Katsushi Tokunaga

List of Publications by Year
in descending order

180 papers	5,248 citations	109321 35 h-index	123424 61 g-index
184 all docs	184 docs citations	184 times ranked	7755 citing authors

#	Article	IF	Citations
1	An ancient retrotransposal insertion causes Fukuyama-type congenital muscular dystrophy. Nature, 1998, 394, 388-392.	27.8	758
2	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, 721-728.	6.2	251
3	FTO polymorphisms in oceanic populations. Journal of Human Genetics, 2007, 52, 1031-1035.	2.3	127
4	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.	1.4	117
5	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.	1.3	115
6	Genetic origins of the Ainu inferred from combined DNA analyses of maternal and paternal lineages. Journal of Human Genetics, 2004, 49, 187-193.	2.3	108
7	GA4GH: International policies and standards for data sharing across genomic research and healthcare. Cell Genomics, 2021, 1, 100029.	6.5	94
8	Genomeâ€wide Association Study of Autism Spectrum Disorder in the East Asian Populations. Autism Research, 2016, 9, 340-349.	3.8	89
9	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.	3.3	83
10	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.	2.5	81
11	Association of TCF7L2 polymorphisms with susceptibility to type 2 diabetes in 4,087 Japanese subjects. Journal of Human Genetics, 2008, 53, 174-180.	2.3	80
12	Recombination and gene conversion-like events may contribute to ABO gene diversity causing various phenotypes. Immunogenetics, 2001, 53, 190-199.	2.4	70
13	Identification of the gene variations in human CD22. Immunogenetics, 1999, 49, 280-286.	2.4	68
14	Associations of human leukocyte antigens with autoimmune diseases: challenges in identifying the mechanism. Journal of Human Genetics, 2015, 60, 697-702.	2.3	62
15	Contribution of HLA Genes to Genetic Predisposition in Diffuse Panbronchiolitis. American Journal of Respiratory and Critical Care Medicine, 1998, 158, 846-850.	5.6	60
16	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.	3.3	59
17	IKZF1, a new susceptibility gene for cold medicineâ€"related Stevens-Johnson syndrome/toxic epidermal necrolysis with severe mucosal involvement. Journal of Allergy and Clinical Immunology, 2015, 135, 1538-1545.e17.	2.9	55
18	Different Alleles Cause an Imbalance in A2 and A2B Phenotypes of the ABO Blood Group. Vox Sanguinis, 1998, 74, 242-247.	1.5	54

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19	Discerning the Origins of the Negritos, First Sundaland People: Deep Divergence and Archaic Admixture. Genome Biology and Evolution, 2017, 9, 2013-2022.	2.5	54
20	Strong Association of the HLA-DR/DQ Locus with Childhood Steroid-Sensitive Nephrotic Syndrome in the Japanese Population. Journal of the American Society of Nephrology: JASN, 2018, 29, 2189-2199.	6.1	54
21	Key HLAâ€ÐRB1â€ÐQB1 haplotypes and role of the BTNL2 gene for response to a hepatitis B vaccine. Hepatology, 2018, 68, 848-858.	7.3	53
22	Genetic variations on the Y chromosome in the Japanese population and implications for modern human Y chromosome lineage. Journal of Human Genetics, 1999, 44, 240-245.	2.3	51
23	DBTSS/DBKERO for integrated analysis of transcriptional regulation. Nucleic Acids Research, 2018, 46, D229-D238.	14.5	48
24	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.	2.3	48
25	Epigenome-wide association study of DNA methylation in panic disorder. Clinical Epigenetics, 2017, 9, 6.	4.1	47
26	HLA class II alleles in Ainu living in Hidaka district, Hokkaido, northern Japan. , 1996, 101, 1-9.		46
27	Genome-wide association studies identifyPRKCBas a novel genetic susceptibility locus for primary biliary cholangitis in the Japanese population. Human Molecular Genetics, 2017, 26, ddw406.	2.9	46
28	Pathogen lineage-based genome-wide association study identified CD53 as susceptible locus in tuberculosis. Journal of Human Genetics, 2017, 62, 1015-1022.	2.3	45
29	Evidence for Host-Bacterial Co-evolution via Genome Sequence Analysis of 480 Thai Mycobacterium tuberculosis Lineage 1 Isolates. Scientific Reports, 2018, 8, 11597.	3.3	44
30	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, 533-537.	2.3	41
31	Association of Cw11 in Japanese patients with psoriasis vulgaris. Tissue Antigens, 1990, 36, 241-242.	1.0	40
32	Appropriate data cleaning methods for genome-wide association study. Journal of Human Genetics, 2008, 53, 886-893.	2.3	40
33	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.	2.5	40
34	Genetics of narcolepsy. Human Genome Variation, 2019, 6, 4.	0.7	40
35	Understanding of HLA-conferred susceptibility to chronic hepatitis B infection requires HLA genotyping-based association analysis. Scientific Reports, 2016, 6, 24767.	3.3	39
36	Common risk variants in NPHS1 and TNFSF15 are associated with childhood steroid-sensitive nephrotic syndrome. Kidney International, 2020, 98, 1308-1322.	5.2	39

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37	Digenic mutations in ALDH2 and ADH5 impair formaldehyde clearance and cause a multisystem disorder, AMeD syndrome. Science Advances, 2020, 6, .	10.3	39
38	Founder-haplotype analysis in Fukuyama-type congenital muscular dystrophy (FCMD). Human Genetics, 1998, 103, 323-327.	3.8	38
39	A polymorphism in CCR1/CCR3 is associated with narcolepsy. Brain, Behavior, and Immunity, 2015, 49, 148-155.	4.1	38
40	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.	3.3	38
41	Possible association of human leucocyte antigen DR1 with delayed sleep phase syndrome. Psychiatry and Clinical Neurosciences, 1999, 53, 527-529.	1.8	37
42	HLA and Human Mate Choice. Tests on Japanese Couples.. Anthropological Science, 2000, 108, 199-214.	0.4	37
43	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.	3.8	36
44	Analysis of Human Leukocyte Antigenâ€G Polymorphism Including Intron 4 in Japanese Couples with Habitual Abortion. American Journal of Reproductive Immunology, 1999, 41, 159-163.	1.2	34
45	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.	2.3	34
46	High-density Association Mapping and Interaction Analysis of PLA2R1 and HLA Regions with Idiopathic Membranous Nephropathy in Japanese. Scientific Reports, 2016, 6, 38189.	3.3	34
47	Association and interaction analyses of NRG1 and ERBB4 genes with schizophrenia in a Japanese population. Journal of Human Genetics, 2008, 53, 929-935.	2.3	33
48	Human leukocyte antigen variants and risk of hepatocellular carcinoma modified by hepatitis C virus genotypes: A genomeâ€wide association study. Hepatology, 2018, 67, 651-661.	7.3	32
49	NAT2 ultra-slow acetylator and risk of anti-tuberculosis drug-induced liver injury. Pharmacogenetics and Genomics, 2018, 28, 167-176.	1.5	32
50	Power of genome-wide linkage disequilibrium testing by using microsatellite markers. Journal of Human Genetics, 2003, 48, 487-491.	2.3	31
51	Genome-Wide Association Study Confirming a Strong Effect of HLA and Identifying Variants inCSAD/lnc-ITGB7-1on Chromosome 12q13.13 Associated With Susceptibility to Fulminant Type 1 Diabetes. Diabetes, 2019, 68, 665-675.	0.6	31
52	The First Pilot Genome-Wide Gene-Environment Study of Depression in the Japanese Population. PLoS ONE, 2016, 11, e0160823.	2.5	30
53	Phenome-wide association study maps new diseases to the human major histocompatibility complex region. Journal of Medical Genetics, 2016, 53, 681-689.	3.2	29
54	Development of a prediction system for anti-tuberculosis drug-induced liver injury in Japanese patients. Human Genome Variation, 2016, 3, 16014.	0.7	29

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55	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.	4.4	29
56	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.	2.5	29
57	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.	3.3	29
58	HLA Class I Analysis Provides Insight Into the Genetic and Epigenetic Background of Immune Evasion in Colorectal Cancer With High Microsatellite Instability. Gastroenterology, 2022, 162, 799-812.	1.3	28
59	Profiling of genes expressed in human monocytes and monocyte-derived dendritic cells using cDNA expression array. British Journal of Haematology, 2001, 114, 191-197.	2.5	27
60	New susceptibility variants to narcolepsy identified in HLA class II region. Human Molecular Genetics, 2015, 24, 891-898.	2.9	27
61	Mutations in rrs , rpsL and gidB in streptomycin-resistant Mycobacterium tuberculosis isolates from Thailand. Journal of Global Antimicrobial Resistance, 2016, 4, 5-10.	2.2	27
62	Identification of the functional variant driving ORMDL3 and GSDMB expression in human chromosome 17q12-21 in primary biliary cholangitis. Scientific Reports, 2017, 7, 2904.	3.3	27
63	X Chromosome Contribution to the Genetic Architecture of Primary Biliary Cholangitis. Gastroenterology, 2021, 160, 2483-2495.e26.	1.3	27
64	Unique characteristics of the Ainu population in Northern Japan. Journal of Human Genetics, 2015, 60, 565-571.	2.3	26
65	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.	3.3	26
66	Determination of Granulocyte-Specific Antigens on Neutrophil Fcgamma Receptor IIIb by PCR-Preferential Homoduplex Formation Assay, and Gene Frequencies in the Japanese Population. Vox Sanguinis, 1999, 77, 218-222.	1.5	25
67	Association of diffuse panbronchiolitis with microsatellite polymorphism of the human interleukin 8 (IL-8) gene. Journal of Human Genetics, 1999, 44, 169-172.	2.3	25
68	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.	2.3	25
69	Support for an association between HLA-DR1 and schizophrenia in the Japanese population. American Journal of Medical Genetics Part A, 2000, 96, 725-727.	2.4	24
70	Human primary biliary cirrhosis-susceptible allele of rs4979462 enhances TNFSF15 expression by binding NF-1. Human Genetics, 2015, 134, 737-747.	3.8	24
71	Role of <scp>HLA</scp>â€<scp>DP</scp> and <scp>HLA</scp>â€<scp>DQ</scp> on the clearance of hepatitis B virus and the risk of chronic infection in a multiethnic population. Liver International, 2017, 37, 1476-1487.	3.9	23
72	The first genome-wide association study identifying new susceptibility loci for obstetric antiphospholipid syndrome. Journal of Human Genetics, 2017, 62, 831-838.	2.3	23

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73	POGLUT1, the putative effector gene driven by rs2293370 in primary biliary cholangitis susceptibility locus chromosome 3q13.33. Scientific Reports, 2019, 9, 102.	3.3	23
74	Analysis of whole Y-chromosome sequences reveals the Japanese population history in the Jomon period. Scientific Reports, 2019, 9, 8556.	3.3	23
75	A Genome-wide Association Study Identifying RAP1A as a Novel Susceptibility Gene for Crohnâ€™s Disease in Japanese Individuals. Journal of Crohn's and Colitis, 2019, 13, 648-658.	1.3	22
76	Comparative FISH mapping of the ancestral fusion point of human chromosome 2. Chromosome Research, 2000, 8, 727-735.	2.2	21
77	Genetic Diversity and Dynamic Distribution of Mycobacterium tuberculosis Isolates Causing Pulmonary and Extrapulmonary Tuberculosis in Thailand. Journal of Clinical Microbiology, 2014, 52, 4267-4274.	3.9	20
78	Disease susceptibility genes shared by primary biliary cirrhosis and Crohnâ€™s disease in the Japanese population. Journal of Human Genetics, 2015, 60, 525-531.	2.3	20
79	NFKB1 and MANBA Confer Disease Susceptibility to PrimaryÂBiliary Cholangitis via Independent Putative PrimaryÂFunctionalÂVariants. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 515-532.	4.5	20
80	Reply to: "Lack of HIF-2Î± 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-2Î± SNP rs17039192 with knee osteoarthritis". Nature Medicine, 2011, 17, 27-29.	30.7	19
81	HLA-A*02:06 and PTGER3 polymorphism exert additive effects in cold medicine-related Stevensâ€"Johnson syndrome with severe ocular complications. Human Genome Variation, 2015, 2, 15023.	0.7	19
82	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.	0.7	19
83	Amino acid position 37 of HLA-DRÎ²1 affects susceptibility to Crohnâ€™s disease in Asians. Human Molecular Genetics, 2018, 27, 3901-3910.	2.9	19
84	A missense variant in PER2 is associated with delayed sleepâ€"wake phase disorder in a Japanese population. Journal of Human Genetics, 2019, 64, 1219-1225.	2.3	19
85	Genomewide Association Study Confirming the Association of NAT2 with Susceptibility to Antituberculosis Drug-Induced Liver Injury in Thai Patients. Antimicrobial Agents and Chemotherapy, 2019, 63, .	3.2	19
86	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.	2.3	18
87	Glypican-5 Increases Susceptibility to Nephrotic Damage in Diabetic Kidney. American Journal of Pathology, 2015, 185, 1889-1898.	3.8	18
88	Evaluation of polygenic risks for narcolepsy and essential hypersomnia. Journal of Human Genetics, 2016, 61, 873-878.	2.3	18
89	Genome-wide association study using the ethnicity-specific Japonica array: identification of new susceptibility loci for cold medicine-related Stevensâ€"Johnson syndrome with severe ocular complications. Journal of Human Genetics, 2017, 62, 485-489.	2.3	18
90	Homoplastic single nucleotide polymorphisms contributed to phenotypic diversity in Mycobacterium tuberculosis. Scientific Reports, 2020, 10, 8024.	3.3	18

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91	HLA-A26 subtype A pockets accommodate acidic N-termini of ligands. Immunogenetics, 1998, 48, 350-353.	2.4	17
92	Association of HLA class I and II gene polymorphisms with acetaminophen-related Stevensâ€"Johnson syndrome with severe ocular complications in Japanese individuals. Human Genome Variation, 2019, 6, 50.	0.7	17
93	The Origin and Composition of Korean Ethnicity Analyzed by Ancient and Present-Day Genome Sequences. Genome Biology and Evolution, 2020, 12, 553-565.	2.5	17
94	Haplotype analyses with the human leucocyte antigen and tumour necrosis factorâ€alpha genes in narcolepsy families. Psychiatry and Clinical Neurosciences, 2001, 55, 37-39.	1.8	16
95	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.	2.3	16
96	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.	4.8	16
97	Epigenome-wide association study of DNA methylation in narcolepsy: an integrated genetic and epigenetic approach. Sleep, 2018, 41, .	1.1	16
98	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.	3.3	16
99	Integrative genome analysis identified the KANNO blood group antigen as prion protein. Transfusion, 2019, 59, 2429-2435.	1.6	16
100	A high-resolution HLA imputation system for the Taiwanese population: a study of the Taiwan Biobank. Pharmacogenomics Journal, 2020, 20, 695-704.	2.0	16
101	Genome-wide association study in patients with pulmonary Mycobacterium avium complex disease. European Respiratory Journal, 2021, 58, 1902269.	6.7	16
102	A common Japanese haplotype HLAâ€A26â€Cw3â€B61â€DR9â€DQ3 carries HLAâ€B*4002. Tissue Antigens, 1992, 40, 257-260.	1.0	15
103	MHC (Major Histocompatibility Complex)-DRB Genes and Polymorphisms in Common Marmoset. Journal of Molecular Evolution, 2000, 51, 214-222.	1.8	15
104	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.	2.3	15
105	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.	2.5	15
106	Immune-related pathways including HLA-DRB1ˆ—13:02 are associated with panic disorder. Brain, Behavior, and Immunity, 2015, 46, 96-103.	4.1	15
107	Fine-mapping analysis revealed complex pleiotropic effect and tissue-specific regulatory mechanism of TNFSF15 in primary biliary cholangitis, Crohnâ€™s disease and leprosy. Scientific Reports, 2016, 6, 31429.	3.3	15
108	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.	3.3	15

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109	New variations of human SHP-1. Immunogenetics, 1999, 49, 577-579.	2.4	14
110	Negative association of the HLA-DRB1*1502-DQB1*0601 haplotype with human narcolepsy. Immunogenetics, 2001, 52, 299-301.	2.4	13
111	Identification of ITPA on chromosome 20 as a susceptibility gene for young-onset tuberculosis. Human Genome Variation, 2016, 3, 15067.	0.7	13
112	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.	0.7	12
113	Novel rare variations of the oxytocin receptor (OXTR) gene in autism spectrum disorder individuals. Human Genome Variation, 2015, 2, 15024.	0.7	11
114	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.	3.3	11
115	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.	2.4	11
116	Identification of a telomeric boundary of the HLA region with potential for predisposition to human narcolepsy. Immunogenetics, 2000, 52, 12-18.	2.4	10
117	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, 1962-1968.	3.9	10
118	Determination of Granulocyte–Specific Antigens on Neutrophil FcÁ Receptor IIIb by PCR–Preferential Homoduplex Formation Assay, and Gene Frequencies in the Japanese Population. Vox Sanguinis, 1999, 77, 218-222.	1.5	10
119	DNAâ€Based Typing of Human Platelet Antigen Systems by Polymerase Chain Reactionâ€Singleâ€Strand Conformation Polymorphism Method. Vox Sanguinis, 1995, 69, 347-351.	1.5	9
120	Establishment of a method of anonymization of DNA samples in genetic research. Journal of Human Genetics, 2003, 48, 327-330.	2.3	9
121	An epigenome-wide methylation study of healthy individuals with or without depressive symptoms. Journal of Human Genetics, 2018, 63, 319-326.	2.3	9
122	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	9
123	Metabolome analysis using cerebrospinal fluid from narcolepsy type 1 patients. Sleep, 2020, 43, .	1.1	9
124	Genome-Wide Association Study Identifies ZNF354C Variants Associated with Depression from Interferon-Based Therapy for Chronic Hepatitis C. PLoS ONE, 2016, 11, e0164418.	2.5	9
125	Haplotype-specific sequence encoding the protein kinase, interferon-inducible double-stranded RNA-dependent activator in the human leukocyte antigen classï¿½II region. Immunogenetics, 2001, 52, 186-194.	2.4	8
126	Identification of a two-SNP PLA2R1 Haplotype and HLA-DRB1 Alleles as Primary Risk Associations in Idiopathic Membranous Nephropathy. Scientific Reports, 2018, 8, 15576.	3.3	8

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127	NELFCD and CTSZ loci are associated with jaundice-stage progression in primary biliary cholangitis in the Japanese population. Scientific Reports, 2018, 8, 8071.	3.3	8
128	Haplotype-specific PCR for NAT2 diplotyping. Human Genome Variation, 2020, 7, 13.	0.7	8
129	Phasing analysis of lung cancer genomes using a long read sequencer. Nature Communications, 2022, 13, .	12.8	8
130	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.	2.3	7
131	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.	2.5	7
132	Genome-Wide Association Study Reveals Host Genetic Factors for Liver Diseases. Journal of Clinical and Translational Hepatology, 2013, 1, 45-50.	1.4	7
133	HLA-DRB1 polymorphism on Ha'ano island of the Kingdom of Tonga. Anthropological Science, 2006, 114, 193-198.	0.4	7
134	Linkage disequilibrium structure of the 5q31-33 region in a Thai population. Journal of Human Genetics, 2008, 53, 850-856.	2.3	6
135	Genome-wide analysis of CNV (copy number variation) and their associations with narcolepsy in a Japanese population. Journal of Human Genetics, 2014, 59, 235-240.	2.3	6
136	Increased expression and altered localization of cathepsin Z are associated with progression to jaundice stage in primary biliary cholangitis. Scientific Reports, 2018, 8, 11808.	3.3	6
137	MGeND: an integrated database for Japanese clinical and genomic information. Human Genome Variation, 2019, 6, 53.	0.7	6
138	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.	2.3	6
139	A human PSMB11 variant affects thymoproteasome processing and CD8+ T cell production. JCI Insight, 2017, 2, .	5.0	6
140	Narcolepsy susceptibility gene CCR3 modulates sleep-wake patterns in mice. PLoS ONE, 2017, 12, e0187888.	2.5	6
141	Genome-wide association study of idiopathic hypersomnia in a Japanese population. Sleep and Biological Rhythms, 2022, 20, 137-148.	1.0	6
142	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, 271-278.	1.2	5
143	Selecting a contingency table in a population-based association study: allele frequency or positivity?. Journal of Human Genetics, 1999, 44, 246-248.	2.3	5
144	Lessons from Genome-Wide Search for Disease-Related Genes with Special Reference to HLA-Disease Associations. Genes, 2014, 5, 84-96.	2.4	5

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145	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.	3.8	5
146	A variant at 9q34.11 is associated with HLA-DQB1*06:02Ânegative essential hypersomnia. Journal of Human Genetics, 2018, 63, 1259-1267.	2.3	5
147	Genome-wide haplotype association analysis of primary biliary cholangitis risk in Japanese. Scientific Reports, 2018, 8, 7806.	3.3	5
148	Sojourn Times and Substitution Rate at Overdominant and Linked Neutral Loci. Genetics, 2000, 155, 921-927.	2.9	5
149	A rare genetic variant in the cleavage site of prepro-orexin is associated with idiopathic hypersomnia. Npj Genomic Medicine, 2022, 7, 29.	3.8	5
150	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, 279-279.	2.5	4
151	Computer Simulation Analysis Suggests Weak Balancing Selection Operative at theMICALocus. Hereditas, 2000, 133, 25-28.	1.4	4
152	Strong linkage disequilibrium of a HbE variant with the (AT)9(T)5 repeat in the BP1 binding site upstream of the Î²-globin gene in the Thai population. Journal of Human Genetics, 2005, 50, 7-11.	2.3	4
153	Risk factors associated with large clusters of tuberculosis patients determined by whole-genome sequencing in a high-tuberculosis-burden country. Tuberculosis, 2020, 125, 101991.	1.9	4
154	Identification of the novel HLAâ€ÐQB1 allele, HLAâ€ÐQB1*05:03:01:04 , in a Japanese individual. Hla, 2019, 94, 466-468.	0.6	3
155	Mapping of susceptible variants for cold medicine-related Stevensâ€"Johnson syndrome by whole-genome resequencing. Npj Genomic Medicine, 2021, 6, 9.	3.8	3
156	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.	3.8	3
157	An Association Study of HLA with the Kinetics of SARS-CoV-2 Spike Specific IgG Antibody Responses to BNT162b2 mRNA Vaccine. Vaccines, 2022, 10, 563.	4.4	3
158	Characterization of the novel <scp>HLAâ€A</scp> allele, A*24:02:01:111 in a Japanese individual. Hla, 2022, 100, 148-149.	0.6	3
159	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
160	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.	0.0	2
161	Power of association test for detecting minor histocompatibility gene causing graft-versus-host disease following bone barrow transplantation. Journal of Human Genetics, 2003, 48, 502-507.	2.3	2
162	Detection of the novel HLAâ€A allele, HLAâ€A*02:01:01:58, in a Japanese individual. Hla, 2019, 94, 435-436.	0.6	2

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163	Discovery of the novel HLAâ€B allele, HLAâ€B*51:01:01:36 in a Japanese individual. Hla, 2019, 94, 445-447.	0.6	2
164	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.	0.7	2
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