Katsushi Tokunaga

List of Publications by Year in Descending Order

173 papers	4,031 citations	31 h-index	55 g-index
183 ext. papers	4,742 ext. citations	5 avg, IF	4.76 L-index

#	Paper	IF	Citations
173	A rare genetic variant in the cleavage site of prepro-orexin is associated with idiopathic hypersomnia.. *Npj Genomic Medicine*, **2022**, 7, 29	6.2	0
172	GA4GH: International policies and standards for data sharing across genomic research and healthcare.. *Cell Genomics*, **2021**, 1, 100029-100029		20
171	HLA Class I Analysis Provides Insight Into the Genetic and Epigenetic Background of Immune Evasion in Colorectal Cancer With High Microsatellite Instability. *Gastroenterology*, **2021**,	13.3	4
170	Characterization of intermediate-sized insertions using whole-genome sequencing data and analysis of their functional impact on gene expression. *Human Genetics*, **2021**, 140, 1201-1216	6.3	0
169	Genome-wide copy number variation analysis of hepatitis B infection in a Japanese population. *Human Genome Variation*, **2021**, 8, 22	1.8	0
168	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. *Gastroenterology*, **2021**, 160, 2483-2495.e26	13.3	9
167	Mapping of susceptible variants for cold medicine-related Stevens-Johnson syndrome by whole-genome resequencing. *Npj Genomic Medicine*, **2021**, 6, 9	6.2	1
166	Haplotype-specific PCR for diplotyping. *Human Genome Variation*, **2020**, 7, 13	1.8	5
165	Homoplastic single nucleotide polymorphisms contributed to phenotypic diversity in Mycobacterium tuberculosis. *Scientific Reports*, **2020**, 10, 8024	4.9	8
164	The Origin and Composition of Korean Ethnicity Analyzed by Ancient and Present-Day Genome Sequences. *Genome Biology and Evolution*, **2020**, 12, 553-565	3.9	7
163	Polo-like kinase 4 and Stromal antigen 3 are not associated with recurrent pregnancy loss caused by embryonic aneuploidy. *Human Genome Variation*, **2020**, 7, 18	1.8	2
162	Metabolome analysis using cerebrospinal fluid from narcolepsy type 1 patients. *Sleep*, **2020**, 43,	1.1	4
161	Common risk variants in NPHS1 and TNFSF15 are associated with childhood steroid-sensitive nephrotic syndrome. *Kidney International*, **2020**, 98, 1308-1322	9.9	17
160	A high-resolution HLA imputation system for the Taiwanese population: a study of the Taiwan Biobank. *Pharmacogenomics Journal*, **2020**, 20, 695-704	3.5	8
159	Digenic mutations in and impair formaldehyde clearance and cause a multisystem disorder, AMeD syndrome. *Science Advances*, **2020**, 6,	14.3	14
158	Risk factors associated with large clusters of tuberculosis patients determined by whole-genome sequencing in a high-tuberculosis-burden country. *Tuberculosis*, **2020**, 125, 101991	2.6	2
157	An optimized genomic VCF workflow for precise identification of Mycobacterium tuberculosis cluster from cross-platform whole genome sequencing data. *Infection, Genetics and Evolution*, **2020**, 79, 104152	4.5	3

156	Epigenome-wide association study of narcolepsy-affected lateral hypothalamic brains, and overlapping DNA methylation profiles between narcolepsy and multiple sclerosis. *Sleep*, **2020**, 43,	1.1	4
155	The association of integration patterns of human papilloma virus and single nucleotide polymorphisms on immune- or DNA repair-related genes in cervical cancer patients. *Scientific Reports*, **2019**, 9, 13132	4.9	3
154	A missense variant in PER2 is associated with delayed sleep-wake phase disorder in a Japanese population. *Journal of Human Genetics*, **2019**, 64, 1219-1225	4.3	11
153	Genetics of narcolepsy. *Human Genome Variation*, **2019**, 6, 4	1.8	26
152	POGLUT1, the putative effector gene driven by rs2293370 in primary biliary cholangitis susceptibility locus chromosome 3q13.33. *Scientific Reports*, **2019**, 9, 102	4.9	14
151	NFKB1 and MANBA Confer Disease Susceptibility to Primary Biliary Cholangitis via Independent Putative Primary Functional Variants. *Cellular and Molecular Gastroenterology and Hepatology*, **2019**, 7, 515-532	7.9	10
150	Genomewide Association Study Confirming the Association of with Susceptibility to Antituberculosis Drug-Induced Liver Injury in Thai Patients. *Antimicrobial Agents and Chemotherapy*, **2019**, 63,	5.9	13
149	Analysis of whole Y-chromosome sequences reveals the Japanese population history in the Jomon period. *Scientific Reports*, **2019**, 9, 8556	4.9	15
148	Integrative genome analysis identified the KANNO blood group antigen as prion protein. *Transfusion*, **2019**, 59, 2429-2435	2.9	6
147	Identification of the novel HLA-DQB1 allele, HLA-DQB1*05:03:01:04, in a Japanese individual. *Hla*, **2019**, 94, 466-468	1.9	3
146	Detection of the novel HLA-A allele, HLA-A*02:01:01:58, in a Japanese individual. *Hla*, **2019**, 94, 435-436	1.9	2
145	Discovery of the novel HLA-B allele, HLA-B*51:01:01:36 in a Japanese individual. *Hla*, **2019**, 94, 445-447	1.9	2
144	Association of HLA class I and II gene polymorphisms with acetaminophen-related Stevens-Johnson syndrome with severe ocular complications in Japanese individuals. *Human Genome Variation*, **2019**, 6, 50	1.8	13
143	Identification of HLA-A*02:06:01 as the primary disease susceptibility HLA allele in cold medicine-related Stevens-Johnson syndrome with severe ocular complications by high-resolution NGS-based HLA typing. *Scientific Reports*, **2019**, 9, 16240	4.9	7
142	A 12-kb structural variation in progressive myoclonic epilepsy was newly identified by long-read whole-genome sequencing. *Journal of Human Genetics*, **2019**, 64, 359-368	4.3	36
141	MGeND: an integrated database for Japanese clinical and genomic information. *Human Genome Variation*, **2019**, 6, 53	1.8	2
140	Genome-Wide Association Study Confirming a Strong Effect of HLA and Identifying Variants in on Chromosome 12q13.13 Associated With Susceptibility to Fulminant Type 1 Diabetes. *Diabetes*, **2019**, 68, 665-675	0.9	17
139	Protective association of HLA-DRB1*13:02, HLA-DRB1*04:06, and HLA-DQB1*06:04 alleles with cervical cancer in a Korean population. *Human Immunology*, **2019**, 80, 107-111	2.3	6

138	A Genome-wide Association Study Identifying RAP1A as a Novel Susceptibility Gene for Crohn Disease in Japanese Individuals. *Journal of Crohn s and Colitis*, **2019**, 13, 648-658	1.5	11
137	Whole-exome sequencing and gene-based rare variant association tests suggest that PLA2G4E might be a risk gene for panic disorder. *Translational Psychiatry*, **2018**, 8, 41	8.6	11
136	Epigenome-wide association study of DNA methylation in narcolepsy: an integrated genetic and epigenetic approach. *Sleep*, **2018**, 41,	1.1	12
135	Genome-wide association study of self-reported food reactions in Japanese identifies shrimp and peach specific loci in the HLA-DR/DQ gene region. *Scientific Reports*, **2018**, 8, 1069	4.9	18
134	DBTSS/DBKERO for integrated analysis of transcriptional regulation. *Nucleic Acids Research*, **2018**, 46, D229-D238	20.1	37
133	An epigenome-wide methylation study of healthy individuals with or without depressive symptoms. *Journal of Human Genetics*, **2018**, 63, 319-326	4.3	7
132	Key HLA-DRB1-DQB1 haplotypes and role of the BTNL2 gene for response to a hepatitis B vaccine. *Hepatology*, **2018**, 68, 848-858	11.2	26
131	Human leukocyte antigen variants and risk of hepatocellular carcinoma modified by hepatitis C virus genotypes: A genome-wide association study. *Hepatology*, **2018**, 67, 651-661	11.2	24
130	Strong Association of the Locus with Childhood Steroid-Sensitive Nephrotic Syndrome in the Japanese Population. *Journal of the American Society of Nephrology: JASN*, **2018**, 29, 2189-2199	12.7	37
129	Evidence for Host-Bacterial Co-evolution via Genome Sequence Analysis of 480 Thai Mycobacterium tuberculosis Lineage 1 Isolates. *Scientific Reports*, **2018**, 8, 11597	4.9	30
128	Increased expression and altered localization of cathepsin Z are associated with progression to jaundice stage in primary biliary cholangitis. *Scientific Reports*, **2018**, 8, 11808	4.9	4
127	Amino acid position 37 of HLA-DR affects susceptibility to Crohn disease in Asians. *Human Molecular Genetics*, **2018**, 27, 3901-3910	5.6	12
126	A variant at 9q34.11 is associated with HLA-DQB1*06:02 negative essential hypersomnia. *Journal of Human Genetics*, **2018**, 63, 1259-1267	4.3	3
125	Identification of a two-SNP PLA2R1 Haplotype and HLA-DRB1 Alleles as Primary Risk Associations in Idiopathic Membranous Nephropathy. *Scientific Reports*, **2018**, 8, 15576	4.9	7
124	Genome-wide association study identified new susceptible genetic variants in HLA class I region for hepatitis B virus-related hepatocellular carcinoma. *Scientific Reports*, **2018**, 8, 7958	4.9	23
123	NAT2 ultra-slow acetylator and risk of anti-tuberculosis drug-induced liver injury: a genotype-based meta-analysis. *Pharmacogenetics and Genomics*, **2018**, 28, 167-176	1.9	20
122	Genome-wide haplotype association analysis of primary biliary cholangitis risk in Japanese. *Scientific Reports*, **2018**, 8, 7806	4.9	3
121	NELFCD and CTSZ loci are associated with jaundice-stage progression in primary biliary cholangitis in the Japanese population. *Scientific Reports*, **2018**, 8, 8071	4.9	7

120	Genome-wide association studies identify PRKCB as a novel genetic susceptibility locus for primary biliary cholangitis in the Japanese population. *Human Molecular Genetics*, **2017**, 26, 650-659	5.6	36
119	Genome-Wide Association Study Identifies Risk Variants for Lichen Planus in Patients With Hepatitis C Virus Infection. *Clinical Gastroenterology and Hepatology*, **2017**, 15, 937-944.e5	6.9	17
118	Human Leukocyte Antigen Class I Genes Associated With Stevens-Johnson Syndrome and Severe Ocular Complications Following Use of Cold Medicine in a Brazilian Population. *JAMA Ophthalmology*, **2017**, 135, 355-360	3.9	23
117	Role of HLA-DP and HLA-DQ on the clearance of hepatitis B virus and the risk of chronic infection in a multiethnic population. *Liver International*, **2017**, 37, 1476-1487	7.9	11
116	Genome-Wide Association Study Identifies TLL1 Variant Associated With Development of Hepatocellular Carcinoma After Eradication of Hepatitis C Virus Infection. *Gastroenterology*, **2017**, 152, 1383-1394	13.3	76
115	Genome-wide association study using the ethnicity-specific Japonica array: identification of new susceptibility loci for cold medicine-related Stevens-Johnson syndrome with severe ocular complications. *Journal of Human Genetics*, **2017**, 62, 485-489	4.3	16
114	The first genome-wide association study identifying new susceptibility loci for obstetric antiphospholipid syndrome. *Journal of Human Genetics*, **2017**, 62, 831-838	4.3	13
113	Epigenome-wide association study of DNA methylation in panic disorder. *Clinical Epigenetics*, **2017**, 9, 6	7.7	39
112	Significance of functional disease-causal/susceptible variants identified by whole-genome analyses for the understanding of human diseases. *Proceedings of the Japan Academy Series B: Physical and Biological Sciences*, **2017**, 93, 657-676	4	4
111	Principal contribution of HLA-DQ alleles, DQB1*06:04 and DQB1*03:01, to disease resistance against primary biliary cholangitis in a Japanese population. *Scientific Reports*, **2017**, 7, 11093	4.9	18
110	Discerning the Origins of the Negritos, First Sundaland People: Deep Divergence and Archaic Admixture. *Genome Biology and Evolution*, **2017**, 9, 2013-2022	3.9	30
109	Association of Human Leukocyte Antigen Class 1 genes with Stevens Johnson Syndrome with severe ocular complications in an Indian population. *Scientific Reports*, **2017**, 7, 15960	4.9	13
108	Identification of the functional variant driving ORMDL3 and GSDMB expression in human chromosome 17q12-21 in primary biliary cholangitis. *Scientific Reports*, **2017**, 7, 2904	4.9	15
107	Pathogen lineage-based genome-wide association study identified CD53 as susceptible locus in tuberculosis. *Journal of Human Genetics*, **2017**, 62, 1015-1022	4.3	31
106	A Subgroup Analysis of Genome-wide Association Study for Panic Disorder. *Major Histocompatibility Complex*, **2017**, 24, 54-64	0.1	
105	A human PSMB11 variant affects thymoproteasome processing and CD8+ T cell production. *JCI Insight*, **2017**, 2,	9.9	6
104	Narcolepsy susceptibility gene CCR3 modulates sleep-wake patterns in mice. *PLoS ONE*, **2017**, 12, e0187888	3.7	4
103	Identification of ITPA on chromosome 20 as a susceptibility gene for young-onset tuberculosis. *Human Genome Variation*, **2016**, 3, 15067	1.8	8

102	Fine-mapping analysis revealed complex pleiotropic effect and tissue-specific regulatory mechanism of TNFSF15 in primary biliary cholangitis, Crohn's disease and leprosy. *Scientific Reports*, **2016**, 6, 31429	4.9	9
101	Understanding of HLA-conferred susceptibility to chronic hepatitis B infection requires HLA genotyping-based association analysis. *Scientific Reports*, **2016**, 6, 24767	4.9	29
100	Evaluation of polygenic risks for narcolepsy and essential hypersomnia. *Journal of Human Genetics*, **2016**, 61, 873-878	4.3	17
99	Genome-wide Association Study of Autism Spectrum Disorder in the East Asian Populations. *Autism Research*, **2016**, 9, 340-9	5.1	59
98	Mutations in rrs, rpsL and gidB in streptomycin-resistant Mycobacterium tuberculosis isolates from Thailand. *Journal of Global Antimicrobial Resistance*, **2016**, 4, 5-10	3.4	17
97	NAT2 variants are associated with drug-induced liver injury caused by anti-tuberculosis drugs in Indonesian patients with tuberculosis. *Journal of Human Genetics*, **2016**, 61, 533-7	4.3	30
96	Genome-Wide Association Study Identifies ZNF354C Variants Associated with Depression from Interferon-Based Therapy for Chronic Hepatitis C. *PLoS ONE*, **2016**, 11, e0164418	3.7	7
95	The First Pilot Genome-Wide Gene-Environment Study of Depression in the Japanese Population. *PLoS ONE*, **2016**, 11, e0160823	3.7	22
94	Phenome-wide association study maps new diseases to the human major histocompatibility complex region. *Journal of Medical Genetics*, **2016**, 53, 681-9	5.8	21
93	Development of a prediction system for anti-tuberculosis drug-induced liver injury in Japanese patients. *Human Genome Variation*, **2016**, 3, 16014	1.8	19
92	High-density Association Mapping and Interaction Analysis of PLA2R1 and HLA Regions with Idiopathic Membranous Nephropathy in Japanese. *Scientific Reports*, **2016**, 6, 38189	4.9	27
91	Polymorphisms in the TMEM132D region are associated with panic disorder in HLA-DRB1*13:02-negative individuals of a Japanese population. *Human Genome Variation*, **2016**, 3, 16001	1.8	7
90	Unique characteristics of the Ainu population in Northern Japan. *Journal of Human Genetics*, **2015**, 60, 565-71	4.3	19
89	Disease susceptibility genes shared by primary biliary cirrhosis and Crohn's disease in the Japanese population. *Journal of Human Genetics*, **2015**, 60, 525-31	4.3	16
88	Glypican-5 Increases Susceptibility to Nephrotic Damage in Diabetic Kidney. *American Journal of Pathology*, **2015**, 185, 1889-98	5.8	13
87	Human primary biliary cirrhosis-susceptible allele of rs4979462 enhances TNFSF15 expression by binding NF-1. *Human Genetics*, **2015**, 134, 737-47	6.3	21
86	Associations of human leukocyte antigens with autoimmune diseases: challenges in identifying the mechanism. *Journal of Human Genetics*, **2015**, 60, 697-702	4.3	42
85	A polymorphism in CCR1/CCR3 is associated with narcolepsy. *Brain, Behavior, and Immunity*, **2015**, 49, 148-55	16.6	30

84	New susceptibility variants to narcolepsy identified in HLA class II region. *Human Molecular Genetics*, **2015**, 24, 891-8	5.6	20
83	Novel rare variations of the oxytocin receptor (OXTR) gene in autism spectrum disorder individuals. *Human Genome Variation*, **2015**, 2, 15024	1.8	9
82	CD14 and IL18 gene polymorphisms associated with colorectal cancer subsite risks among atomic bomb survivors. *Human Genome Variation*, **2015**, 2, 15035	1.8	1
81	HLA-A*02:06 and PTGER3 polymorphism exert additive effects in cold medicine-related Stevens-Johnson syndrome with severe ocular complications. *Human Genome Variation*, **2015**, 2, 15023	1.8	18
80	An association analysis of HLA-DQB1 with narcolepsy without cataplexy and idiopathic hypersomnia with/without long sleep time in a Japanese population. *Human Genome Variation*, **2015**, 2, 15031	1.8	16
79	Detection of Hereditary 1,25-Hydroxyvitamin D-Resistant Rickets Caused by Uniparental Disomy of Chromosome 12 Using Genome-Wide Single Nucleotide Polymorphism Array. *PLoS ONE*, **2015**, 10, e0131157	3.7	13
78	IKZF1, a new susceptibility gene for cold medicine-related Stevens-Johnson syndrome/toxic epidermal necrolysis with severe mucosal involvement. *Journal of Allergy and Clinical Immunology*, **2015**, 135, 1538-45.e17	11.5	50
77	Immune-related pathways including HLA-DRB1(*)13:02 are associated with panic disorder. *Brain, Behavior, and Immunity*, **2015**, 46, 96-103	16.6	11
76	Independent strong association of HLA-A*02:06 and HLA-B*44:03 with cold medicine-related Stevens-Johnson syndrome with severe mucosal involvement. *Scientific Reports*, **2014**, 4, 4862	4.9	67
75	Novel DNA chip based on a modified DigiTag2 assay for high-throughput species identification and genotyping of Mycobacterium tuberculosis complex isolates. *Journal of Clinical Microbiology*, **2014**, 52, 1962-8	9.7	8
74	Genome-wide analysis of CNV (copy number variation) and their associations with narcolepsy in a Japanese population. *Journal of Human Genetics*, **2014**, 59, 235-40	4.3	5
73	Strong association between hla-a*02:06 and acetaminophen-related stevens-johnson syndrome with severe mucosal involvements in the Japanese. *Clinical and Translational Allergy*, **2014**, 4, P11	5.2	78
72	HLA association with antipyretic analgesics-induced Stevens-Johnson Syndrome/toxic epidermal necrolysis with severe ocular surface complications in japanese patients. *Clinical and Translational Allergy*, **2014**, 4, P89	5.2	78
71	A new sister journal to the Journal of Human Genetics-for the interest and benefit of the global community of human genome researchers. *Human Genome Variation*, **2014**, 1, 14003	1.8	
70	Trans-ethnic study confirmed independent associations of HLA-A*02:06 and HLA-B*44:03 with cold medicine-related Stevens-Johnson syndrome with severe ocular surface complications. *Scientific Reports*, **2014**, 4, 5981	4.9	55
69	New susceptibility and resistance HLA-DP alleles to HBV-related diseases identified by a trans-ethnic association study in Asia. *PLoS ONE*, **2014**, 9, e86449	3.7	28
68	Association of functional polymorphisms in interferon regulatory factor 2 (IRF2) with susceptibility to systemic lupus erythematosus: a case-control association study. *PLoS ONE*, **2014**, 9, e109764	3.7	6
67	Lessons from Genome-Wide Search for Disease-Related Genes with Special Reference to HLA-Disease Associations. *Genes*, **2014**, 5, 84-96	4.2	3

66	Genetic diversity and dynamic distribution of Mycobacterium tuberculosis isolates causing pulmonary and extrapulmonary tuberculosis in Thailand. *Journal of Clinical Microbiology*, **2014**, 52, 4267-74	9.7	19
65	A genome-wide association study for diabetic retinopathy in a Japanese population: potential association with a long intergenic non-coding RNA. *PLoS ONE*, **2014**, 9, e111715	3.7	62
64	Applications of HLA gene polymorphisms. *Major Histocompatibility Complex*, **2014**, 21, 87-95	0.1	
63	Genome-Wide Association Study Reveals Host Genetic Factors for Liver Diseases. *Journal of Clinical and Translational Hepatology*, **2013**, 1, 45-50	5.2	4
62	Genome-wide association study identifies TNFSF15 and POU2AF1 as susceptibility loci for primary biliary cirrhosis in the Japanese population. *American Journal of Human Genetics*, **2012**, 91, 721-8	11	201
61	Reply to: "Lack of HIF-2 in limb bud mesenchyme causes a modest and transient delay of endochondral bone development" and "Replication studies in various ethnic populations do not support the association of the HIF-2 SNP rs17039192 with knee osteoarthritis". *Nature Medicine*, 2011, 17, 27-29	50.5	18
60	Combining effects of polymorphism of tumor necrosis factor 5C flanking region and HLA-DRB1 on radiological progression in patients with rheumatoid arthritis. *Modern Rheumatology*, **2009**, 19, 134-139	3.3	1
59	Association of TCF7L2 polymorphisms with susceptibility to type 2 diabetes in 4,087 Japanese subjects. *Journal of Human Genetics*, **2008**, 53, 174-180	4.3	76
58	A functional SNP in the NKX2.5-binding site of ITPR3 promoter is associated with susceptibility to systemic lupus erythematosus in Japanese population. *Journal of Human Genetics*, **2008**, 53, 151-162	4.3	21
57	Polymorphisms of promoter and coding regions of the arylamine N-acetyltransferase 2 (NAT2) gene in the Indonesian population: proposal for a new nomenclature. *Journal of Human Genetics*, **2008**, 53, 201-209	4.3	28
56	Linkage disequilibrium structure of the 5q31-33 region in a Thai population. *Journal of Human Genetics*, **2008**, 53, 850-856	4.3	5
55	Appropriate data cleaning methods for genome-wide association study. *Journal of Human Genetics*, **2008**, 53, 886-893	4.3	34
54	Association and interaction analyses of NRG1 and ERBB4 genes with schizophrenia in a Japanese population. *Journal of Human Genetics*, **2008**, 53, 929-935	4.3	27
53	The genotypes of GYPA and GYPB carrying the MNSs antigens are not associated with cerebral malaria. *Journal of Human Genetics*, **2007**, 52, 476-479	4.3	1
52	De novo polyalanine expansion of PHOX2B in congenital central hypoventilation syndrome: unequal sister chromatid exchange during paternal gametogenesis. *Journal of Human Genetics*, **2007**, 52, 921-925	4.3	14
51	FTO polymorphisms in oceanic populations. *Journal of Human Genetics*, **2007**, 52, 1031-1035	4.3	118
50	MEL1 at 1p36.3 Is Fused to Several Partner Genes Including HOXA9 Located at Different Chromosomal Bands from 3q21.3 in t(1;3)(p36.3;q21.3)-Leukemia.. *Blood*, **2007**, 110, 3499-3499	2.2	2
49	Role of B cell inhibitory receptor polymorphisms in systemic lupus erythematosus: a negative times a negative makes a positive. *Journal of Human Genetics*, **2006**, 51, 741-750	4.3	15

48	Polymorphisms in the ABO blood group gene in three populations in the New Georgia group of the Solomon Islands. *Journal of Human Genetics*, **2006**, 51, 407-411	4.3	15
47	HLA-DRB1 polymorphism on Haʻano island of the Kingdom of Tonga. *Anthropological Science*, **2006**, 114, 193-198	1.3	5
46	Strong linkage disequilibrium of a HbE variant with the (AT)9(T)5 repeat in the BP1 binding site upstream of the beta-globin gene in the Thai population. *Journal of Human Genetics*, **2005**, 50, 7-11	4.3	2
45	Genetic origins of the Ainu inferred from combined DNA analyses of maternal and paternal lineages. *Journal of Human Genetics*, **2004**, 49, 187-193	4.3	99
44	Comparative study of the haplotype structure and linkage disequilibrium of chromosome 1p36.2 region in the Korean and Japanese populations. *Journal of Human Genetics*, **2004**, 49, 603-609	4.3	6
43	Establishment of a method of anonymization of DNA samples in genetic research. *Journal of Human Genetics*, **2003**, 48, 327-330	4.3	9
42	Power of genome-wide linkage disequilibrium testing by using microsatellite markers. *Journal of Human Genetics*, **2003**, 48, 487-491	4.3	28
41	Power of association test for detecting minor histocompatibility gene causing graft-versus-host disease following bone marrow transplantation [correction]. *Journal of Human Genetics*, **2003**, 48, 502-507	4.3	2
40	HLA-DRB1 Polymorphism of Balopa Islanders in Papua New Guinea. *Anthropological Science*, **2003**, 111, 157-164	1.3	2
39	Negative association of the HLA-DRB1*1502-DQB1*0601 haplotype with human narcolepsy. *Immunogenetics*, **2001**, 52, 299-301	3.2	11
38	Haplotype-specific sequence encoding the protein kinase, interferon-inducible double-stranded RNA-dependent activator in the human leukocyte antigen class II region. *Immunogenetics*, **2001**, 52, 186-94	3.2	6
37	Recombination and gene conversion-like events may contribute to ABO gene diversity causing various phenotypes. *Immunogenetics*, **2001**, 53, 190-9	3.2	64
36	Profiling of genes expressed in human monocytes and monocyte-derived dendritic cells using cDNA expression array. *British Journal of Haematology*, **2001**, 114, 191-7	4.5	25
35	Haplotype analyses with the human leucocyte antigen and tumour necrosis factor-alpha genes in narcolepsy families. *Psychiatry and Clinical Neurosciences*, **2001**, 55, 37-9	6.2	12
34	Support for an association between HLA-DR1 and schizophrenia in the Japanese population. *American Journal of Medical Genetics Part A*, **2000**, 96, 725-7		22
33	Novel single nucleotide polymorphisms (SNPs) at positions 497 (T/G) and 829 (T/C) in the human c-FOS gene and haplotype association. *Human Mutation*, **2000**, 16, 279	4.7	4
32	Computer simulation analysis suggests weak balancing selection operative at the MICA locus. *Hereditas*, **2000**, 133, 25-8	2.4	4
31	Comparative FISH mapping of the ancestral fusion point of human chromosome 2. *Chromosome Research*, **2000**, 8, 727-35	4.4	14

30	MHC (major histocompatibility complex)-DRB genes and polymorphisms in common marmoset. *Journal of Molecular Evolution*, **2000**, 51, 214-22	3.1	13
29	Identification of a telomeric boundary of the HLA region with potential for predisposition to human narcolepsy. *Immunogenetics*, **2000**, 52, 12-8	3.2	10
28	HLA and Human Mate Choice. Tests on Japanese Couples.. *Anthropological Science*, **2000**, 108, 199-214	1.3	32
27	Sojourn times and substitution rate at overdominant and linked neutral loci. *Genetics*, **2000**, 155, 921-7	4	5
26	HLA-DRB1 alleles encoding the shared epitope associated with rheumatoid arthritis confer additional susceptibility to seronegative spondyloarthropathies in HLA-B27-positive Japanese individuals. *Japanese Journal of Rheumatology*, **1999**, 9, 55-64		
25	Possible association of human leucocyte antigen DR1 with delayed sleep phase syndrome. *Psychiatry and Clinical Neurosciences*, **1999**, 53, 527-9	6.2	34
24	Determination of Granulocyte-Specific Antigens on Neutrophil Fc Receptor IIIb by PCR-Preferential Homoduplex Formation Assay, and Gene Frequencies in the Japanese Population. *Vox Sanguinis*, **1999**, 77, 218-222	3.1	25
23	Analysis of human leukocyte antigen-G polymorphism including intron 4 in Japanese couples with habitual abortion. *American Journal of Reproductive Immunology*, **1999**, 41, 159-63	3.8	30
22	Identification of the gene variations in human CD22. *Immunogenetics*, **1999**, 49, 280-6	3.2	50
21	New variations of human SHP-1. *Immunogenetics*, **1999**, 49, 577-9	3.2	11
20	HLA-DRB1 alleles encoding the shared epitope associated with rheumatoid arthritis confer additional susceptibility to seronegative spondyloarthropathies in HLA-B27-positive Japanese individuals. *Japanese Journal of Rheumatology*, **1999**, 9, 55-64		1
19	Association of diffuse panbronchiolitis with microsatellite polymorphism of the human interleukin 8 (IL-8) gene. *Journal of Human Genetics*, **1999**, 44, 169-72	4.3	24
18	Genetic variations on the Y chromosome in the Japanese population and implications for modern human Y chromosome lineage. *Journal of Human Genetics*, **1999**, 44, 240-5	4.3	47
17	Selecting a contingency table in a population-based association study: allele frequency or positivity?. *Journal of Human Genetics*, **1999**, 44, 246-8	4.3	3
16	Determination of granulocyte-specific antigens on neutrophil FcA receptor IIIb by PCR-preferential homoduplex formation assay, and gene frequencies in the Japanese population. *Vox Sanguinis*, **1999**, 77, 218-22	3.1	8
15	An ancient retrotransposal insertion causes Fukuyama-type congenital muscular dystrophy. *Nature*, **1998**, 394, 388-92	50.4	665
14	Human lymphocytes obtained from decidual tissue express killer activatory receptors as well as killer inhibitory receptors: analysis using a single strand conformation polymorphism method. *American Journal of Reproductive Immunology*, **1998**, 39, 271-8	3.8	4
13	Founder-haplotype analysis in Fukuyama-type congenital muscular dystrophy (FCMD). *Human Genetics*, **1998**, 103, 323-7	6.3	35

12	HLA-A26 subtype A pockets accommodate acidic N-termini of ligands. *Immunogenetics*, **1998**, 48, 350-3	3.2	17
11	Different Alleles Cause an Imbalance in A2 and A2B Phenotypes of the ABO Blood Group. *Vox Sanguinis*, **1998**, 74, 242-247	3.1	49
10	Contribution of HLA genes to genetic predisposition in diffuse panbronchiolitis. *American Journal of Respiratory and Critical Care Medicine*, **1998**, 158, 846-50	10.2	45
9	DNA typing of HLA-A2, A26 and B61 alleles using the PCR-RFLP method.. *Major Histocompatibility Complex*, **1997**, 3, 205-212	0.1	1
8	Sequence analysis of a serological subtype, LA-A9HH, observed in Japanese and the confirmatory sequence of A*2408.. *Major Histocompatibility Complex*, **1996**, 3, 9-14	0.1	2
7	HLA class II alleles in Ainu living in Hidaka District, Hokkaido, northern Japan. *American Journal of Physical Anthropology*, **1996**, 101, 1-9	2.5	38
6	DNA-based typing of human platelet antigen systems by polymerase chain reaction-single-strand conformation polymorphism method. *Vox Sanguinis*, **1995**, 69, 347-51	3.1	4
5	Genetic polymorphisms in the fourth component of complement (C4) and in properdin factor B (BF) in Japanese patients with palmoplantar pustulosis. *Journal of Dermatology*, **1992**, 19, 353-5	1.6	
4	A common Japanese haplotype HLA-A26-Cw3-B61-DR9-DQ3 carries HLA-B*4002. *Tissue Antigens*, **1992**, 40, 257-60		15
3	Sequence Variation of Human Platelet Membrane Glycoprotein IIIa Associated with the Yuka/Yukb Alloantigen System.. *Proceedings of the Japan Academy Series B: Physical and Biological Sciences*, **1991**, 67, 102-106	4	28
2	Association of Cw11 in Japanese patients with psoriasis vulgaris. *Tissue Antigens*, **1990**, 36, 241-2		37
1	Genome-wide association study of idiopathic hypersomnia in a Japanese population. *Sleep and Biological Rhythms*,1	1.3	1