Xueling Sim

List of Publications by Year
in descending order

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Version: 2024-02-01

156 papers	23,257 citations	16451 64 h-index	9589 142 g-index
177 all docs	177 docs citations	177 times ranked	29922 citing authors

#	Article	IF	Citations
1	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. Journal of Human Genetics, 2022, 67, 87-93.	2.3	27
2	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744.	7.1	51
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	6.2	24
4	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations. Communications Biology, 2022, 5, 329.	4.4	21
5	Circulating Metabolic Biomarkers Are Consistently Associated With Type 2 Diabetes Risk in Asian and European Populations. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2751-e2761.	3.6	8
6	Genetics in chronic kidney disease: conclusions from a Kidney Disease: Improving Global Outcomes (KDIGO) Controversies Conference. Kidney International, 2022, 101, 1126-1141.	5.2	46
7	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.	5.5	9
8	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
9	Multidisciplinary Effort to Drive Precision-Medicine for the Future. Frontiers in Digital Health, 2022, 4, 845405.	2.8	3
10	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
11	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.	5.2	18
12	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. Briefings in Bioinformatics, 2021, 22, .	6.5	8
13	Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013.	1.7	2
14	Association of leukocyte telomere length with chronic kidney disease in East Asians with type 2 diabetes: a Mendelian randomization study. CKJ: Clinical Kidney Journal, 2021, 14, 2371-2376.	2.9	12
15	Association of Genetic Variants for Plasma LRG1 With Rapid Decline in Kidney Function in Patients With Type 2 Diabetes. Journal of Clinical Endocrinology and Metabolism, 2021, 106, 2384-2394.	3.6	9
16	Cohort profile: The Singapore Breast Cancer Cohort (SGBCC), a multi-center breast cancer cohort for evaluation of phenotypic risk factors and genetic markers. PLoS ONE, 2021, 16, e0250102.	2.5	11
17	Progress in Defining the Genetic Contribution to Type 2 Diabetes in Individuals of East Asian Ancestry. Current Diabetes Reports, 2021, 21, 17.	4.2	5
18	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. Human Genetics and Genomics Advances, 2021, 2, 100029.	1.7	23

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19	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	21.4	341
20	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	12.8	49
21	APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups. Lipids in Health and Disease, 2021, 20, 113.	3.0	12
22	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.	4.1	17
23	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	27.8	353
24	Serum acylcarnitines and amino acids and risk of type 2 diabetes in a multiethnic Asian population. BMJ Open Diabetes Research and Care, 2020, 8, e001315.	2.8	22
25	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
26	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. Nature Communications, 2020, 11, 3833.	12.8	88
27	Coffee, Black Tea, and Green Tea Consumption in Relation to Plasma Metabolites in an Asian Population. Molecular Nutrition and Food Research, 2020, 64, e2000527.	3.3	11
28	Diet, Physical Activity and Adiposity as Determinants of Circulating Amino Acid Levels in a Multiethnic Asian Population. Nutrients, 2020, 12, 2603.	4.1	8
29	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 3854-3864.	3.6	9
30	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. Communications Biology, 2020, 3, 755.	4.4	10
31	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
32	Identification of type 2 diabetes loci in 433,540 East Asian individuals. Nature, 2020, 582, 240-245.	27.8	282
33	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. European Journal of Epidemiology, 2020, 35, 685-697.	5.7	9
34	Cohort profile: the Singapore diabetic cohort study. BMJ Open, 2020, 10, e036443.	1.9	3
35	Exploring Factors Underlying Ethnic Difference in Age-related Macular Degeneration Prevalence. Ophthalmic Epidemiology, 2020, 27, 399-408.	1.7	5
36	Genome-wide meta-analysis associates GPSM1 with type 2 diabetes, a plausible gene involved in skeletal muscle function. Journal of Human Genetics, 2020, 65, 411-420.	2.3	6

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37	Association of G6PD variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. BMJ Open Diabetes Research and Care, 2020, 8, e001091.	2.8	12
38	Multiple Biomarkers Improved Prediction for the Risk of Type 2 Diabetes Mellitus in Singapore Chinese Men and Women. Diabetes and Metabolism Journal, 2020, 44, 295.	4.7	6
39	Genetic variants linked to myopic macular degeneration in persons with high myopia: CREAM Consortium. PLoS ONE, 2019, 14, e0220143.	2.5	12
40	Feeding-Related Knowledge, Attitudes, and Practices among Grandparents in Singapore. Nutrients, 2019, 11, 1696.	4.1	11
41	Associations with metabolites in Chinese suggest new metabolic roles in Alzheimerâ€™s and Parkinsonâ€™s diseases. Human Molecular Genetics, 2019, 29, 189-201.	2.9	12
42	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. Cell, 2019, 179, 736-749.e15.	28.9	126
43	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
44	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits. JAMA Network Open, 2019, 2, e1910915.	5.9	41
45	Factors influencing communication of traditional Chinese medicine use between patients and doctors: A multisite cross-sectional study. Journal of Integrative Medicine, 2019, 17, 396-403.	3.1	8
46	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
47	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376.	12.8	64
48	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
49	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	27.8	248
50	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.	2.9	31
51	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.	21.4	112
52	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
53	Fish and marine fatty acids intakes, theFADSgenotypes and long-term weight gain: a prospective cohort study. BMJ Open, 2019, 9, e022877.	1.9	5
54	Ethnicity-Specific Skeletal Muscle Transcriptional Signatures and Their Relevance to Insulin Resistance in Singapore. Journal of Clinical Endocrinology and Metabolism, 2019, 104, 465-486.	3.6	4

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55	Large-scale lipidomics identifies associations between plasma sphingolipids and T2DM incidence. JCI Insight, 2019, 4, .	5.0	92
56	303-OR: ADA Presidents' Select Abstract: Transethnic Association Study of Type 2 Diabetes in More than a Million Individuals. Diabetes, 2019, 68, 303-OR.	0.6	2
57	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. Human Molecular Genetics, 2018, 27, 1664-1674.	2.9	30
58	Cohort Profile: The Singapore Multi-Ethnic Cohort (MEC) study. International Journal of Epidemiology, 2018, 47, 699-699j.	1.9	67
59	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.	6.2	123
60	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.1	28
61	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.6	136
62	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. Nature Communications, 2018, 9, 5052.	12.8	75
63	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
64	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
65	Gene-diet interaction effects on BMI levels in the Singapore Chinese population. Nutrition Journal, 2018, 17, 31.	3.4	11
66	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166.	2.5	94
67	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
68	Discovery and Fine-Mapping of Type 2 Diabetes Susceptibility Loci in Diverse Populations Using More than a Million Individuals. Diabetes, 2018, 67, .	0.6	0
69	A genome-wide association study of corneal astigmatism: The CREAM Consortium. Molecular Vision, 2018, 24, 127-142.	1.1	10
70	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
71	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.	2.9	120
72	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. Journal of the American Heart Association, 2017, 6, .	3.7	89

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73	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.	2.9	135
74	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.	0.6	47
75	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. Circulation: Cardiovascular Genetics, 2017, 10, e001527.	5.1	26
76	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
77	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
78	The contribution of recently identified adult BMI risk loci to paediatric obesity in a Singaporean Chinese childhood dataset. Pediatric Obesity, 2017, 12, e46-e50.	2.8	9
79	HDL-cholesterol levels and risk of age-related macular degeneration: a multiethnic genetic study using Mendelian randomization. International Journal of Epidemiology, 2017, 46, 1891-1902.	1.9	73
80	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
81	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.	3.3	28
82	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.	8.4	341
83	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. PLoS Genetics, 2017, 13, e1007021.	3.5	27
84	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. PLoS Genetics, 2017, 13, e1007079.	3.5	49
85	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
86	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
87	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics, 2016, 48, 1171-1184.	21.4	362
88	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.6	17
89	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	2.9	21
90	Novel Genetic Loci Associated With Retinal Microvascular Diameter. Circulation: Cardiovascular Genetics, 2016, 9, 45-54.	5.1	28

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91	Evaluation of transethnic fine mapping with population-specific and cosmopolitan imputation reference panels in diverse Asian populations. European Journal of Human Genetics, 2016, 24, 592-599.	2.8	4
92	Genome-Wide Association Meta-analysis Identifies Novel Variants Associated With Fasting Plasma Glucose in East Asians. Diabetes, 2015, 64, 291-298.	0.6	59
93	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876.	3.5	95
94	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. Human Molecular Genetics, 2015, 24, 1791-1800.	2.9	105
95	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. Human Molecular Genetics, 2014, 23, 5492-5504.	2.9	192
96	Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494.	3.5	351
97	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
98	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.	6.2	109
99	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
100	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
101	Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. Diabetologia, 2013, 56, 1291-1305.	6.3	94
102	Genome-wide Association Analysis of Blood-Pressure Traits in African-Ancestry Individuals Reveals Common Associated Genes in African and Non-African Populations. American Journal of Human Genetics, 2013, 93, 545-554.	6.2	189
103	Overlap Between Common Genetic Polymorphisms Underpinning Kidney Traits and Cardiovascular Disease Phenotypes: The CKDGen Consortium. American Journal of Kidney Diseases, 2013, 61, 889-898.	1.9	31
104	Genetic Variation in CDH13 Is Associated With Lower Plasma Adiponectin Levels but Greater Adiponectin Sensitivity in East Asian Populations. Diabetes, 2013, 62, 4277-4283.	0.6	48
105	Meta-analysis of genome-wide association studies in five cohorts reveals common variants in RBFOX1, a regulator of tissue-specific splicing, associated with refractive error. Human Molecular Genetics, 2013, 22, 2754-2764.	2.9	60
106	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. Nature Genetics, 2013, 45, 197-201.	21.4	247
107	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
108	Genetic Association of Refractive Error and Axial Length with 15q14 but Not 15q25 in the Blue Mountains Eye Study Cohort. Ophthalmology, 2013, 120, 292-297.	5.2	26

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109	Genome-Wide Association Study Identifies a Novel Locus Contributing to Type 2 Diabetes Susceptibility in Sikhs of Punjabi Origin From India. Diabetes, 2013, 62, 1746-1755.	0.6	167
110	Seven new loci associated with age-related macular degeneration. Nature Genetics, 2013, 45, 433-439.	21.4	687
111	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. Human Molecular Genetics, 2013, 22, 4653-4660.	2.9	29
112	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. Human Molecular Genetics, 2013, 22, 2303-2311.	2.9	63
113	Insights into the Genetic Architecture of Early Stage Age-Related Macular Degeneration: A Genome-Wide Association Study Meta-Analysis. PLoS ONE, 2013, 8, e53830.	2.5	108
114	Genome-Wide Association Study of Retinopathy in Individuals without Diabetes. PLoS ONE, 2013, 8, e54232.	2.5	22
115	Genetic Loci for Retinal Arteriolar Microcirculation. PLoS ONE, 2013, 8, e65804.	2.5	27
116	Are C-Reactive Protein Associated Genetic Variants Associated with Serum Levels and Retinal Markers of Microvascular Pathology in Asian Populations from Singapore?. PLoS ONE, 2013, 8, e67650.	2.5	23
117	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.	2.5	24
118	Genetic Associations of Type 2 Diabetes with Islet Amyloid Polypeptide Processing and Degrading Pathways in Asian Populations. PLoS ONE, 2013, 8, e62378.	2.5	7
119	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 4365-4365.	2.9	2
120	Natural positive selection and northâ€“south genetic diversity in East Asia. European Journal of Human Genetics, 2012, 20, 102-110.	2.8	42
121	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.	2.8	13
122	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. Nature Genetics, 2012, 44, 67-72.	21.4	545
123	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. Human Molecular Genetics, 2012, 21, 437-445.	2.9	69
124	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.	3.8	67
125	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. Nature Genetics, 2012, 44, 1142-1146.	21.4	196
126	Meta-analysis identifies common variants associated with body mass index in east Asians. Nature Genetics, 2012, 44, 307-311.	21.4	372

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127	Meta-analysis identifies multiple loci associated with kidney functionâ€“related traits in east Asian populations. Nature Genetics, 2012, 44, 904-909.	21.4	254
128	Estimating the number of true discoveries in genomeâ€wide association studies. Statistics in Medicine, 2012, 31, 1177-1189.	1.6	3
129	Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. International Journal of Obesity, 2012, 36, 159-163.	3.4	83
130	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. Nature Genetics, 2011, 43, 984-989.	21.4	481
131	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. Nature, 2011, 478, 103-109.	27.8	1,855
132	Genome-Wide Association Studies Reveal Genetic Variants in CTNND2 for High Myopia in Singapore Chinese. Ophthalmology, 2011, 118, 368-375.	5.2	118
133	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. Nature Genetics, 2011, 43, 531-538.	21.4	516
134	SgD-CNV, a database for common and rare copy number variants in three Asian populations. Human Mutation, 2011, 32, 1341-1349.	2.5	27
135	A method for identifying haplotypes carrying the causative allele in positive natural selection and genome-wide association studies. Bioinformatics, 2011, 27, 822-828.	4.1	8
136	Candidate Gene Association Study for Diabetic Retinopathy in Persons with Type 2 Diabetes: The Candidate Gene Association Resource (CARe). , 2011, 52, 7593.		82
137	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. Human Molecular Genetics, 2011, 20, 649-658.	2.9	140
138	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.	2.9	91
139	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. Human Molecular Genetics, 2011, 20, 2273-2284.	2.9	168
140	Copy number polymorphisms in new HapMap III and Singapore populations. Journal of Human Genetics, 2011, 56, 552-560.	2.3	1
141	Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. Human Molecular Genetics, 2011, 20, 3693-3698.	2.9	51
142	Transferability of Type 2 Diabetes Implicated Loci in Multi-Ethnic Cohorts from Southeast Asia. PLoS Genetics, 2011, 7, e1001363.	3.5	131
143	Genome-Wide Meta-Analysis of Five Asian Cohorts Identifies PDGFRA as a Susceptibility Locus for Corneal Astigmatism. PLoS Genetics, 2011, 7, e1002402.	3.5	35
144	Patterns of linkage disequilibrium in different populations: implications and opportunities for lipid-associated loci identified from genome-wide association studies. Current Opinion in Lipidology, 2010, 21, 104-115.	2.7	11

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145	Identifying candidate causal variants via transâ€population fineâ€mapping. Genetic Epidemiology, 2010, 34, 653-664.	1.3	31
146	Genomic copy number variations in three Southeast Asian populations. Human Mutation, 2010, 31, 851-857.	2.5	26
147	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
148	Learning in Glaucoma Genetic Risk Assessment. , 2010, 2010, 6182-5.		3
149	Identification of New Genetic Risk Variants for Type 2 Diabetes. PLoS Genetics, 2010, 6, e1001127.	3.5	193
150	Four Novel Loci (19q13, 6q24, 12q24, and 5q14) Influence the Microcirculation In Vivo. PLoS Genetics, 2010, 6, e1001184.	3.5	134
151	Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. Journal of Lipid Research, 2009, 50, 514-520.	4.2	53
152	Singapore Genome Variation Project: A haplotype map of three Southeast Asian populations. Genome Research, 2009, 19, 2154-2162.	5.5	146
153	Gender differences in the trend of colorectal cancer incidence in Singapore, 1968â€“2002. International Journal of Colorectal Disease, 2008, 23, 461-467.	2.2	35
154	Incidence, mortality and survival patterns of prostate cancer among residents in Singapore from 1968 to 2002. BMC Cancer, 2008, 8, 368.	2.6	10
155	FTO Variants Are Associated With Obesity in the Chinese and Malay Populations in Singapore. Diabetes, 2008, 57, 2851-2857.	0.6	152
156	Ethnic differences in the time trend of female breast cancer incidence: Singapore, 1968 â€“ 2002. BMC Cancer, 2006, 6, 261.	2.6	78