeghers syndrome within a 6-cM region of chromosome 19p13.3. *Human Genetics*, **1998**, 102, 203-6	6.3	17
16	Genomic organization and mutational analysis of HERG, a gene responsible for familial long QT syndrome. *Human Genetics*, **1998**, 102, 435-9	6.3	75
15	Genomic organization and mutational analysis of KVLQT1, a gene responsible for familial long QT syndrome. *Human Genetics*, **1998**, 103, 290-4	6.3	32
14	Identification by differential display of eight known genes induced during in vivo intimal hyperplasia. *Journal of Human Genetics*, **1998**, 43, 9-13	4.3	8
13	Heterozygosities and allelic frequencies of 358 dinucleotide-repeat marker loci in the Japanese population. *Journal of Human Genetics*, **1998**, 43, 165-8	4.3	6
12	Homozygosity mapping of a gene responsible for gelatinous drop-like corneal dystrophy to chromosome 1p. *American Journal of Human Genetics*, **1998**, 63, 1073-7	11	39
11	Isolation and chromosomal mapping of the human homolog of perilipin (PLIN), a rat adipose tissue-specific gene, by differential display method. *Genomics*, **1998**, 48, 254-7	4.3	29
10	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, 378-81	4.3	15
9	Novel mechanism of HERG current suppression in LQT2: shift in voltage dependence of HERG inactivation. *Circulation Research*, **1998**, 83, 415-22	15.7	82
8	Four novel KVLQT1 and four novel HERG mutations in familial long-QT syndrome. *Circulation*, **1997**, 95, 565-7	16.7	76
7	Molecular cloning and mapping of a human cDNA for cytosolic malate dehydrogenase (MDH1). *Genomics*, **1996**, 32, 128-30	4.3	14
6	Construction of a normalized directionally cloned cDNA library from adult heart and analysis of 3040 clones by partial sequencing. *Genomics*, **1996**, 35, 231-5	4.3	20
5	Molecular cloning of a human cDNA encoding putative cysteine protease (PRSC1) and its chromosome assignment to 14q32.1. *Cytogenetic and Genome Research*, **1996**, 74, 120-3	1.9	9

4	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, 802-4	3.2	10
3	Genetic linkage analyses of Romano-Ward syndrome (RWS) in 13 Japanese families. *Human Genetics*, **1994**, 94, 380-4	6.3	6
2	Assignment of the human caltractin gene (CALT) to Xq28 by fluorescence in situ hybridization. *Genomics*, **1994**, 24, 609-10	4.3	4
1	Identification of myocardial infarction-susceptible genes and their functional analyses79-88		