

Xueling Sim

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

157
papers

16,253
citations

54
h-index

127
g-index

177
ext. papers

20,333
ext. citations

12.3
avg, IF

4.48
L-index

#	Paper	IF	Citations
157	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. <i>JAMA Oncology</i> , 2022 ,	13.4	4
156	Identification of genetic effects underlying type 2 diabetes in South Asian and European populations.. <i>Communications Biology</i> , 2022 , 5, 329	6.7	2
155	Overlap of high-risk individuals predicted by family history, and genetic and non-genetic breast cancer risk prediction models: implications for risk stratification.. <i>BMC Medicine</i> , 2022 , 20, 150	11.4	0
154	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. <i>Nature Genetics</i> , 2022 ,	36.3	7
153	Multidisciplinary Effort to Drive Precision-Medicine for the Future.. <i>Frontiers in Digital Health</i> , 2022 , 4, 845405	2.3	0
152	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. <i>Genome Medicine</i> , 2022 , 14, 51	14.4	0
151	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. <i>Molecular Psychiatry</i> , 2021 , 26, 2111-2125	15.1	3
150	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
149	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. <i>Clinical Epigenetics</i> , 2021 , 13, 195	7.7	1
148	Association of leukocyte telomere length with chronic kidney disease in East Asians with type 2 diabetes: a Mendelian randomization study. <i>CKJ: Clinical Kidney Journal</i> , 2021 , 14, 2371-2376	4.5	0
147	Association of Genetic Variants for Plasma LRG1 With Rapid Decline in Kidney Function in Patients With Type 2 Diabetes. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 2384-2394	5.6	4
146	Cohort profile: The Singapore Breast Cancer Cohort (SGBCC), a multi-center breast cancer cohort for evaluation of phenotypic risk factors and genetic markers. <i>PLoS ONE</i> , 2021 , 16, e0250102	3.7	2
145	Progress in Defining the Genetic Contribution to Type 2 Diabetes in Individuals of East Asian Ancestry. <i>Current Diabetes Reports</i> , 2021 , 21, 17	5.6	2
144	Genetic discovery and risk characterization in type 2 diabetes across diverse populations. <i>Human Genetics and Genomics Advances</i> , 2021 , 2, 100029-100029	0.8	7
143	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021 , 53, 840-860	36.3	44
142	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. <i>Nature Communications</i> , 2021 , 12, 3505	17.4	5
141	Using off-target data from whole-exome sequencing to improve genotyping accuracy, association analysis and polygenic risk prediction. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3

140	Analyses of biomarker traits in diverse UK biobank participants identify associations missed by European-centric analysis strategies. <i>Journal of Human Genetics</i> , 2021 ,	4.3	6
139	APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups. <i>Lipids in Health and Disease</i> , 2021 , 20, 113	4.4	2
138	Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , 2020 , 582, 240-245	50.4	89
137	Mendelian randomization analysis does not support causal associations of birth weight with hypertension risk and blood pressure in adulthood. <i>European Journal of Epidemiology</i> , 2020 , 35, 685-697 ^{12.1}	12.1	2
136	Cohort profile: the Singapore diabetic cohort study. <i>BMJ Open</i> , 2020 , 10, e036443	3	2
135	Exploring Factors Underlying Ethnic Difference in Age-related Macular Degeneration Prevalence. <i>Ophthalmic Epidemiology</i> , 2020 , 27, 399-408	1.9	2
134	Genome-wide meta-analysis associates GPSM1 with type 2 diabetes, a plausible gene involved in skeletal muscle function. <i>Journal of Human Genetics</i> , 2020 , 65, 411-420	4.3	3
133	Association of variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. <i>BMJ Open Diabetes Research and Care</i> , 2020 , 8,	4.5	7
132	Associations with metabolites in Chinese suggest new metabolic roles in Alzheimer's and Parkinson's diseases. <i>Human Molecular Genetics</i> , 2020 , 29, 189-201	5.6	5
131	Multiple Biomarkers Improved Prediction for the Risk of Type 2 Diabetes Mellitus in Singapore Chinese Men and Women. <i>Diabetes and Metabolism Journal</i> , 2020 , 44, 295-306	5	2
130	Serum acylcarnitines and amino acids and risk of type 2 diabetes in a multiethnic Asian population. <i>BMJ Open Diabetes Research and Care</i> , 2020 , 8,	4.5	8
129	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020 , 52, 1314-1332	36.3	26
128	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. <i>Nature Communications</i> , 2020 , 11, 3833	17.4	31
127	Coffee, Black Tea, and Green Tea Consumption in Relation to Plasma Metabolites in an Asian Population. <i>Molecular Nutrition and Food Research</i> , 2020 , 64, e2000527	5.9	5
126	Diet, Physical Activity and Adiposity as Determinants of Circulating Amino Acid Levels in a Multiethnic Asian Population. <i>Nutrients</i> , 2020 , 12,	6.7	1
125	Genome-Wide Association for HbA1c in Malay Identified Deletion on SLC4A1 that Influences HbA1c Independent of Glycemia. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020 , 105,	5.6	4
124	Common variants in SOX-2 and congenital cataract genes contribute to age-related nuclear cataract. <i>Communications Biology</i> , 2020 , 3, 755	6.7	3
123	Association of Birth Weight With Type 2 Diabetes and Glycemic Traits: A Mendelian Randomization Study. <i>JAMA Network Open</i> , 2019 , 2, e1910915	10.4	14

122	Factors influencing communication of traditional Chinese medicine use between patients and doctors: A multisite cross-sectional study. <i>Journal of Integrative Medicine</i> , 2019 , 17, 396-403	4	4
121	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019 , 188, 1033-1054	3.8	39
120	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019 , 10, 376	17.4	41
119	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
118	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019 , 570, 71-76	50.4	129
117	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019 , 28, 2615-2633	5.6	14
116	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019 , 51, 636-648	36.3	59
115	Genetic variants linked to myopic macular degeneration in persons with high myopia: CREAM Consortium. <i>PLoS ONE</i> , 2019 , 14, e0220143	3.7	5
114	Feeding-Related Knowledge, Attitudes, and Practices among Grandparents in Singapore. <i>Nutrients</i> , 2019 , 11,	6.7	2
113	Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. <i>Cell</i> , 2019 , 179, 736-749.e15	56.2	51
112	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
111	Large-scale lipidomics identifies associations between plasma sphingolipids and T2DM incidence. <i>JCI Insight</i> , 2019 , 5,	9.9	49
110	303-OR: ADA Presidents Select Abstract: Transethnic Association Study of Type 2 Diabetes in More than a Million Individuals. <i>Diabetes</i> , 2019 , 68, 303-OR	0.9	1
109	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
108	Fish and marine fatty acids intakes, the genotypes and long-term weight gain: a prospective cohort study. <i>BMJ Open</i> , 2019 , 9, e022877	3	2
107	Ethnicity-Specific Skeletal Muscle Transcriptional Signatures and Their Relevance to Insulin Resistance in Singapore. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019 , 104, 465-486	5.6	3
106	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. <i>Human Molecular Genetics</i> , 2018 , 27, 1664-1674	5.6	20
105	Cohort Profile: The Singapore Multi-Ethnic Cohort (MEC) study. <i>International Journal of Epidemiology</i> , 2018 , 47, 699-699j	7.8	34

104	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018 , 102, 375-400	11	59
103	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 379-384	11.5	21
102	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018 , 67, 1414-1427	0.9	71
101	Gene-diet interaction effects on BMI levels in the Singapore Chinese population. <i>Nutrition Journal</i> , 2018 , 17, 31	4.3	7
100	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018 , 13, e0198166	3.7	31
99	A genome-wide association study of corneal astigmatism: The CREAM Consortium. <i>Molecular Vision</i> , 2018 , 24, 127-142	2.3	5
98	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018 , 50, 26-41	36.3	186
97	Interethnic analyses of blood pressure loci in populations of East Asian and European descent. <i>Nature Communications</i> , 2018 , 9, 5052	17.4	29
96	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018 , 50, 1505-1513	36.3	675
95	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018 , 50, 834-848	36.3	135
94	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
93	New insights into the genetics of primary open-angle glaucoma based on meta-analyses of intraocular pressure and optic disc characteristics. <i>Human Molecular Genetics</i> , 2017 , 26, 438-453	5.6	80
92	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017 , 6,	6	65
91	Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , 2017 , 26, 1770-1784	5.6	90
90	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
89	Genome-Wide Association Study Meta-Analysis of Long-Term Average Blood Pressure in East Asians. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10, e001527		20
88	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017 , 49, 1758-1766	36.6	310
87	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		33

86	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. <i>PLoS Medicine</i> , 2017 , 14, e1002383	11.6	223
85	Estimation of kinship coefficient in structured and admixed populations using sparse sequencing data. <i>PLoS Genetics</i> , 2017 , 13, e1007021	6	13
84	The contribution of recently identified adult BMI risk loci to paediatric obesity in a Singaporean Chinese childhood dataset. <i>Pediatric Obesity</i> , 2017 , 12, e46-e50	4.6	5
83	HDL-cholesterol levels and risk of age-related macular degeneration: a multiethnic genetic study using Mendelian randomization. <i>International Journal of Epidemiology</i> , 2017 , 46, 1891-1902	7.8	45
82	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
81	Genome-wide association study identifies a missense variant at APOA5 for coronary artery disease in Multi-Ethnic Cohorts from Southeast Asia. <i>Scientific Reports</i> , 2017 , 7, 17921	4.9	14
80	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. <i>PLoS Genetics</i> , 2017 , 13, e1007079	6	33
79	Evaluation of transethnic fine mapping with population-specific and cosmopolitan imputation reference panels in diverse Asian populations. <i>European Journal of Human Genetics</i> , 2016 , 24, 592-9	5.3	4
78	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016 , 48, 1151-1161	36.3	181
77	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016 , 48, 1171-1184	36.3	251
76	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. <i>BMC Proceedings</i> , 2016 , 10, 71-77	2.3	14
75	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016 , 25, 2070-2081	5.6	20
74	Novel Genetic Loci Associated With Retinal Microvascular Diameter. <i>Circulation: Cardiovascular Genetics</i> , 2016 , 9, 45-54		18
73	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
72	Identification and functional characterization of G6PC2 coding variants influencing glycemic traits define an effector transcript at the G6PC2-ABCB11 locus. <i>PLoS Genetics</i> , 2015 , 11, e1004876	6	76
71	Meta-analysis of genome-wide association studies of adult height in East Asians identifies 17 novel loci. <i>Human Molecular Genetics</i> , 2015 , 24, 1791-800	5.6	71
70	Genome-wide association meta-analysis identifies novel variants associated with fasting plasma glucose in East Asians. <i>Diabetes</i> , 2015 , 64, 291-8	0.9	43
69	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , 2014 , 94, 233-45	11	170

68	Gene-age interactions in blood pressure regulation: a large-scale investigation with the CHARGE, Global BPgen, and ICBP Consortia. <i>American Journal of Human Genetics</i> , 2014 , 95, 24-38	11	80
67	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014 , 46, 234-44	36.3	784
66	Simulation of Finnish population history, guided by empirical genetic data, to assess power of rare-variant tests in Finland. <i>American Journal of Human Genetics</i> , 2014 , 94, 710-20	11	19
65	Meta-analysis of genome-wide association studies in East Asian-ancestry populations identifies four new loci for body mass index. <i>Human Molecular Genetics</i> , 2014 , 23, 5492-504	5.6	141
64	Distribution and medical impact of loss-of-function variants in the Finnish founder population. <i>PLoS Genetics</i> , 2014 , 10, e1004494	6	243
63	Genome-wide association study in a Chinese population identifies a susceptibility locus for type 2 diabetes at 7q32 near PAX4. <i>Diabetologia</i> , 2013 , 56, 1291-305	10.3	85
62	Genome-wide association analysis of blood-pressure traits in African-ancestry individuals reveals common associated genes in African and non-African populations. <i>American Journal of Human Genetics</i> , 2013 , 93, 545-54	11	145
61	Overlap between common genetic polymorphisms underpinning kidney traits and cardiovascular disease phenotypes: the CKDGen consortium. <i>American Journal of Kidney Diseases</i> , 2013 , 61, 889-98	7.4	26
60	Genetic variation in CDH13 is associated with lower plasma adiponectin levels but greater adiponectin sensitivity in East Asian populations. <i>Diabetes</i> , 2013 , 62, 4277-83	0.9	36
59	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. <i>Human Molecular Genetics</i> , 2013 , 22, 2754-64	5.6	52
58	Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. <i>Nature Genetics</i> , 2013 , 45, 197-201	36.3	212
57	Functional variants at the 11q13 risk locus for breast cancer regulate cyclin D1 expression through long-range enhancers. <i>American Journal of Human Genetics</i> , 2013 , 92, 489-503	11	167
56	Genetic association of refractive error and axial length with 15q14 but not 15q25 in the Blue Mountains Eye Study cohort. <i>Ophthalmology</i> , 2013 , 120, 292-7	7.3	25
55	Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. <i>Diabetes</i> , 2013 , 62, 1746-55	0.9	129
54	Seven new loci associated with age-related macular degeneration. <i>Nature Genetics</i> , 2013 , 45, 433-9, 439e1-3	16.3	577
53	Genome-wide association study of intraocular pressure identifies the GLCCI1/ICA1 region as a glaucoma susceptibility locus. <i>Human Molecular Genetics</i> , 2013 , 22, 4653-60	5.6	24
52	Comparing methods for performing trans-ethnic meta-analysis of genome-wide association studies. <i>Human Molecular Genetics</i> , 2013 , 22, 2303-11	5.6	48
51	Insights into the genetic architecture of early stage age-related macular degeneration: a genome-wide association study meta-analysis. <i>PLoS ONE</i> , 2013 , 8, e53830	3.7	79

50	Genome-wide association study of retinopathy in individuals without diabetes. <i>PLoS ONE</i> , 2013 , 8, e542327	3.7	11
49	Genetic loci for retinal arteriolar microcirculation. <i>PLoS ONE</i> , 2013 , 8, e65804	3.7	19
48	Are C-reactive protein associated genetic variants associated with serum levels and retinal markers of microvascular pathology in Asian populations from Singapore?. <i>PLoS ONE</i> , 2013 , 8, e67650	3.7	18
47	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. <i>PLoS ONE</i> , 2013 , 8, e79767	3.7	20
46	Genetic associations of type 2 diabetes with islet amyloid polypeptide processing and degrading pathways in asian populations. <i>PLoS ONE</i> , 2013 , 8, e62378	3.7	6
45	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. <i>Human Molecular Genetics</i> , 2012 , 21, 437-45	5.6	61
44	Large scale international replication and meta-analysis study confirms association of the 15q14 locus with myopia. The CREAM consortium. <i>Human Genetics</i> , 2012 , 131, 1467-80	6.3	57
43	Genome-wide association analyses identify three new susceptibility loci for primary angle closure glaucoma. <i>Nature Genetics</i> , 2012 , 44, 1142-1146	36.3	160
42	Meta-analysis identifies common variants associated with body mass index in east Asians. <i>Nature Genetics</i> , 2012 , 44, 307-11	36.3	301
41	Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. <i>Nature Genetics</i> , 2012 , 44, 904-9	36.3	201
40	Estimating the number of true discoveries in genome-wide association studies. <i>Statistics in Medicine</i> , 2012 , 31, 1177-89	2.3	3
39	Replication of 13 obesity loci among Singaporean Chinese, Malay and Asian-Indian populations. <i>International Journal of Obesity</i> , 2012 , 36, 159-63	5.5	70
38	Identification of four novel variants that influence central corneal thickness in multi-ethnic Asian populations. <i>Human Molecular Genetics</i> , 2012 , 21, 4365-4365	5.6	2
37	Natural positive selection and north-south genetic diversity in East Asia. <i>European Journal of Human Genetics</i> , 2012 , 20, 102-10	5.3	38
36	A statistical method for region-based meta-analysis of genome-wide association studies in genetically diverse populations. <i>European Journal of Human Genetics</i> , 2012 , 20, 469-75	5.3	12
35	Meta-analysis of genome-wide association studies identifies eight new loci for type 2 diabetes in east Asians. <i>Nature Genetics</i> , 2011 , 44, 67-72	36.3	475
34	Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2011 , 43, 984-9	36.3	406
33	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011 , 478, 103-9	50.4	1564

32	Genome-wide association studies reveal genetic variants in CTNND2 for high myopia in Singapore Chinese. <i>Ophthalmology</i> , 2011 , 118, 368-75	7.3	103
31	Meta-analysis of genome-wide association studies identifies common variants associated with blood pressure variation in east Asians. <i>Nature Genetics</i> , 2011 , 43, 531-8	36.3	442
30	SgD-CNV, a database for common and rare copy number variants in three Asian populations. <i>Human Mutation</i> , 2011 , 32, 1341-9	4.7	25
29	A method for identifying haplotypes carrying the causative allele in positive natural selection and genome-wide association studies. <i>Bioinformatics</i> , 2011 , 27, 822-8	7.2	6
28	Candidate gene association study for diabetic retinopathy in persons with type 2 diabetes: the Candidate Gene Association Resource (CARE) 2011 , 52, 7593-602		73
27	Collagen-related genes influence the glaucoma risk factor, central corneal thickness. <i>Human Molecular Genetics</i> , 2011 , 20, 649-58	5.6	127
26	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. <i>Human Molecular Genetics</i> , 2011 , 20, 1864-72	5.6	79
25	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011 , 20, 2273-84	5.6	146
24	Copy number polymorphisms in new HapMap III and Singapore populations. <i>Journal of Human Genetics</i> , 2011 , 56, 552-60	4.3	1
23	Association of variants in FRAP1 and PDGFRA with corneal curvature in Asian populations from Singapore. <i>Human Molecular Genetics</i> , 2011 , 20, 3693-8	5.6	46
22	Transferability of type 2 diabetes implicated loci in multi-ethnic cohorts from Southeast Asia. <i>PLoS Genetics</i> , 2011 , 7, e1001363	6	119
21	Genome-wide meta-analysis of five Asian cohorts identifies PDGFRA as a susceptibility locus for corneal astigmatism. <i>PLoS Genetics</i> , 2011 , 7, e1002402	6	33
20	Biological, clinical and population relevance of 95 loci for blood lipids. <i>Nature</i> , 2010 , 466, 707-13	50.4	2742
19	Learning in glaucoma genetic risk assessment. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2010 , 2010, 6182-5	0.9	2
18	Identification of new genetic risk variants for type 2 diabetes. <i>PLoS Genetics</i> , 2010 , 6, e1001127	6	168
17	Four novel Loci (19q13, 6q24, 12q24, and 5q14) influence the microcirculation in vivo. <i>PLoS Genetics</i> , 2010 , 6, e1001184	6	111
16	Patterns of linkage disequilibrium in different populations: implications and opportunities for lipid-associated loci identified from genome-wide association studies. <i>Current Opinion in Lipidology</i> , 2010 , 21, 104-15	4.4	10
15	Identifying candidate causal variants via trans-population fine-mapping. <i>Genetic Epidemiology</i> , 2010 , 34, 653-64	2.6	27

14	Genomic copy number variations in three Southeast Asian populations. <i>Human Mutation</i> , 2010 , 31, 851-74.7	20
13	Polymorphisms at newly identified lipid-associated loci are associated with blood lipids and cardiovascular disease in an Asian Malay population. <i>Journal of Lipid Research</i> , 2009 , 50, 514-520	6.3 41
12	Singapore Genome Variation Project: a haplotype map of three Southeast Asian populations. <i>Genome Research</i> , 2009 , 19, 2154-62	9.7 129
11	Incidence, mortality and survival patterns of prostate cancer among residents in Singapore from 1968 to 2002. <i>BMC Cancer</i> , 2008 , 8, 368	4.8 9
10	FTO variants are associated with obesity in the Chinese and Malay populations in Singapore. <i>Diabetes</i> , 2008 , 57, 2851-7	0.9 133
9	Gender differences in the trend of colorectal cancer incidence in Singapore, 1968-2002. <i>International Journal of Colorectal Disease</i> , 2008 , 23, 461-7	3 30
8	Ethnic differences in the time trend of female breast cancer incidence: Singapore, 1968-2002. <i>BMC Cancer</i> , 2006 , 6, 261	4.8 65
7	The Trans-Ancestral Genomic Architecture of Glycaemic Traits	1
6	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes	1
5	Rare coding variants in 35 genes associate with circulating lipid levels in a multi-ancestry analysis of 170,000 exomes	2
4	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution	1
3	Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries	2
2	Identification of type 2 diabetes loci in 433,540 East Asian individuals	4
1	Tissue-Specific Alteration of Metabolic Pathways Influences Glycemic Regulation	4