Kazuyoshi Hosomichi

List of Publications by Year
in descending order

139	4,328	117571	123376
papers	citations	34 h-index	61 g-index

142	142	142	6872
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The HLA genomic loci map: expression, interaction, diversity and disease. Journal of Human Genetics, 2009, 54, 15-39.	1.1	640
2	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. Genome Research, 2008, 18, 1100-1111.	2.4	456
3	Next-generation sequencing: impact of exome sequencing in characterizing Mendelian disorders. Journal of Human Genetics, 2012, 57, 621-632.	1.1	177
4	The impact of next-generation sequencing technologies on HLA research. Journal of Human Genetics, 2015, 60, 665-673.	1.1	173
5	Comparative Genomic Analysis of Two Avian (Quail and Chicken) MHC Regions. Journal of Immunology, 2004, 172, 6751-6763.	0.4	145
6	Phase-defined complete sequencing of the HLA genes by next-generation sequencing. BMC Genomics, 2013, 14, 355.	1.2	121
7	Extended Gene Map Reveals Tripartite Motif, C-Type Lectin, and Ig Superfamily Type Genes within a Subregion of the Chicken MHC-B Affecting Infectious Disease. Journal of Immunology, 2007, 178, 7162-7172.	0.4	114
8	Rapid Evolution of Major Histocompatibility Complex Class I Genes in Primates Generates New Disease Alleles in Humans via Hitchhiking Diversity. Genetics, 2006, 173, 1555-1570.	1.2	100
9	Gene Expression Profiling Reveals Distinct Molecular Signatures Associated With the Rupture of Intracranial Aneurysm. Stroke, 2014, 45, 2239-2245.	1.0	100
10	A new genotype of bovine leukemia virus in South America identified by NGS-based whole genome sequencing and molecular evolutionary genetic analysis. Retrovirology, 2016, 13, 4.	0.9	88
11	Contribution of Mutation, Recombination, and Gene Conversion to Chicken Mhc-B Haplotype Diversity. Journal of Immunology, 2008, 181, 3393-3399.	0.4	86
12	Oligogenic familial hypercholesterolemia, LDL cholesterol, and coronary artery disease. Journal of Clinical Lipidology, 2018, 12, 1436-1444.	0.6	81
13	Genetic and phenotypic landscape of the major histocompatibilty complex region in the Japanese population. Nature Genetics, 2019, 51, 470-480.	9.4	75
14	CRISPR/Cas9-mediated gene knockout in the mouse brain using in utero electroporation. Scientific Reports, 2016, 6, 20611.	1.6	73
15	Genome-wide association study revealed novel loci which aggravate asymptomatic hyperuricaemia into gout. Annals of the Rheumatic Diseases, 2019, 78, 1430-1437.	0.5	73
16	Identification of an HLA class I allele closely involved in the autoantigen presentation in acquired aplastic anemia. Blood, 2017, 129, 2908-2916.	0.6	71
17	Folding of the Cerebral Cortex Requires Cdk5 in Upper-Layer Neurons in Gyrencephalic Mammals. Cell Reports, 2017, 20, 2131-2143.	2.9	62
18	A partial nuclear genome of the Jomons who lived 3000 years ago in Fukushima, Japan. Journal of Human Genetics, 2017, 62, 213-221.	1.1	58

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19	Late Jomon male and female genome sequences from the Funadomari site in Hokkaido, Japan. Anthropological Science, 2019, 127, 83-108.	0.2	58
20	The major histocompatibility complex (Mhc) class IIB region has greater genomic structural flexibility and diversity in the quail than the chicken. BMC Genomics, 2006, 7, 322.	1.2	54
21	A third broad lineage of major histocompatibility complex (MHC) class I in teleost fish; MHC class II linkage and processed genes. Immunogenetics, 2007, 59, 305-321.	1.2	52
22	BG1 has a major role in MHC-linked resistance to malignant lymphoma in the chicken. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 16740-16745.	3.3	52
23	Exome resequencing combined with linkage analysis identifies novel PTH1R variants in primary failure of tooth eruption in Japanese. Journal of Bone and Mineral Research, 2011, 26, 1655-1661.	3.1	52
24	A homozygous SFTPA1 mutation drives necroptosis of type II alveolar epithelial cells in patients with idiopathic pulmonary fibrosis. Journal of Experimental Medicine, 2019, 216, 2724-2735.	4.2	49
25	Comprehensive genetic testing approach for major inherited kidney diseases, using next-generation sequencing with a custom panel. Clinical and Experimental Nephrology, 2017, 21, 63-75.	0.7	47
26	Multiple common and rare variants of ABCG2 cause gout. RMD Open, 2017, 3, e000464.	1.8	46
27	A BAC-based contig map of the cynomolgus macaque (Macaca fascicularis) major histocompatibility complex genomic region. Genomics, 2007, 89, 402-412.	1.3	45
28	Exome sequencing identifies novel rheumatoid arthritis-susceptible variants in the BTNL2. Journal of Human Genetics, 2013, 58, 210-215.	1.1	43
29	MHC class I A loci polymorphism and diversity in three Southeast Asian populations of cynomolgus macaque. Immunogenetics, 2009, 61, 635-648.	1.2	40
30	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. PLoS Genetics, 2016, 12, e1005893.	1.5	40
31	Comprehensive microbiome analysis of tonsillar crypts in IgA nephropathy. Nephrology Dialysis Transplantation, 2017, 32, gfw343.	0.4	40
32	Comparative genomics of the poultry major histocompatibility complex. Animal Science Journal, 2006, 77, 151-162.	0.6	38
33	Primordial Linkage ofÎ²2-Microglobulinto the MHC. Journal of Immunology, 2011, 186, 3563-3571.	0.4	37
34	TRIM39 and RNF39 are associated with BehÃ§etâ€™s disease independently of HLA-Bâˆ—51 and -Aâˆ—26. Biochemical and Biophysical Research Communications, 2010, 401, 533-537.	1.0	36
35	Novel cynomolgus macaque MHC-DPB1 polymorphisms in three South-East Asian populations*. Tissue Antigens, 2006, 67, 297-306.	1.0	32
36	Detection of Ancestry Informative HLA Alleles Confirms the Admixed Origins of Japanese Population. PLoS ONE, 2013, 8, e60793.	1.1	31

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37	Nutritional and hormonal regulation of uncoupling protein 2. IUBMB Life, 2009, 61, 1123-1131.	1.5	29
38	A Bead-based Normalization for Uniform Sequencing depth (BeNUS) protocol for multi-samples sequencing exemplified by HLA-B. BMC Genomics, 2014, 15, 645.	1.2	29
39	Paradoxical development of polymyositis-like autoimmunity through augmented expression of autoimmune regulator (AIRE). Journal of Autoimmunity, 2018, 86, 75-92.	3.0	26
40	Dysfunctional missense variant of OAT10/SLC22A13 decreases gout risk and serum uric acid levels. Annals of the Rheumatic Diseases, 2020, 79, 164-166.	0.5	26
41	A nonsynonymous variant of IL1A is associated with endometriosis in Japanese population. Journal of Human Genetics, 2013, 58, 517-520.	1.1	25
42	Subtype-specific gout susceptibility loci and enrichment of selection pressure on ABCG2 and ALDH2 identified by subtype genome-wide meta-analyses of clinically defined gout patients. Annals of the Rheumatic Diseases, 2020, 79, 657-665.	0.5	24
43	Structure and evolution of the filaggrin gene repeated region in primates. BMC Evolutionary Biology, 2017, 17, 10.	3.2	23
44	Next-generation sequencing identifies contribution of both class I and II HLA genes on susceptibility of multiple sclerosis in Japanese. Journal of Neuroinflammation, 2019, 16, 162.	3.1	22
45	HLA loci predisposing to immune TTP in Japanese: potential role of the shared ADAMTS13 peptide bound to different HLA-DR. Blood, 2020, 135, 2413-2419.	0.6	22
46	Comparative genome analysis of the major histocompatibility complex (MHC) class I B/C segments in primates elucidated by genomic sequencing in common marmoset (Callithrix jacchus). Immunogenetics, 2011, 63, 485-499.	1.2	21
47	Aggregation of rare/low-frequency variants of the mitochondria respiratory chain-related proteins in rheumatoid arthritis patients. Journal of Human Genetics, 2015, 60, 449-454.	1.1	21
48	Germline Variants of Prostate Cancer in Japanese Families. PLoS ONE, 2016, 11, e0164233.	1.1	21
49	Comprehensive genetic exploration of selective tooth agenesis of mandibular incisors by exome sequencing. Human Genome Variation, 2017, 4, 17005.	0.4	20
50	Sustained clonal hematopoiesis by HLA-lacking hematopoietic stem cells without driver mutations in aplastic anemia. Blood Advances, 2018, 2, 1000-1012.	2.5	20
51	A catalog of the pathogenic mutations of LDL receptor gene in Japanese familial hypercholesterolemia. Journal of Clinical Lipidology, 2020, 14, 346-351.e9.	0.6	20
52	Silver Nanoscale Hexagonal Column Chips for Detecting Cell-free DNA and Circulating Nucleosomes in Cancer Patients. Scientific Reports, 2015, 5, 10455.	1.6	19
53	Alopecia areata susceptibility variant in MHC region impacts expressions of genes contributing to hair keratinization and is involved in hair loss. EBioMedicine, 2020, 57, 102810.	2.7	19
54	Identification of heat shock protein 70 genes HSPA2, HSPA5 and HSPA8 from the Japanese quail, Coturnix japonica. Animal Science Journal, 2008, 79, 171-181.	0.6	17

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55	Molecular Characterization of an Intact p53 Pathway Subtype in High-Grade Serous Ovarian Cancer. PLoS ONE, 2014, 9, e114491.	1.1	17
56	Rapid and cost-effective high-throughput sequencing for identification of germline mutations of BRCA1 and BRCA2. Journal of Human Genetics, 2017, 62, 561-567.	1.1	17
57	Localized astrogenesis regulates gyrification of the cerebral cortex. Science Advances, 2022, 8, eabi5209.	4.7	17
58	A frequent nonsense mutation in exon 1 across certain HLA-A and -B alleles in leukocytes of patients with acquired aplastic anemia. Haematologica, 2021, 106, 1581-1590.	1.7	15
59	Deficiency of the splicing factor RBM10 limits EGFR inhibitor response in EGFR-mutant lung cancer. Journal of Clinical Investigation, 2022, 132, .	3.9	15
60	MHC classï¿½IIB gene sequences and expression in quails (Coturnix japonica) selected for high and low antibody responses. Immunogenetics, 2004, 56, 280-91.	1.2	14
61	Human Endogenous Retrovirus (HERVK9) Structural Polymorphism With Haplotypic HLA-A Allelic Associations. Genetics, 2008, 180, 445-457.	1.2	14
62	HLA-DPB1*04:01 allele is associated with non-obstructive azoospermia in Japanese patients. Human Genetics, 2013, 132, 1405-1411.	1.8	14
63	Immune-Mediated Hematopoietic Failure after Allogeneic Hematopoietic Stem Cell Transplantation: A Common Cause of Late Graft Failure in Patients with Complete Donor Chimerism. Biology of Blood and Marrow Transplantation, 2018, 24, 43-49.	2.0	14
64	Evolutionary Relations of Hexanchiformes Deep-Sea Sharks Elucidated by Whole Mitochondrial Genome Sequences. BioMed Research International, 2013, 2013, 1-11.	0.9	12
65	Aire Controls Heterogeneity of Medullary Thymic Epithelial Cells for the Expression of Self-Antigens. Journal of Immunology, 2022, 208, 303-320.	0.4	12
66	Whole-exome sequencing analysis of supernumerary teeth occurrence in Japanese individuals. Human Genome Variation, 2017, 4, 16046.	0.4	11
67	The ATF6Î²-calreticulin axis promotes neuronal survival under endoplasmic reticulum stress and excitotoxicity. Scientific Reports, 2021, 11, 13086.	1.6	11
68	First Japanese Family With PDX1-MODY (MODY4): A Novel PDX1 Frameshift Mutation, Clinical Characteristics, and Implications. Journal of the Endocrine Society, 2022, 6, bvab159.	0.1	11
69	Escape hematopoiesis by HLA-B5401-lacking hematopoietic stem progenitor cells in men with acquired aplastic anemia. Haematologica, 2019, 104, e447-e450.	1.7	10
70	MCPIP1 reduces HBV-RNA by targeting its epsilon structure. Scientific Reports, 2020, 10, 20763.	1.6	10
71	HLA class I alleleâ€“lacking leukocytes predict rare clonal evolution to MDS/AML in patients with acquired aplastic anemia. Blood, 2021, 137, 3576-3580.	0.6	10
72	Possible Association between Dysfunction of Vitamin D Binding Protein (GC Globulin) and Migraine Attacks. PLoS ONE, 2014, 9, e105319.	1.1	9

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73	A de novo mutation of the LDL receptor gene as the cause of familial hypercholesterolemia identified using whole exome sequencing. Clinica Chimica Acta, 2016, 453, 194-196.	0.5	9
74	Tissue-specific autoimmunity controlled by Aire in thymic and peripheral tolerance mechanisms. International Immunology, 2020, 32, 117-131.	1.8	9
75	Polygenic risk scores for low-density lipoprotein cholesterol and familial hypercholesterolemia. Journal of Human Genetics, 2021, 66, 1079-1087.	1.1	9
76	Basic characterization of 90 kDa heat shock protein genes HSP90AA1, HSP90AB1, HSP90B1 and TRAP1 expressed in Japanese quail (Coturnix japonica). Animal Science Journal, 2010, 81, 513-518.	0.6	8
77	Exploration of genetic factors determining cleft side in a pair of monozygotic twins with mirror-image cleft lip and palate using whole-genome sequencing and comparison of craniofacial morphology. Archives of Oral Biology, 2018, 96, 33-38.	0.8	8
78	Identification of cDNA for the HSPA2, HSPA5 and HSPA8 orthologs of the heat shock protein 70 family from guinea fowl (Numida meleagris). Animal Science Journal, 2005, 76, 519-524.	0.6	7
79	Genetic and family structure in a group of 165 common bottlenose dolphins caught off the Japanese coast. Marine Mammal Science, 2013, 29, 474-496.	0.9	7
80	High Order Formation and Evolution of Hornerin in Primates. Genome Biology and Evolution, 2018, 10, 3167-3175.	1.1	7
81	Identification of candidate PAX2-regulated genes implicated in human kidney development. Scientific Reports, 2021, 11, 9123.	1.6	7
82	Primary analysis of <scp>DNA</scp> polymorphisms in the <scp>TRIM</scp> region (<scp>MHC</scp> subregion) of the <scp>J</scp>apanese quail, <scp>C</scp>oturnix japonica. Animal Science Journal, 2013, 84, 90-96.	0.6	6
83	Aire Controls in Trans the Production of Medullary Thymic Epithelial Cells Expressing Ly-6C/Ly-6G. Journal of Immunology, 2018, 201, 3244-3257.	0.4	6
84	Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. Cell Genomics, 2022, 2, 100101.	3.0	6
85	AMBRA1 is involved in T cell receptor-mediated metabolic reprogramming through an ATG7-independent pathway. Biochemical and Biophysical Research Communications, 2017, 491, 1098-1104.	1.0	5
86	Wholeâ€genome sequencing in a pair of monozygotic twins with discordant cleft lip and palate subtypes. Oral Diseases, 2018, 24, 1303-1309.	1.5	5
87	A Targeted Genetic Association Study of the Rare Type of Osteomyelitis. Journal of Dental Research, 2020, 99, 271-276.	2.5	5
88	A novel RFX6 heterozygous mutation (p.R652X) in maturityâ€onset diabetes mellitus: A case report. Journal of Diabetes Investigation, 2021, 12, 1914-1918.	1.1	5
89	NOTCH alteration in EGFR-mutated lung adenocarcinoma leads to histological small-cell carcinoma transformation under EGFR-TKI treatment. Translational Lung Cancer Research, 2021, 10, 4161-4173.	1.3	5
90	No evidence of bovine leukemia virus proviral DNA and antibodies in human specimens from Japan. Retrovirology, 2022, 19, 7.	0.9	5

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91	HLA-A allele associations with viral MER9-LTR nucleotide sequences at two distinct loci within the MHC alpha block. Immunogenetics, 2009, 61, 257-270.	1.2	4
92	Next-generation sequencing analysis identifies genomic alterations in pathological morphologies: A case of pulmonary carcinosarcoma harboring EGFR mutations. Lung Cancer, 2018, 122, 146-150.	0.9	4
93	HLA-B*39:01:01 is a novel risk factor for antithyroid drug-induced agranulocytosis in Japanese population. Pharmacogenomics Journal, 2021, 21, 94-101.	0.9	4
94	Allelic and haplotypic HLA diversity in indigenous Malaysian populations explored using Next Generation Sequencing. Human Immunology, 2022, 83, 17-26.	1.2	4
95	Dysbiotic gut microbiota in pancreatic cancer patients form correlation networks with the oral microbiota and prognostic factors. American Journal of Cancer Research, 2021, 11, 3163-3175.	1.4	4
96	Predictors associated with a better response to the Japanese aluminumâ€free hepatitis A vaccine, Aimmugen^{Â®}, for people living with HIV. Hepatology Research, 2022, 52, 227-234.	1.8	4
97	Biased expression of mutant alleles in cancer-related genes in esophageal squamous cell carcinoma. Esophagus, 2022, 19, 294-302.	1.0	4
98	Comprehensive Comparison of Novel Bovine Leukemia Virus (BLV) Integration Sites between B-Cell Lymphoma Lines BLSC-KU1 and BLSC-KU17 Using the Viral DNA Capture High-Throughput Sequencing Method. Viruses, 2022, 14, 995.	1.5	4
99	Exact break point of a 50Âkb deletion 8Âkb centromeric of the HLA-A locus with HLA-A*24:02: the same deletion observed in other A*24 alleles and A*23:01 allele. Immunogenetics, 2011, 63, 467-474.	1.2	3
100	Genome-wide linkage and exome analyses identify variants of HMCN1for splenic epidermoid cyst. BMC Medical Genetics, 2014, 15, 115.	2.1	3
101	Correction of the <scp>HLAâ€DQB1</scp>*04:01:01 sequence at position 79 in exon 1. Hla, 2016, 87, 57-58.	0.4	3
102	RXRB Is an MHC-Encoded Susceptibility Gene Associated with Anti-Topoisomerase IÂAntibody-Positive Systemic Sclerosis. Journal of Investigative Dermatology, 2017, 137, 1878-1886.	0.3	3
103	Identification of a novel variant of the RET proto-oncogene in a novel family with Hirschsprungâ€™s disease. Pediatric Surgery International, 2017, 33, 1041-1046.	0.6	3
104	No novel, high penetrant gene might remain to be found in Japanese patients with unknown MODY. Journal of Human Genetics, 2018, 63, 821-829.	1.1	3
105	Molecular features of tumor-derived genetic alterations in circulating cell-free DNA in virtue of autopsy analysis. Scientific Reports, 2021, 11, 8398.	1.6	3
106	Somatic mutations in oral squamous cell carcinomas in 98 Japanese patients and their clinical implications. Cancer Treatment and Research Communications, 2021, 29, 100456.	0.7	3
107	RHEB is a potential therapeutic target in T cell acute lymphoblastic leukemia. Biochemical and Biophysical Research Communications, 2022, 621, 74-79.	1.0	3
108	Development of polymorphic Genetic Markers in the Quail Mhc (Coja) Region. Major Histocompatibility Complex, 2005, 11, 241-251.	0.2	2

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109	Identification of novel exonic mobile element insertions in epithelial ovarian cancers. Human Genome Variation, 2015, 2, 15030.	0.4	2
110	New PCNT candidate missense variant in a patient with oral and maxillofacial osteodysplasia: a case report. BMC Medical Genetics, 2019, 20, 126.	2.1	2
111	Characterization of LILRB3 and LILRA6 allelic variants in the Japanese population. Journal of Human Genetics, 2021, 66, 739-748.	1.1	2
112	Whole-Genome Sequencing of a 900-Year-Old Human Skeleton Supports Two Past Migration Events from the Russian Far East to Northern Japan. Genome Biology and Evolution, 2021, 13, .	1.1	2
113	Effect of Î²3â€adrenergic receptor gene polymorphism andÂlifestyle on overweight Japanese rural residents: AÂcrossâ€sectional study. Obesity Science and Practice, 2022, 8, 199-207.	1.0	2
114	Effects of functional variants of vitamin C transporter genes on apolipoprotein E E4-associated risk of cognitive decline: The Nakajima study. PLoS ONE, 2021, 16, e0259663.	1.1	2
115	Familial idiopathic basal ganglia calcification with a heterozygous missense variant (c.<scp>902C</scp>>T/p.<scp>P307L</scp>) in <scp>SLC20A2</scp> showing widespread cerebrovascular lesions. Neuropathology, 2022, 42, 126-133.	0.7	2
116	Association between Vitamin Intake and Chronic Kidney Disease According to a Variant Located Upstream of the PTGS1 Gene: A Cross-Sectional Analysis of Shika Study. Nutrients, 2022, 14, 2082.	1.7	2
117	Contribution of mutation, recombination, and gene conversion to chicken Mhc-B haplotype diversity. Journal of Immunology, 2010, 184, 5415-5415.	0.4	1
118	Orthognathic surgery induces genomewide changes longitudinally in DNA methylation in saliva. Oral Diseases, 2019, 25, 508-514.	1.5	1
119	A toddler with phylloid-type pigmentary mosaicism and ambiguous genitalia resulting from trisomy 14 induced by a der(Y)t(Y;14). Human Genome Variation, 2020, 7, 28.	0.4	1
120	Analysis of HLA gene polymorphisms in East Africans reveals evidence of gene flow in two Semitic populations from Sudan. European Journal of Human Genetics, 2021, 29, 1259-1271.	1.4	1
121	Relationships among the Î²3-adrenargic receptor gene Trp64Arg polymorphism, hypertension, and insulin resistance in a Japanese population. PLoS ONE, 2021, 16, e0255444.	1.1	1
122	Sequence analysis of functional Mhc class II Î² genes on quails of high- and low-IgG strains, developed by line breeding based on serum IgG concentration. Journal of Animal Genetics, 2004, 32, 3-10.	0.1	1
123	Glucokinase-maturity onset diabetes mellitus in the young suggested by factory-calibrated glucose monitoring data: a case report. Endocrine Journal, 2022, 69, 473-477.	0.7	1
124	Association Between Serum 25-Hydroxyvitamin D Concentrations, CDX2 Polymorphism in Promoter Region of Vitamin D Receptor Gene, and Chronic Pain in Rural Japanese Residents. Journal of Pain Research, 0, Volume 15, 1475-1485.	0.8	1
125	Correction for Goto et al., BG1 has a major role in MHC-linked resistance to malignant lymphoma in the chicken. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8041-8041.	3.3	0
126	The impact of next-generation sequencing technologies on MHC research. Journal of Animal Genetics, 2015, 43, 25-32.	0.5	0

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127	3102Comprehensive genotyping and phenotyping in patients with severe hypercholesterolemia. European Heart Journal, 2017, 38, .	1.0	0
128	3073Leveraging transcriptome sequencing for detecting novel disease-related pathways using human cardiac sarcoidosis myocardium biopsies. European Heart Journal, 2019, 40, .	1.0	0
129	Deciphering Novel Disease Mechanism in Cardiomyopathy by Transcriptome Sequencing. Impact, 2019, 2019, 10-12.	0.0	0
130	A case of MODY5-like manifestations without mutations or deletions in coding and minimal promoter regions of the HNF1B gene. Endocrine Journal, 2020, 67, 981-988.	0.7	0
131	Positional effects of polymorphisms in probe-target sequences on genoplot images of oligonucleotide microarrays. Genetics and Molecular Research, 2010, 9, 524-531.	0.3	0
132	The Admixed Origin of Japanese Population from HLA Alleles. Major Histocompatibility Complex, 2014, 21, 37-44.	0.2	0
133	Identification of an HLA Class I Allele Closely Involved in the Pathogenesis of Acquired Aplastic Anemia. Blood, 2016, 128, 729-729.	0.6	0
134	HLA Class I Allele-Lacking Hematopoietic Stem/Progenitor Cells Support Long-Term Clonal Hematopoiesis without Oncogenic Driver Mutations in Acquired Aplastic Anemia. Blood, 2016, 128, 3894-3894.	0.6	0
135	Loss-of-Function Mutations in HLA-Class I Alleles in Acquire Aplastic Anemia: Evidence for the Involvement of Limited Class I Alleles in the Auto-Antigen Presentation of Aplastic Anemia. Blood, 2018, 132, 2584-2584.	0.6	0
136	A Common HLA Allelic Mutation of exon1 in Leukocytes Defines Class I Alleles Responsible for Autoantigen Presentation of Acquired Aplastic Anemia. Blood, 2019, 134, 1215-1215.	0.6	0
137	Minor GPI(-) Granulocyte Populations in Patients with Acquired Aplastic Anemia and Healthy Individuals Are Derived from a Few Piga-Mutated Hematopoietic Stem Progenitor Cells. Blood, 2021, 138, 2181-2181.	0.6	0
138	Clonal Hematopoiesis By HLA Class I Allele-Lacking Hematopoietic Stem Cells and Concomitant Aberrant Stem Cells Is Rarely Associated with Clonal Evolution to Secondary Myelodysplastic Syndrome and Acute Myeloid Leukemia in Patients with Acquired Aplastic Anemia. Blood, 2020, 136, 1-2.	0.6	0
139	Immune-mediated thrombotic thrombocytopenic purpura and HLA. Major Histocompatibility Complex, 2022, 29, 42-51.	0.2	0