Chiea-Chuen Khor

List of Publications by Year
in descending order

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206 papers	17,045 citations	16411 64 h-index	19136 118 g-index
215 all docs	215 docs citations	215 times ranked	27341 citing authors

#	Article	IF	Citations
1	LoFreq: a sequence-quality aware, ultra-sensitive variant caller for uncovering cell-population heterogeneity from high-throughput sequencing datasets. Nucleic Acids Research, 2012, 40, 11189-11201.	6.5	1,074
2	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
3	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
4	High-density genetic mapping identifies new susceptibility loci for rheumatoid arthritis. Nature Genetics, 2012, 44, 1336-1340.	9.4	558
5	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
6	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	9.4	481
7	Genome-wide meta-analyses of multiancestry cohorts identify multiple new susceptibility loci for refractive error and myopia. Nature Genetics, 2013, 45, 314-318.	9.4	398
8	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
9	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	3.9	341
10	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
11	Genome-wide association study identifies FCGR2A as a susceptibility locus for Kawasaki disease. Nature Genetics, 2011, 43, 1241-1246.	9.4	297
12	Trans-ancestry genome-wide association study identifies 12 genetic loci influencing blood pressure and implicates a role for DNA methylation. Nature Genetics, 2015, 47, 1282-1293.	9.4	294
13	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	13.7	282
14	Genome-wide association study identifies variants in the CFH region associated with host susceptibility to meningococcal disease. Nature Genetics, 2010, 42, 772-776.	9.4	275
15	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. Nature Genetics, 2013, 45, 155-163.	9.4	269
16	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
17	Genome-Wide Expression Profiling Identifies Type 1 Interferon Response Pathways in Active Tuberculosis. PLoS ONE, 2012, 7, e45839.	1.1	213
18	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. Nature Genetics, 2014, 46, 1126-1130.	9.4	212

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19	Genome-wide association analysis identifies TXNRD2, ATXN2 and FOXC1 as susceptibility loci for primary open-angle glaucoma. Nature Genetics, 2016, 48, 189-194.	9.4	211
20	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2012, 44, 1142-1146.	9.4	196
21	Genome-wide meta-analysis identifies 127 open-angle glaucoma loci with consistent effect across ancestries. Nature Communications, 2021, 12, 1258.	5.8	196
22	Genome-wide association study identifies susceptibility loci for dengue shock syndrome at MICB and PLCE1. Nature Genetics, 2011, 43, 1139-1141.	9.4	181
23	Frequent transmission of the Mycobacterium tuberculosis Beijing lineage and positive selection for the EsxW Beijing variant in Vietnam. Nature Genetics, 2018, 50, 849-856.	9.4	167
24	Common variants near ABCA1 and in PMM2 are associated with primary open-angle glaucoma. Nature Genetics, 2014, 46, 1115-1119.	9.4	160
25	Identification of two new loci at IL23R and RAB32 that influence susceptibility to leprosy. Nature Genetics, 2011, 43, 1247-1251.	9.4	159
26	Cloning and variation of ground state intestinal stem cells. Nature, 2015, 522, 173-178.	13.7	156
27	Deep Whole-Genome Sequencing of 100 Southeast Asian Malays. American Journal of Human Genetics, 2013, 92, 52-66.	2.6	153
28	New loci and coding variants confer risk for age-related macular degeneration in East Asians. Nature Communications, 2015, 6, 6063.	5.8	147
29	Genome-wide association study identifies five new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2016, 48, 556-562.	9.4	147
30	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Human Molecular Genetics, 2011, 20, 649-658.	1.4	140
31	Nine Loci for Ocular Axial Length Identified through Genome-wide Association Studies, Including Shared Loci with Refractive Error. American Journal of Human Genetics, 2013, 93, 264-277.	2.6	139
32	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.	1.4	135
33	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
34	Cartography of opportunistic pathogens and antibiotic resistance genes in a tertiary hospital environment. Nature Medicine, 2020, 26, 941-951.	15.2	130
35	CISHand Susceptibility to Infectious Diseases. New England Journal of Medicine, 2010, 362, 2092-2101.	13.9	129
36	Exome chip meta-analysis identifies novel loci and East Asianâ€“specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	9.4	129

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37	Global gene expression profiling identifies new therapeutic targets in acute Kawasaki disease. Genome Medicine, 2014, 6, 541.	3.6	126
38	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	13.5	126
39	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400.	2.6	123
40	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics.. Human Molecular Genetics, 2017, 26, ddw399.	1.4	120
41	Genome-Wide Association Studies Reveal Genetic Variants in CTNND2 for High Myopia in Singapore Chinese. Ophthalmology, 2011, 118, 368-375.	2.5	118
42	Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115.	13.9	116
43	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	9.4	114
44	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
45	Genome-wide association study identifies seven novel susceptibility loci for primary open-angle glaucoma. Human Molecular Genetics, 2018, 27, 1486-1496.	1.4	111
46	Gene-Age Interactions in Blood Pressure Regulation: A Large-Scale Investigation with the CHARGE, Global BPgen, and ICBP Consortia. American Journal of Human Genetics, 2014, 95, 24-38.	2.6	109
47	Identification of new susceptibility loci for IgA nephropathy in Han Chinese. Nature Communications, 2015, 6, 7270.	5.8	109
48	A common variant near TGFBR3 is associated with primary open angle glaucoma. Human Molecular Genetics, 2015, 24, 3880-3892.	1.4	105
49	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	1.4	105
50	Meta-analysis of geneâ€“environment-wide association scans accounting for education level identifies additional loci for refractive error. Nature Communications, 2016, 7, 11008.	5.8	104
51	A common variant mapping to CACNA1A is associated with susceptibility to exfoliation syndrome. Nature Genetics, 2015, 47, 387-392.	9.4	97
52	Genetic Variants on Chromosome 1q41 Influence Ocular Axial Length and High Myopia. PLoS Genetics, 2012, 8, e1002753.	1.5	95
53	Genome-wide association studies in Asians confirm the involvement of ATOH7 and TGFBR3, and further identify CARD10 as a novel locus influencing optic disc area. Human Molecular Genetics, 2011, 20, 1864-1872.	1.4	91
54	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. Nature Communications, 2014, 5, 4883.	5.8	89

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55	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	5.8	88
56	Variation at HLA-DRB1 is associated with resistance to enteric fever. Nature Genetics, 2014, 46, 1333-1336.	9.4	85
57	CFH and VIPR2 as susceptibility loci in choroidal thickness and pachychoroid disease central serous chorioretinopathy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6261-6266.	3.3	85
58	Genetic risk of extranodal natural killer T-cell lymphoma: a genome-wide association study. Lancet Oncology, The, 2016, 17, 1240-1247.	5.1	84
59	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
60	Genetic variants and cellular stressors associated with exfoliation syndrome modulate promoter activity of a lncRNA within theLOXL1locus. Human Molecular Genetics, 2015, 24, 6552-6563.	1.4	76
61	Metaâ€analysis of Genomeâ€Wide Association Studies Identifies Novel Loci Associated With Optic Disc Morphology. Genetic Epidemiology, 2015, 39, 207-216.	0.6	72
62	Brain-derived neurotrophic factor genetic polymorphism (rs6265) is protective against chemotherapy-associated cognitive impairment in patients with early-stage breast cancer. Neuro-Oncology, 2016, 18, 244-251.	0.6	71
63	Identification of myopia-associated WNT7B polymorphisms provides insights into the mechanism underlying the development of myopia. Nature Communications, 2015, 6, 6689.	5.8	70
64	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 437-445.	1.4	69
65	ABCC5, a Gene That Influences the Anterior Chamber Depth, Is Associated with Primary Angle Closure Glaucoma. PLoS Genetics, 2014, 10, e1004089.	1.5	68
66	A missense variant in FGD6 confers increased risk of polypoidal choroidal vasculopathy. Nature Genetics, 2016, 48, 640-647.	9.4	68
67	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. Human Genetics, 2012, 131, 1467-1480.	1.8	67
68	Transethnic Replication of Association of CTG18.1 Repeat Expansion ofTCF4Gene With Fuchs' Corneal Dystrophy in Chinese Implies Common Causal Variant. , 2014, 55, 7073.		64
69	Loci for human leukocyte telomere length in the Singaporean Chinese population and trans-ethnic genetic studies. Nature Communications, 2019, 10, 2491.	5.8	64
70	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. Human Molecular Genetics, 2013, 22, 2303-2311.	1.4	63
71	Education influences the association between genetic variants and refractive error: a meta-analysis of five Singapore studies. Human Molecular Genetics, 2014, 23, 546-554.	1.4	63
72	Cross-ancestry genome-wide association analysis of corneal thickness strengthens link between complex and Mendelian eye diseases. Nature Communications, 2018, 9, 1864.	5.8	63

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73	Multiple Nonglycemic Genomic Loci Are Newly Associated With Blood Level of Glycated Hemoglobin in East Asians. Diabetes, 2014, 63, 2551-2562.	0.3	61
74	Genome-wide association study identifies ZFHX1B as a susceptibility locus for severe myopia. Human Molecular Genetics, 2013, 22, 5288-5294.	1.4	59
75	Mutational spectrum of Barrettâ€™s stem cells suggests paths to initiation of a precancerous lesion. Nature Communications, 2016, 7, 10380.	5.8	57
76	Pseudoexfoliation syndrome-associated genetic variants affect transcription factor binding and alternative splicing of LOXL1. Nature Communications, 2017, 8, 15466.	5.8	57
77	Genome-wide linkage and association mapping identify susceptibility alleles in ABCC4 for Kawasaki disease. Journal of Medical Genetics, 2011, 48, 467-472.	1.5	56
78	Replication and Meta-Analysis of GWAS Identified Susceptibility Loci in Kawasaki Disease Confirm the Importance of B Lymphoid Tyrosine Kinase (BLK) in Disease Susceptibility. PLoS ONE, 2013, 8, e72037.	1.1	55
79	A genome-wide association study of n-3 and n-6 plasma fatty acids in a Singaporean Chinese population. Genes and Nutrition, 2015, 10, 53.	1.2	53
80	Association ofTCF4Gene Polymorphisms with Fuchs' Corneal Dystrophy in the Chinese. , 2011, 52, 5573.		51
81	Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. Human Molecular Genetics, 2011, 20, 3693-3698.	1.4	51
82	Association of Genetic Variants With Primary Open-Angle Glaucoma Among Individuals With African Ancestry. JAMA - Journal of the American Medical Association, 2019, 322, 1682.	3.8	50
83	Sensitive detection of chromatin-altering polymorphisms reveals autoimmune disease mechanisms. Nature Methods, 2015, 12, 458-464.	9.0	49
84	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
85	Genetic Variation in the SLC8A1 Calcium Signaling Pathway Is Associated With Susceptibility to Kawasaki Disease and Coronary Artery Abnormalities. Circulation: Cardiovascular Genetics, 2016, 9, 559-568.	5.1	45
86	TM4SF20 Ancestral Deletion and Susceptibility to a Pediatric Disorder of Early Language Delay and Cerebral White Matter Hyperintensities. American Journal of Human Genetics, 2013, 93, 197-210.	2.6	43
87	Genome-wide association study of B cell non-Hodgkin lymphoma identifies 3q27 as a susceptibility locus in the Chinese population. Nature Genetics, 2013, 45, 804-807.	9.4	43
88	Insights into the Genetic Structure and Diversity of 38 South Asian Indians from Deep Whole-Genome Sequencing. PLoS Genetics, 2014, 10, e1004377.	1.5	43
89	Natural positive selection and northâ€“south genetic diversity in East Asia. European Journal of Human Genetics, 2012, 20, 102-110.	1.4	42
90	Genome-Wide Meta-Analysis Identifies Three Novel Susceptibility Loci and Reveals Ethnic Heterogeneity of Genetic Susceptibility for IgA Nephropathy. Journal of the American Society of Nephrology: JASN, 2020, 31, 2949-2963.	3.0	42

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91	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	2.6	42
92	ISL1 is a major susceptibility gene for classic bladder exstrophy and a regulator of urinary tract development. Scientific Reports, 2017, 7, 42170.	1.6	41
93	Whole-exome sequencing implicates UBE3D in age-related macular degeneration in East Asian populations. Nature Communications, 2015, 6, 6687.	5.8	40
94	Hostâ€“pathogen interactions revealed by human genome-wide surveys. Trends in Genetics, 2012, 28, 233-243.	2.9	39
95	Establishing multiple omics baselines for three Southeast Asian populations in the Singapore Integrative Omics Study. Nature Communications, 2017, 8, 653.	5.8	39
96	Genome-wide association analyses identify two susceptibility loci for pachychoroid disease central serous chorioretinopathy. Communications Biology, 2019, 2, 468.	2.0	39
97	Genetic Variants of MICB and PLCE1 and Associations with Non-Severe Dengue. PLoS ONE, 2013, 8, e59067.	1.1	39
98	Genome-Wide Meta-Analysis of Five Asian Cohorts Identifies PDGFRA as a Susceptibility Locus for Corneal Astigmatism. PLoS Genetics, 2011, 7, e1002402.	1.5	35
99	Meta-analysis of genome-wide association studies in multiethnic Asians identifies two loci for age-related nuclear cataract. Human Molecular Genetics, 2014, 23, 6119-6128.	1.4	35
100	Association of Common SIX6 Polymorphisms With Peripapillary Retinal Nerve Fiber Layer Thickness: The Singapore Chinese Eye Study. Investigative Ophthalmology and Visual Science, 2015, 56, 478-483.	3.3	35
101	Shared genetic variants for polypoidal choroidal vasculopathy and typical neovascular age-related macular degeneration in East Asians. Journal of Human Genetics, 2017, 62, 1049-1055.	1.1	35
102	Predictive role of NUDT15 variants on thiopurine-induced myelotoxicity in Asian inflammatory bowel disease patients. Pharmacogenomics, 2018, 19, 31-43.	0.6	34
103	Natural resistance to Meningococcal Disease related to CFH loci: Meta-analysis of genome-wide association studies. Scientific Reports, 2016, 6, 35842.	1.6	33
104	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
105	A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633.	1.4	31
106	MMP20 and ARMS2/HTRA1 Are Associated with Neovascular Lesion Size in Age-Related Macular Degeneration. Ophthalmology, 2015, 122, 2295-2302.e2.	2.5	30
107	Disruption of vascular homeostasis in patients with Kawasaki disease: Involvement of vascular endothelial growth factor and angiopoietins. Arthritis and Rheumatism, 2012, 64, 306-315.	6.7	29
108	mcr-1in Multidrug-ResistantblaKPC-2-Producing Clinical Enterobacteriaceae Isolates in Singapore. Antimicrobial Agents and Chemotherapy, 2016, 60, 6435-6437.	1.4	29

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109	Analysis of non-synonymous-coding variants of Parkinson's disease-related pathogenic and susceptibility genes in East Asian populations. Human Molecular Genetics, 2014, 23, 3891-3897.	1.4	28
110	Aggregate Effects of Intraocular Pressure and Cup-to-Disc Ratio Genetic Variants on Glaucoma in a Multiethnic Asian Population. Ophthalmology, 2015, 122, 1149-1157.	2.5	28
111	Targeted next-generation sequencing to diagnose disorders of HDL cholesterol. Journal of Lipid Research, 2015, 56, 1993-2001.	2.0	28
112	Glaucoma Genetics. Asia-Pacific Journal of Ophthalmology, 2016, 5, 256-259.	1.3	28
113	Genome-wide association study identifies a missense variant at APOA5 for coronary artery disease in Multi-Ethnic Cohorts from Southeast Asia. Scientific Reports, 2017, 7, 17921.	1.6	28
114	Pseudoexfoliation syndrome and glaucoma: from genes to disease mechanisms. Current Opinion in Ophthalmology, 2021, 32, 118-128.	1.3	28
115	SgD-CNV, a database for common and rare copy number variants in three Asian populations. Human Mutation, 2011, 32, 1341-1349.	1.1	27
116	Coordinated Genetic Scaling of the Human Eye: Shared Determination of Axial Eye Length and Corneal Curvature. , 2013, 54, 1715.		27
117	Characterizing the genetic differences between two distinct migrant groups from Indo-European and Dravidian speaking populations in India. BMC Genetics, 2014, 15, 86.	2.7	27
118	Pharmacogenetics of UGT1A4, UGT2B7 and UGT2B15 and Their Influence on Tamoxifen Disposition in Asian Breast Cancer Patients. Clinical Pharmacokinetics, 2016, 55, 1239-1250.	1.6	27
119	Characteristics of p.Gln368Ter Myocilin Variant and Influence of Polygenic Risk on Glaucoma Penetrance in the UK Biobank. Ophthalmology, 2021, 128, 1300-1311.	2.5	27
120	Polygenic risk scores for prediction of breast cancer risk in Asian populations. Genetics in Medicine, 2022, 24, 586-600.	1.1	27
121	Coding Variants at Hexa-allelic Amino Acid 13 of HLA-DRB1 Explain Independent SNP Associations with Follicular Lymphoma Risk. American Journal of Human Genetics, 2013, 93, 167-172.	2.6	26
122	Different Hereditary Contribution of theCFHGene Between Polypoidal Choroidal Vasculopathy and Age-Related Macular Degeneration in Chinese Han People. , 2014, 55, 2534.		25
123	The genetic variants underlying breast cancer treatment-induced chronic and late toxicities: A systematic review. Cancer Treatment Reviews, 2014, 40, 1199-1214.	3.4	25
124	Genetics of Exfoliation Syndrome. Journal of Glaucoma, 2018, 27, S12-S14.	0.8	25
125	A Study Assessing the Association of Glycated Hemoglobin A1C (HbA1C) Associated Variants with HbA1C, Chronic Kidney Disease and Diabetic Retinopathy in Populations of Asian Ancestry. PLoS ONE, 2013, 8, e79767.	1.1	24
126	Genome-wide association study for refractive astigmatism reveals genetic co-determination with spherical equivalent refractive error: the CREAM consortium. Human Genetics, 2015, 134, 131-146.	1.8	24

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127	Keratoconus-susceptibility gene identification by corneal thickness genome-wide association study and artificial intelligence IBM Watson. Communications Biology, 2020, 3, 410.	2.0	24
128	Lack of Association Between Primary Angle-Closure Glaucoma Susceptibility Loci and the Ocular Biometric Parameters Anterior Chamber Depth and Axial Length. , 2013, 54, 5824.		23
129	A Novel Splice-Site Mutation in ALS2 Establishes the Diagnosis of Juvenile Amyotrophic Lateral Sclerosis in a Family with Early Onset Anarthria and Generalized Dystonias. PLoS ONE, 2014, 9, e113258.	1.1	22
130	CMPK1 and RBP3 are associated with corneal curvature in Asian populations. Human Molecular Genetics, 2014, 23, 6129-6136.	1.4	22
131	Characterising private and shared signatures of positive selection in 37 Asian populations. European Journal of Human Genetics, 2017, 25, 499-508.	1.4	22
132	Evaluation of Primary Angle-Closure Glaucoma Susceptibility Loci in Patients with Early Stages of Angle-Closure Disease. Ophthalmology, 2018, 125, 664-670.	2.5	22
133	The protective variant rs7173049 at LOXL1 locus impacts on retinoic acid signaling pathway in pseudoexfoliation syndrome. Human Molecular Genetics, 2019, 28, 2531-2548.	1.4	22
134	Multi-trait genome-wide association study identifies new loci associated with optic disc parameters. Communications Biology, 2019, 2, 435.	2.0	22
135	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. Nature Communications, 2020, 11, 3761.	5.8	22
136	A Genetic Variant in TGFBR3-CDC7 Is Associated with Visual Field Progression in Primary Open-Angle Glaucoma Patients fromÂSingapore. Ophthalmology, 2015, 122, 2416-2422.	2.5	20
137	Patient-Based Transcriptome-Wide Analysis Identify Interferon and Ubiquination Pathways as Potential Predictors of Influenza A Disease Severity. PLoS ONE, 2014, 9, e111640.	1.1	19
138	The genetics of angle closure glaucoma. Experimental Eye Research, 2019, 189, 107835.	1.2	19
139	Pharmacogenetics of irinotecan, doxorubicin and docetaxel transporters in Asian and Caucasian cancer patients: a comparative review. Drug Metabolism Reviews, 2016, 48, 502-540.	1.5	18
140	Genetic Studies of Hypertrophic Cardiomyopathy in Singaporeans Identify Variants in TNNI3 and TNNT2 That Are Common in Chinese Patients. Circulation Genomic and Precision Medicine, 2020, 13, 424-434.	1.6	18
141	Genetic loci and prioritization of genes for kidney function decline derived from a meta-analysis of 62 longitudinal genome-wide association studies. Kidney International, 2022, 102, 624-639.	2.6	18
142	Genotypeâ€“Phenotype Correlation Analysis for Three Primary Angle Closure Glaucoma-Associated Genetic Polymorphisms. , 2014, 55, 1143.		17
143	Interaction effects between Paraoxonase 1 variants and cigarette smoking on risk of coronary heart disease in a Singaporean Chinese population. Atherosclerosis, 2015, 240, 40-45.	0.4	17
144	Impact of BMI and waist circumference on epigenome-wide DNA methylation and identification of epigenetic biomarkers in blood: an EWAS in multi-ethnic Asian individuals. Clinical Epigenetics, 2021, 13, 195.	1.8	17

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145	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
146	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051.	5.8	16
147	A homozygousFITM2mutation causes a deafness-dystonia syndrome with motor regression and signs of ichthyosis and sensory neuropathy. DMM Disease Models and Mechanisms, 2017, 10, 105-118.	1.2	16
148	Effect of plasma polyunsaturated fatty acid levels on leukocyte telomere lengths in the Singaporean Chinese population. Nutrition Journal, 2020, 19, 119.	1.5	16
149	Association of Rare CYP39A1 Variants With Exfoliation Syndrome Involving the Anterior Chamber of the Eye. JAMA - Journal of the American Medical Association, 2021, 325, 753.	3.8	16
150	Low frequency variants associated with leukocyte telomere length in the Singapore Chinese population. Communications Biology, 2021, 4, 519.	2.0	15
151	The genetic basis for adult onset glaucoma: Recent advances and future directions. Progress in Retinal and Eye Research, 2022, 90, 101066.	7.3	15
152	TNFRSF10A-LOC389641 rs13278062 But Not REST-C4orf14-POLR2B-IGFBP7 rs1713985 Was Found Associated With Age-Related Macular Degeneration in a Chinese Population. , 2013, 54, 8199.		14
153	A statistical method for region-based meta-analysis of genome-wide association studies in genetically diverse populations. European Journal of Human Genetics, 2012, 20, 469-475.	1.4	13
154	The Contribution of Genetic Architecture to the 10-Year Incidence of Age-Related Macular Degeneration in the Fellow Eye. , 2015, 56, 5353.		13
155	Whole-Genome Sequencing Analysis of Serially Isolated Multi-Drug and Extensively Drug Resistant Mycobacterium tuberculosis from Thai Patients. PLoS ONE, 2016, 11, e0160992.	1.1	13
156	Large-scale genotyping identifies a new locus at 22q13.2 associated with female breast size. Journal of Medical Genetics, 2013, 50, 666-673.	1.5	12
157	Impact of Measurement Error on Testing Genetic Association with Quantitative Traits. PLoS ONE, 2014, 9, e87044.	1.1	12
158	Evaluation of Primary Angle-Closure Glaucoma Susceptibility Loci for Estimating Angle Closure Disease Severity. Ophthalmology, 2021, 128, 403-409.	2.5	12
159	Utility of genetic and non-genetic risk factors in predicting coronary heart disease in Singaporean Chinese. European Journal of Preventive Cardiology, 2017, 24, 153-160.	0.8	11
160	Gene-diet interaction effects on BMI levels in the Singapore Chinese population. Nutrition Journal, 2018, 17, 31.	1.5	11
161	An Evaluation of DNA Methyltransferase 1 (DNMT1) Single Nucleotide Polymorphisms and Chemotherapy-Associated Cognitive Impairment: A Prospective, Longitudinal Study. Scientific Reports, 2019, 9, 14570.	1.6	11
162	NAFLD polygenic risk score and risk of hepatocellular carcinoma in an East Asian population. Hepatology Communications, 2022, 6, 2310-2321.	2.0	11

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163	Strategies for identifying the genetic basis of dyslipidemia: genome-wide association studies vs. the resequencing of extremes. Current Opinion in Lipidology, 2010, 21, 123-127.	1.2	10
164	Combined genotype and haplotype tests for region-based association studies. BMC Genomics, 2013, 14, 569.	1.2	10
165	ADP ribosyl-cyclases (CD38 / CD157), social skills and friendship. Psychoneuroendocrinology, 2017, 78, 185-192.	1.3	10
166	Integration of Genetic and Biometric Risk Factors for Detection of Primary Angle Closure Glaucoma. American Journal of Ophthalmology, 2019, 208, 160-165.	1.7	10
167	An intronic FTO variant rs16952570 confers protection against thiopurine-induced myelotoxicities in multiethnic Asian IBD patients. Pharmacogenomics Journal, 2020, 20, 505-515.	0.9	10
168	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	2.0	10
169	Histone acetylome-wide associations in immune cells from individuals with active Mycobacterium tuberculosis infection. Nature Microbiology, 2022, 7, 312-326.	5.9	9
170	Overlap of high-risk individuals predicted by family history, and genetic and non-genetic breast cancer risk prediction models: implications for risk stratification. BMC Medicine, 2022, 20, 150.	2.3	9
171	Mapping the genetic diversity of HLA haplotypes in the Japanese populations. Scientific Reports, 2015, 5, 17855.	1.6	8
172	Linking a genomeâ€wide association study signal to a LRRK2 coding variant in Parkinson's disease. Movement Disorders, 2016, 31, 484-487.	2.2	8
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174	Revealing the molecular signatures of host-pathogen interactions. Genome Biology, 2011, 12, 229.	13.9	7
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