

# Shuhua Xu

## List of Publications by Citations

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151  
papers

4,247  
citations

31  
h-index

60  
g-index

170  
ext. papers

5,979  
ext. citations

7.5  
avg. IF

5.05  
L-index

#	Paper	IF	Citations
151	Mapping human genetic diversity in Asia. <i>Science</i> , <b>2009</b> , 326, 1541-5	33.3	444
150	Genomic dissection of population substructure of Han Chinese and its implication in association studies. <i>American Journal of Human Genetics</i> , <b>2009</b> , 85, 762-74	11	264
149	A genome-wide search for signals of high-altitude adaptation in Tibetans. <i>Molecular Biology and Evolution</i> , <b>2011</b> , 28, 1003-11	8.3	231
148	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , <b>2019</b> , 51, 1670-1678	36.3	185
147	<i>Gossypium barbadense</i> genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. <i>Scientific Reports</i> , <b>2015</b> , 5, 14139	4.9	165
146	Genetic control of floral zygomorphy in pea ( <i>Pisum sativum</i> L.). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 10414-9	11.5	148
145	Analysis of genomic admixture in Uyghur and its implication in mapping strategy. <i>American Journal of Human Genetics</i> , <b>2008</b> , 82, 883-94	11	142
144	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. <i>Nature Communications</i> , <b>2019</b> , 10, 4892	17.4	140
143	Ancestral Origins and Genetic History of Tibetan Highlanders. <i>American Journal of Human Genetics</i> , <b>2016</b> , 99, 580-594	11	124
142	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D24-D33	20.1	119
141	A genome-wide analysis of admixture in Uyghurs and a high-density admixture map for disease-gene discovery. <i>American Journal of Human Genetics</i> , <b>2008</b> , 83, 322-36	11	100
140	The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. <i>European Journal of Human Genetics</i> , <b>2011</b> , 19, 224-30	5.3	66
139	Population genetic structure of peninsular Malaysia Malay sub-ethnic groups. <i>PLoS ONE</i> , <b>2011</b> , 6, e18313	3.7	62
138	Genetic dating indicates that the Asian-Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 4574-9	11.5	60
137	Genome-wide detection of natural selection in African Americans pre- and post-admixture. <i>Genome Research</i> , <b>2012</b> , 22, 519-27	9.7	60
136	The p.Ser267Phe variant in SLC10A1 is associated with resistance to chronic hepatitis B. <i>Hepatology</i> , <b>2015</b> , 61, 1251-60	11.2	59
135	Down-Regulation of EPAS1 Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 818-830	8.3	58

134	Human migration through bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum revealed by Y chromosomes. <i>PLoS ONE</i> , <b>2011</b> , 6, e24282	3.7	58
133	Genetic structure, divergence and admixture of Han Chinese, Japanese and Korean populations. <i>Hereditas</i> , <b>2018</b> , 155, 19	2.4	48
132	Neanderthal introgression at chromosome 3p21.31 was under positive natural selection in East Asians. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 683-95	8.3	46
131	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. <i>Genome Biology</i> , <b>2017</b> , 18, 115	18.3	40
130	A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 54-66	11	40
129	A map of copy number variations in Chinese populations. <i>PLoS ONE</i> , <b>2011</b> , 6, e27341	3.7	40
128	PanSNPdb: the Pan-Asian SNP genotyping database. <i>PLoS ONE</i> , <b>2011</b> , 6, e21451	3.7	40
127	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. <i>Molecular Biology and Evolution</i> , <b>2017</b> , 34, 2572-2582	8.3	38
126	Identification of functional mutations in GATA4 in patients with congenital heart disease. <i>PLoS ONE</i> , <b>2013</b> , 8, e62138	3.7	38
125	A spatial analysis of genetic structure of human populations in China reveals distinct difference between maternal and paternal lineages. <i>European Journal of Human Genetics</i> , <b>2008</b> , 16, 705-17	5.3	38
124	<i>Helicobacter pylori</i> induces increased expression of the vitamin d receptor in immune responses. <i>Helicobacter</i> , <b>2014</b> , 19, 37-47	4.9	37
123	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , <b>2022</b> ,	50.4	35
122	Adaptation of human skin color in various populations. <i>Hereditas</i> , <b>2018</b> , 155, 1	2.4	34
121	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 559-575	5.6	33
120	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. <i>European Journal of Human Genetics</i> , <b>2014</b> , 22, 248-53	5.3	31
119	PGG.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D971-D976	20.1	31
118	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. <i>Molecular Biology and Evolution</i> , <b>2016</b> , 33, 1177-87	8.3	28
117	PEAS V1.0: a package for elementary analysis of SNP data. <i>Molecular Ecology Resources</i> , <b>2010</b> , 10, 1085-88.4		28

116	Haplotype-sharing analysis showing Uyghurs are unlikely genetic donors. <i>Molecular Biology and Evolution</i> , <b>2009</b> , 26, 2197-206	8.3	27
115	A systematic characterization of genes underlying both complex and Mendelian diseases. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 1611-24	5.6	27
114	Principal component analysis reveals the 1000 Genomes Project does not sufficiently cover the human genetic diversity in Asia. <i>Frontiers in Genetics</i> , <b>2013</b> , 4, 127	4.5	26
113	Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. <i>Infection, Genetics and Evolution</i> , <b>2012</b> , 12, 142-8	4.5	25
112	Exploring population admixture dynamics via empirical and simulated genome-wide distribution of ancestral chromosomal segments. <i>American Journal of Human Genetics</i> , <b>2012</b> , 91, 849-62	11	25
111	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , <b>2018</b> , 37, 241-251	4.3	24
110	Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations. <i>Molecular Genetics and Genomics</i> , <b>2018</b> , 293, 1293-1300	3.1	23
109	Neanderthal origin of the haplotypes carrying the functional variant Val92Met in the MC1R in modern humans. <i>Molecular Biology and Evolution</i> , <b>2014</b> , 31, 1994-2003	8.3	23
108	The population genomic landscape of human genetic structure, admixture history and local adaptation in Peninsular Malaysia. <i>Human Genetics</i> , <b>2014</b> , 133, 1169-85	6.3	23
107	Homozygous p.Ser267Phe in SLC10A1 is associated with a new type of hypercholanemia and implications for personalized medicine. <i>Scientific Reports</i> , <b>2017</b> , 7, 9214	4.9	23
106	Novel genetic loci affecting facial shape variation in humans. <i>ELife</i> , <b>2019</b> , 8,	8.9	22
105	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , <b>2017</b> , 12, e0185487	3.7	21
104	Quantitating and dating recent gene flow between European and East Asian populations. <i>Scientific Reports</i> , <b>2015</b> , 5, 9500	4.9	20
103	Variation and signatures of selection on the human face. <i>Journal of Human Evolution</i> , <b>2014</b> , 75, 143-52	3.1	20
102	Genetic evidence supports linguistic affinity of Mlabri--a hunter-gatherer group in Thailand. <i>BMC Genetics</i> , <b>2010</b> , 11, 18	2.6	20
101	Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. <i>European Journal of Human Genetics</i> , <b>2014</b> , 22, 930-7	5.3	19
100	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. <i>European Journal of Human Genetics</i> , <b>2015</b> , 23, 536-42	5.3	18
99	Gastric precancerous lesions are associated with gene variants in <i>Helicobacter pylori</i> -susceptible ethnic Malays. <i>World Journal of Gastroenterology</i> , <b>2013</b> , 19, 3615-22	5.6	18

98	Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. <i>Human Genetics</i> , <b>2016</b> , 135, 1279-1286	6.3	18
97	Dissecting the genetic structure and admixture of four geographical Malay populations. <i>Scientific Reports</i> , <b>2015</b> , 5, 14375	4.9	17
96	Differential positive selection of malaria resistance genes in three indigenous populations of Peninsular Malaysia. <i>Human Genetics</i> , <b>2015</b> , 134, 375-92	6.3	17
95	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. <i>Journal of Medical Genetics</i> , <b>2014</b> , 51, 614-22	5.8	17
94	Genome-wide landscapes of human local adaptation in Asia. <i>PLoS ONE</i> , <b>2013</b> , 8, e54224	3.7	17
93	Dissecting linkage disequilibrium in African-American genomes: roles of markers and individuals. <i>Molecular Biology and Evolution</i> , <b>2007</b> , 24, 2049-58	8.3	17
92	Ancestry variation and footprints of natural selection along the genome in Latin American populations. <i>Scientific Reports</i> , <b>2016</b> , 6, 21766	4.9	17
91	Pooled analysis of genome-wide association studies of cervical intraepithelial neoplasia 3 (CIN3) identifies a new susceptibility locus. <i>Oncotarget</i> , <b>2016</b> , 7, 42216-42224	3.3	16
90	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. <i>Journal of Genetics and Genomics</i> , <b>2018</b> , 45, 419-432	4	16
89	Characterising private and shared signatures of positive selection in 37 Asian populations. <i>European Journal of Human Genetics</i> , <b>2017</b> , 25, 499-508	5.3	15
88	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. <i>Human Genetics</i> , <b>2018</b> , 137, 161-173	6.3	15
87	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. <i>National Science Review</i> , <b>2019</b> , 6, 1201-1222	10.8	15
86	Length Distribution of Ancestral Tracks under a General Admixture Model and Its Applications in Population History Inference. <i>Scientific Reports</i> , <b>2016</b> , 6, 20048	4.9	15
85	EDARV370A associated facial characteristics in Uyghur population revealing further pleiotropic effects. <i>Human Genetics</i> , <b>2016</b> , 135, 99-108	6.3	15
84	Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys. <i>Nature Communications</i> , <b>2019</b> , 10, 5525	17.4	15
83	Differential Natural Selection of Human Zinc Transporter Genes between African and Non-African Populations. <i>Scientific Reports</i> , <b>2015</b> , 5, 9658	4.9	14
82	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. <i>PLoS Genetics</i> , <b>2018</b> , 14, e1007640	6	14
81	Triose Kinase Controls the Lipogenic Potential of Fructose and Dietary Tolerance. <i>Cell Metabolism</i> , <b>2020</b> , 32, 605-618.e7	24.6	13

80	MultiWaver 2.0: modeling discrete and continuous gene flow to reconstruct complex population admixtures. <i>European Journal of Human Genetics</i> , <b>2019</b> , 27, 133-139	5.3	13
79	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , <b>2018</b> , 41, 1-12	4.2	13
78	Phylogeography of Y-chromosome haplogroup O3a2b2-N6 reveals patrilineal traces of Austronesian populations on the eastern coastal regions of Asia. <i>PLoS ONE</i> , <b>2017</b> , 12, e0175080	3.7	12
77	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. <i>European Journal of Human Genetics</i> , <b>2018</b> , 26, 1687-1696	5.3	12
76	Nomogram to predict lymph node metastasis in patients with early oesophageal squamous cell carcinoma. <i>British Journal of Surgery</i> , <b>2018</b> , 105, 1464-1470	5.3	12
75	Analysis of genome-wide RNA-sequencing data suggests age of the CEPH/Utah (CEU) lymphoblastoid cell lines systematically biases gene expression profiles. <i>Scientific Reports</i> , <b>2015</b> , 5, 7960	4.9	12
74	The history and evolution of the Denisovan- haplotype in Tibetans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	12
73	PGG.SNV: understanding the evolutionary and medical implications of human single nucleotide variations in diverse populations. <i>Genome Biology</i> , <b>2019</b> , 20, 215	18.3	11
72	Inference of multiple-wave admixtures by length distribution of ancestral tracks. <i>Heredity</i> , <b>2018</b> , 121, 52-63	3.6	11
71	Increased genetic diversity of ADME genes in African Americans compared with their putative ancestral source populations and implications for pharmacogenomics. <i>BMC Genetics</i> , <b>2014</b> , 15, 52	2.6	11
70	HIF2A Variants Were Associated with Different Levels of High-Altitude Hypoxia among Native Tibetans. <i>PLoS ONE</i> , <b>2015</b> , 10, e0137956	3.7	11
69	The influence of admixture and consanguinity on population genetic diversity in Middle East. <i>Journal of Human Genetics</i> , <b>2014</b> , 59, 615-22	4.3	11
68	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. <i>The HUGO Journal</i> , <b>2014</b> , 8, 5		11
67	Paleolithic Contingent in Modern Japanese: Estimation and Inference using Genome-wide Data. <i>Scientific Reports</i> , <b>2012</b> , 2, 355	4.9	11
66	assembly of a Tibetan genome and identification of novel structural variants associated with high-altitude adaptation. <i>National Science Review</i> , <b>2020</b> , 7, 391-402	10.8	11
65	A new method for modeling coalescent processes with recombination. <i>BMC Bioinformatics</i> , <b>2014</b> , 15, 273	3.6	10
64	Identification of close relatives in the HUGO Pan-Asian SNP database. <i>PLoS ONE</i> , <b>2011</b> , 6, e29502	3.7	10
63	Response to Li et al.. <i>American Journal of Human Genetics</i> , <b>2009</b> , 85, 937-939	11	10

62	AncestryPainter: A Graphic Program for Displaying Ancestry Composition of Populations and Individuals. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2018</b> , 16, 382-385	6.5	10
61	Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions. <i>Heredity</i> , <b>2017</b> , 118, 503-510	3.6	9
60	Modeling Continuous Admixture Using Admixture-Induced Linkage Disequilibrium. <i>Scientific Reports</i> , <b>2017</b> , 7, 43054	4.9	9
59	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2016</b> , 14, 253-261	6.5	9
58	Towards understanding the low prevalence of Helicobacter pylori in Malays: genetic variants among Helicobacter pylori-negative ethnic Malays in the north-eastern region of Peninsular Malaysia and Han Chinese and South Indians. <i>Journal of Digestive Diseases</i> , <b>2013</b> , 14, 196-202	3.3	9
57	plays a role in the high-altitude adaptation of Tibetans. <i>Zoological Research</i> , <b>2017</b> , 38, 155-162	3.4	9
56	Reintroduction of a Homocysteine Level-Associated Allele into East Asians by Neanderthal Introgression. <i>Molecular Biology and Evolution</i> , <b>2015</b> , 32, 3108-13	8.3	8
55	A probabilistic method for testing and estimating selection differences between populations. <i>Genome Research</i> , <b>2015</b> , 25, 1903-9	9.7	8
54	Genome-wide comparison of allele-specific gene expression between African and European populations. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 1067-1077	5.6	8
53	Dissimilarity of contemporary and historical gene flow in a wild carrot ( <i>Daucus carota</i> ) metapopulation under contrasting levels of human disturbance: implications for risk assessment and management of transgene introgression. <i>Annals of Botany</i> , <b>2013</b> , 112, 1361-70	4.1	8
52	Ancestry informative marker set for han chinese population. <i>G3: Genes, Genomes, Genetics</i> , <b>2012</b> , 2, 339-41	3.1	8
51	Human population admixture in Asia. <i>Genomics and Informatics</i> , <b>2012</b> , 10, 133-44	1.9	8
50	Deleted in Colorectal Cancer (DCC) gene polymorphism is associated with H. pylori infection among susceptible Malays from the north-eastern region of Peninsular Malaysia. <i>Hepato-Gastroenterology</i> , <b>2013</b> , 60, 124-8		8
49	Signature of positive selection of PTK6 gene in East Asian populations: a cross talk for Helicobacter pylori invasion and gastric cancer endemicity. <i>Molecular Genetics and Genomics</i> , <b>2015</b> , 290, 1741-52	3.1	7
48	PGG.Population: a database for understanding the genomic diversity and genetic ancestry of human populations. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D984-D993	20.1	7
47	Fine-scale population structure of Malays in Peninsular Malaysia and Singapore and implications for association studies. <i>Human Genomics</i> , <b>2015</b> , 9, 16	6.8	7
46	A genome-wide characterization of copy number variations in native populations of Peninsular Malaysia. <i>European Journal of Human Genetics</i> , <b>2018</b> , 26, 886-897	5.3	6
45	Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genome-wide SNP data. <i>Annals of Human Genetics</i> , <b>2018</b> , 82, 216-226	2.2	6

44	Genetic diversity and natural selection footprints of the glycine amidinotransferase gene in various human populations. <i>Scientific Reports</i> , <b>2016</b> , 6, 18755	4.9	6
43	Models, methods and tools for ancestry inference and admixture analysis. <i>Quantitative Biology</i> , <b>2017</b> , 5, 236-250	3.9	6
42	Identification of two maternal transmission ratio distortion loci in pedigrees of the Framingham heart study. <i>Scientific Reports</i> , <b>2013</b> , 3, 2147	4.9	6
41	Natural Selection and Functional Potentials of Human Noncoding Elements Revealed by Analysis of Next Generation Sequencing Data. <i>PLoS ONE</i> , <b>2015</b> , 10, e0129023	3.7	6
40	A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. <i>Heredity</i> , <b>2018</b> , 120, 83-89	3.6	6
39	contributes to high-altitude adaptation in Tibetans by regulating nitric oxide production. <i>Zoological Research</i> , <b>2017</b> , 38, 163-170	3.4	5
38	Assessing genome-wide copy number variation in the Han Chinese population. <i>Journal of Medical Genetics</i> , <b>2017</b> , 54, 685-692	5.8	5
37	Population genomics of East Asian ethnic groups. <i>Hereditas</i> , <b>2020</b> , 157, 49	2.4	4
36	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. <i>Journal of Medical Genetics</i> , <b>2013</b> , 50, 534-42	5.8	4
35	The history and evolution of the Denisovan-EPAS1 haplotype in Tibetans		4
34	Genetic Origins and Sex-Biased Admixture of the Huis. <i>Molecular Biology and Evolution</i> , <b>2021</b> , 38, 3804-3819	3.9	4
33	Complete sequence data support lack of balancing selection on PRNP in a natural Chinese population. <i>Journal of Human Genetics</i> , <b>2006</b> , 51, 451-454	4.3	3
32	AdmixSim: A Forward-Time Simulator for Various Complex Scenarios of Population Admixture. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 601439	4.5	3
31	Genomic diversity and post-admixture adaptation in the Uyghurs.. <i>National Science Review</i> , <b>2022</b> , 9, nwab124	10.24	3
30	Haplotype-resolved de novo assembly of a Tujia genome suggests the necessity for high-quality population-specific genome references.. <i>Cell Systems</i> , <b>2022</b> ,	10.6	3
29	A comparative analysis of genetic diversity of candidate genes associated with type 2 diabetes in worldwide populations. <i>Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji</i> , <b>2016</b> , 38, 543-559	1.4	3
28	Convergent adaptive evolution-how common, or how rare?. <i>National Science Review</i> , <b>2020</b> , 7, 945-946	10.8	2
27	Chromosome-wide haplotype sharing: a measure integrating recombination information to reconstruct the phylogeny of human populations. <i>Annals of Human Genetics</i> , <b>2011</b> , 75, 694-706	2.2	2



26	A design of multi-source samples as a shared control for association studies in genetically stratified populations. <i>Cell Research</i> , <b>2009</b> , 19, 913-5	24.7	2
25	Refining models of archaic admixture in Eurasia with ArchaicSeeker 2.0. <i>Nature Communications</i> , <b>2021</b> , 12, 6232	17.4	2
24	AdmixSim: A Forward-Time Simulator for Various and Complex Scenarios of Population Admixture		2
23	Shared Signature of Recent Positive Selection on the TSBP1-BTNL2-HLA-DRA Genes in Five Native Populations from North Borneo. <i>Genome Biology and Evolution</i> , <b>2020</b> , 12, 2245-2257	3.9	2
22	Y-LineageTracker: a high-throughput analysis framework for Y-chromosomal next-generation sequencing data. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 114	3.6	2
21	The HuaBiao project: whole-exome sequencing of 5000 Han Chinese individuals. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 1032-1035	4	2
20	A Probabilistic Method for Estimating the Sharing of Identity by Descent for Populations with Migration. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2016</b> , 13, 281-90	3	1
19	CNVbase: Batch identification of novel and rare copy number variations based on multi-ethnic population data. <i>Journal of Genetics and Genomics</i> , <b>2017</b> , 44, 367-370	4	1
18	Genetic connections and convergent evolution of tropical indigenous peoples in Asia.. <i>Molecular Biology and Evolution</i> , <b>2021</b> ,	8.3	1
17	AdmixSim 2: a forward-time simulator for modeling complex population admixture. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 506	3.6	1
16	Trio deep-sequencing does not reveal unexpected mutations in Cas9-edited monkeys		1
15	De novo assembly of a Tibetan genome and identification of novel structural variants associated with high altitude adaptation		1
14	A genome-wide association study of facial morphology identifies novel genetic loci in Han Chinese. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 198-207	4	1
13	Paternal gene pool of Malays in Southeast Asia and its applications for the early expansion of Austronesians. <i>American Journal of Human Biology</i> , <b>2021</b> , 33, e23486	2.7	1
12	RET compound inheritance in Chinese patients with Hirschsprung disease: lack of penetrance from insufficient gene dysfunction. <i>Human Genetics</i> , <b>2021</b> , 140, 813-825	6.3	1
11	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. <i>Journal of Genetics and Genomics</i> , <b>2021</b> , 48, 972-983	4	1
10	Reply to Denham and Donohue: Asian-Papuan genetic admixture is in excellent agreement with Austronesian dispersal in eastern Indonesia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E2578-E2578	11.5	0
9	The Peopling and Migration History of the Natives in Peninsular Malaysia and Borneo: A Glimpse on the Studies Over the Past 100 years.. <i>Frontiers in Genetics</i> , <b>2022</b> , 13, 767018	4.5	0

- 8 Reply to Lack of evidence for a role of PIWIL1 variants in human male infertility. *Cell*, **2021**, 184, 1943-1944. 4.2 ○
- 7 Large-scale genome-wide scans do not support petaloid toenail as a Mendelian trait. *Journal of Genetics and Genomics*, **2016**, 43, 702-704 4 ○
- 6 Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. *BMC Genomics*, **2019**, 20, 842 4.5 ○
- 5 Improved NGS variant calling tool for the locus.. *Gut*, **2022**, 71, 1000-1001. 19.2 ○
- 4 Detecting archaic introgression and modeling multiple-wave admixture with ArchaicSeeker 2.0.. *STAR Protocols*, **2022**, 3, 101314 1.4 ○
- 3 A mechanism of nitric oxide regulation in high-altitude Tibetans. *National Science Review*, **2018**, 5, 531-531. 1.8
- 2 Population Genomics of High-Altitude Adaptation. *Evolutionary Studies*, **2021**, 67-100 2.5
- 1 A protocol for applying a population-specific reference genome assembly to population genetics and medical studies. *STAR Protocols*, **2022**, 3, 101440 1.4