Shuhua Xu

List of Publications by Year
in descending order

150 papers	7,365 citations	101384 36 h-index	74018 75 g-index
170 all docs	170 docs citations	170 times ranked	9470 citing authors

#	Article	IF	Citations
1	Mapping genomic loci implicates genes and synaptic biology in schizophrenia. Nature, 2022, 604, 502-508.	13.7	929
2	Mapping Human Genetic Diversity in Asia. Science, 2009, 326, 1541-1545.	6.0	557
3	Comparative genetic architectures of schizophrenia in East Asian and European populations. Nature Genetics, 2019, 51, 1670-1678.	9.4	440
4	Genomic Dissection of Population Substructure of Han Chinese and Its Implication in Association Studies. American Journal of Human Genetics, 2009, 85, 762-774.	2.6	338
5	A Genome-Wide Search for Signals of High-Altitude Adaptation in Tibetans. Molecular Biology and Evolution, 2011, 28, 1003-1011.	3.5	311
6	Gossypium barbadense genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. Scientific Reports, 2015, 5, 14139.	1.6	271
7	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. Nature Communications, 2019, 10, 4892.	5.8	256
8	Ancestral Origins and Genetic History of Tibetan Highlanders. American Journal of Human Genetics, 2016, 99, 580-594.	2.6	208
9	Genetic control of floral zygomorphy in pea (*Pisum sativum* L.). Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 10414-10419.	3.3	195
10	Database Resources of the National Genomics Data Center in 2020. Nucleic Acids Research, 2020, 48, D24-D33.	6.5	165
11	Analysis of Genomic Admixture in Uyghur and Its Implication in Mapping Strategy. American Journal of Human Genetics, 2008, 82, 883-894.	2.6	164
12	A Genome-wide Analysis of Admixture in Uyghurs and a High-Density Admixture Map for Disease-Gene Discovery. American Journal of Human Genetics, 2008, 83, 322-336.	2.6	125
13	Genetic structure, divergence and admixture of Han Chinese, Japanese and Korean populations. Hereditas, 2018, 155, 19.	0.5	90
14	Genome-wide detection of natural selection in African Americans pre- and post-admixture. Genome Research, 2012, 22, 519-527.	2.4	89
15	Down-Regulation of *EPAS1* Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia. Molecular Biology and Evolution, 2017, 34, msw280.	3.5	87
16	Genetic dating indicates that the Asian–Papuan admixture through Eastern Indonesia corresponds to the Austronesian expansion. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4574-4579.	3.3	82
17	The Y-chromosome landscape of the Philippines: extensive heterogeneity and varying genetic affinities of Negrito and non-Negrito groups. European Journal of Human Genetics, 2011, 19, 224-230.	1.4	78
18	The p.Ser267Phe variant in SLC10A1 is associated with resistance to chronic hepatitis B. Hepatology, 2015, 61, 1251-1260.	3.6	78

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19	Population Genetic Structure of Peninsular Malaysia Malay Sub-Ethnic Groups. PLoS ONE, 2011, 6, e18312.	1.1	75
20	Human Migration through Bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum Revealed by Y Chromosomes. PLoS ONE, 2011, 6, e24282.	1.1	75
21	A 3.4-kb Copy-Number Deletion near EPAS1 Is Significantly Enriched in High-Altitude Tibetans but Absent from the Denisovan Sequence. American Journal of Human Genetics, 2015, 97, 54-66.	2.6	69
22	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. Genome Biology, 2017, 18, 115.	3.8	67
23	Adaptation of human skin color in various populations. Hereditas, 2018, 155, 1.	0.5	66
24	Neanderthal Introgression at Chromosome 3p21.31 Was Under Positive Natural Selection in East Asians. Molecular Biology and Evolution, 2014, 31, 683-695.	3.5	63
25	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. Molecular Biology and Evolution, 2017, 34, 2572-2582.	3.5	63
26	Novel genetic loci affecting facial shape variation in humans. ELife, 2019, 8, .	2.8	58
27	*H*elicobacter pylori Induces Increased Expression of the Vitamin D Receptor in Immune Responses. Helicobacter, 2014, 19, 37-47.	1.6	53
28	PanSNPdb: The Pan-Asian SNP Genotyping Database. PLoS ONE, 2011, 6, e21451.	1.1	53
29	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. Human Molecular Genetics, 2018, 27, 559-575.	1.4	51
30	PGG.Han: the Han Chinese genome database and analysis platform. Nucleic Acids Research, 2020, 48, D971-D976.	6.5	51
31	Identification of Functional Mutations in GATA4 in Patients with Congenital Heart Disease. PLoS ONE, 2013, 8, e62138.	1.1	49
32	The history and evolution of the Denisovan-*EPAS1* haplotype in Tibetans. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	48
33	Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations. Molecular Genetics and Genomics, 2018, 293, 1293-1300.	1.0	46
34	A spatial analysis of genetic structure of human populations in China reveals distinct difference between maternal and paternal lineages. European Journal of Human Genetics, 2008, 16, 705-717.	1.4	45
35	A Map of Copy Number Variations in Chinese Populations. PLoS ONE, 2011, 6, e27341.	1.1	44
36	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. Molecular Biology and Evolution, 2016, 33, 1177-1187.	3.5	43

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37	A panel of ancestry informative markers to estimate and correct potential effects of population stratification in Han Chinese. European Journal of Human Genetics, 2014, 22, 248-253.	1.4	39
38	PEAS V1.0: a package for elementary analysis of SNP data. Molecular Ecology Resources, 2010, 10, 1085-1088.	2.2	38
39	Principal component analysis reveals the 1000 Genomes Project does not sufficiently cover the human genetic diversity in Asia. Frontiers in Genetics, 2013, 4, 127.	1.1	38
40	Variation and signatures of selection on the human face. Journal of Human Evolution, 2014, 75, 143-152.	1.3	38
41	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. Forensic Science International: Genetics, 2018, 37, 241-251.	1.6	38
42	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. Journal of Genetics and Genomics, 2018, 45, 419-432.	1.7	38
43	Exploring Population Admixture Dynamics via Empirical and Simulated Genome-wide Distribution of Ancestral Chromosomal Segments. American Journal of Human Genetics, 2012, 91, 849-862.	2.6	36
44	Homozygous p.Ser267Phe in SLC10A1 is associated with a new type of hypercholanemia and implications for personalized medicine. Scientific Reports, 2017, 7, 9214.	1.6	36
45	A systematic characterization of genes underlying both complex and Mendelian diseases. Human Molecular Genetics, 2012, 21, 1611-1624.	1.4	35
46	Haplotype-Sharing Analysis Showing Uyghurs Are Unlikely Genetic Donors. Molecular Biology and Evolution, 2009, 26, 2197-2206.	3.5	34
47	Triose Kinase Controls the Lipogenic Potential of Fructose and Dietary Tolerance. Cell Metabolism, 2020, 32, 605-618.e7.	7.2	32
48	Genetic evidence supports linguistic affinity of Mlabri - a hunter-gatherer group in Thailand. BMC Genetics, 2010, 11, 18.	2.7	30
49	Neanderthal Origin of the Haplotypes Carrying the Functional Variant Val92Met in the MC1R in Modern Humans. Molecular Biology and Evolution, 2014, 31, 1994-2003.	3.5	30
50	Distribution of ancestral chromosomal segments in admixed genomes and its implications for inferring population history and admixture mapping. European Journal of Human Genetics, 2014, 22, 930-937.	1.4	30
51	The population genomic landscape of human genetic structure, admixture history and local adaptation in Peninsular Malaysia. Human Genetics, 2014, 133, 1169-1185.	1.8	30
52	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. National Science Review, 2019, 6, 1201-1222.	4.6	30
53	PGG.SNV: understanding the evolutionary and medical implications of human single nucleotide variations in diverse populations. Genome Biology, 2019, 20, 215.	3.8	30
54	Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. Infection, Genetics and Evolution, 2012, 12, 142-148.	1.0	29

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55	Ancestry variation and footprints of natural selection along the genome in Latin American populations. Scientific Reports, 2016, 6, 21766.	1.6	29
56	Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys. Nature Communications, 2019, 10, 5525.	5.8	29
57	Y-LineageTracker: a high-throughput analysis framework for Y-chromosomal next-generation sequencing data. BMC Bioinformatics, 2021, 22, 114.	1.2	29
58	*De novo* assembly of a Tibetan genome and identification of novel structural variants associated with high-altitude adaptation. National Science Review, 2020, 7, 391-402.	4.6	28
59	Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. Human Genetics, 2016, 135, 1279-1286.	1.8	27
60	The fine-scale genetic structure and evolution of the Japanese population. PLoS ONE, 2017, 12, e0185487.	1.1	27
61	Quantitating and Dating Recent Gene Flow between European and East Asian Populations. Scientific Reports, 2015, 5, 9500.	1.6	25
62	AncestryPainter: A Graphic Program for Displaying Ancestry Composition of Populations and Individuals. Genomics, Proteomics and Bioinformatics, 2018, 16, 382-385.	3.0	25
63	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. Systematic and Applied Microbiology, 2018, 41, 1-12.	1.2	24
64	Pooled analysis of genome-wide association studies of cervical intraepithelial neoplasia 3 (CIN3) identifies a new susceptibility locus. Oncotarget, 0, 7, 42216-42224.	0.8	24
65	Dissecting the genetic structure and admixture of four geographical Malay populations. Scientific Reports, 2015, 5, 14375.	1.6	23
66	Length Distribution of Ancestral Tracks under a General Admixture Model and Its Applications in Population History Inference. Scientific Reports, 2016, 6, 20048.	1.6	23
67	EDARV370A associated facial characteristics in Uyghur population revealing further pleiotropic effects. Human Genetics, 2016, 135, 99-108.	1.8	23
68	Nomogram to predict lymph node metastasis in patients with early oesophageal squamous cell carcinoma. British Journal of Surgery, 2018, 105, 1464-1470.	0.1	23
69	MultiWaver 2.0: modeling discrete and continuous gene flow to reconstruct complex population admixtures. European Journal of Human Genetics, 2019, 27, 133-139.	1.4	23
70	Dissecting Linkage Disequilibrium in African-American Genomes: Roles of Markers and Individuals. Molecular Biology and Evolution, 2007, 24, 2049-2058.	3.5	22
71	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. Journal of Medical Genetics, 2014, 51, 614-622.	1.5	22
72	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. European Journal of Human Genetics, 2015, 23, 536-542.	1.4	22

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73	Differential Natural Selection of Human Zinc Transporter Genes between African and Non-African Populations. Scientific Reports, 2015, 5, 9658.	1.6	22
74	Characterising private and shared signatures of positive selection in 37 Asian populations. European Journal of Human Genetics, 2017, 25, 499-508.	1.4	22
75	The HuaBiao project: whole-exome sequencing of 5000 Han Chinese individuals. Journal of Genetics and Genomics, 2021, 48, 1032-1035.	1.7	22
76	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. European Journal of Human Genetics, 2018, 26, 1687-1696.	1.4	21
77	Genetic Origins and Sex-Biased Admixture of the Huis. Molecular Biology and Evolution, 2021, 38, 3804-3819.	3.5	21
78	Genome-Wide Landscapes of Human Local Adaptation in Asia. PLoS ONE, 2013, 8, e54224.	1.1	20
79	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. Human Genetics, 2018, 137, 161-173.	1.8	20
80	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. PLoS Genetics, 2018, 14, e1007640.	1.5	20
81	Genomic diversity and post-admixture adaptation in the Uyghurs. National Science Review, 2022, 9, nwab124.	4.6	20
82	Gastric precancerous lesions are associated with gene variants inHelicobacter pylori-susceptible ethnic Malays. World Journal of Gastroenterology, 2013, 19, 3615.	1.4	20
83	Differential positive selection of malaria resistance genes in three indigenous populations of Peninsular Malaysia. Human Genetics, 2015, 134, 375-392.	1.8	19
84	Inference of multiple-wave admixtures by length distribution of ancestral tracks. Heredity, 2018, 121, 52-63.	1.2	19
85	Refining models of archaic admixture in Eurasia with ArchaicSeeker 2.0. Nature Communications, 2021, 12, 6232.	5.8	19
86	Population genomics of East Asian ethnic groups. Hereditas, 2020, 157, 49.	0.5	18
87	Deleted in Colorectal Cancer (DCC) gene polymorphism is associated with H. pylori infection among susceptible Malays from the north-eastern region of Peninsular Malaysia. Hepato-Gastroenterology, 2013, 60, 124-8.	0.5	18
88	The influence of admixture and consanguinity on population genetic diversity in Middle East. Journal of Human Genetics, 2014, 59, 615-622.	1.1	17
89	Modeling Continuous Admixture Using Admixture-Induced Linkage Disequilibrium. Scientific Reports, 2017, 7, 43054.	1.6	17
90	A new method for modeling coalescent processes with recombination. BMC Bioinformatics, 2014, 15, 273.	1.2	16

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91	Analysis of Genome-Wide RNA-Sequencing Data Suggests Age of the CEPH/Utah (CEU) Lymphoblastoid Cell Lines Systematically Biases Gene Expression Profiles. Scientific Reports, 2015, 5, 7960.	1.6	16
92	Phylogeography of Y-chromosome haplogroup O3a2b2-N6 reveals patrilineal traces of Austronesian populations on the eastern coastal regions of Asia. PLoS ONE, 2017, 12, e0175080.	1.1	16
93	HIF2A Variants Were Associated with Different Levels of High-Altitude Hypoxia among Native Tibetans. PLoS ONE, 2015, 10, e0137956.	1.1	15
94	Precision Medicine: What Challenges Are We Facing?. Genomics, Proteomics and Bioinformatics, 2016, 14, 253-261.	3.0	15
95	Genome-wide comparison of allele-specific gene expression between African and European populations. Human Molecular Genetics, 2018, 27, 1067-1077.	1.4	15
96	Identification of Close Relatives in the HUGO Pan-Asian SNP Database. PLoS ONE, 2011, 6, e29502.	1.1	14
97	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. The HUGO Journal, 2014, 8, 5.	4.1	14
98	GCH1åŸºå›åœ¨è—æ—é«˜åŽŸé€‚åº"ä¸æŒ‡¥ä½œç"". Zoological Research, 2017, 38, 155-162.	0.9	14
99	A design of multi-source samples as a shared control for association studies in genetically stratified populations. Cell Research, 2009, 19, 913-915.	5.7	13
100	Paleolithic Contingent in Modern Japanese: Estimation and Inference using Genome-wide Data. Scientific Reports, 2012, 2, 355.	1.6	13
101	Towards understanding the low prevalence of <i><scp>H</scp>elicobacter pylori</i> in <scp>M</scp>alays: Genetic variants among <i>Helicobacter pylori</i>â€negative ethnic <scp>M</scp>alays in the northâ€eastern region of Peninsular <scp>M</scp>alaysia and <scp>H</scp>an <scp>C</scp>hinese and <scp>S</scp>outh <scp>I</scp>ndians. Journal of Digestive Diseases, 2013, 14, 196-202.	0.7	13
102	Increased genetic diversity of ADME genes in African Americans compared with their putative ancestral source populations and implications for Pharmacogenomics. BMC Genetics, 2014, 15, 52.	2.7	13
103	Models, methods and tools for ancestry inference and admixture analysis. Quantitative Biology, 2017, 5, 236-250.	0.3	13
104	Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genomeâ€wide SNP data. Annals of Human Genetics, 2018, 82, 216-226.	0.3	13
105	Reintroduction of a Homocysteine Level-Associated Allele into East Asians by Neanderthal Introgression. Molecular Biology and Evolution, 2015, 32, msv176.	3.5	12
106	Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions. Heredity, 2017, 118, 503-510.	1.2	12
107	PGG.Population: a database for understanding the genomic diversity and genetic ancestry of human populations. Nucleic Acids Research, 2018, 46, D984-D993.	6.5	12
108	Response to Li etÂal.. American Journal of Human Genetics, 2009, 85, 937-939.	2.6	11

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109	Dissimilarity of contemporary and historical gene flow in a wild carrot (Daucus carota) metapopulation under contrasting levels of human disturbance: implications for risk assessment and management of transgene introgression. Annals of Botany, 2013, 112, 1361-1370.	1.4	11
110	Genetic diversity and natural selection footprints of the glycine amidinotransferase gene in various human populations. Scientific Reports, 2016, 6, 18755.	1.6	11
111	A genome-wide characterization of copy number variations in native populations of Peninsular Malaysia. European Journal of Human Genetics, 2018, 26, 886-897.	1.4	11
112	Human Population Admixture in Asia. Genomics and Informatics, 2012, 10, 133.	0.4	11
113	A probabilistic method for testing and estimating selection differences between populations. Genome Research, 2015, 25, 1903-1909.	2.4	10
114	EP300åŸºå›€è¿‡è¡¨è¾¾ƒæŽ§ä¸€æº°åŒ—æº°å•æˆ°°åŠ©©è—æ—ä°°ç¾µ€¢,å°"é«˜åŽŸä½Žæº°§çŽˆ¢ƒ. Zoological Research, 2017, 38, 163-17	0.9	10
115	Haplotype-resolved de novo assembly of a Tujia genome suggests the necessity for high-quality population-specific genome references. Cell Systems, 2022, 13, 321-333.e6.	2.9	10
116	Signature of positive selection of PTK6 gene in East Asian populations: a cross talk for Helicobacter pylori invasion and gastric cancer endemicity. Molecular Genetics and Genomics, 2015, 290, 1741-1752.	1.0	9
117	Ancestry Informative Marker Set for Han Chinese Population. G3: Genes, Genomes, Genetics, 2012, 2, 339-341.	0.8	8
118	Fine-scale population structure of Malays in Peninsular Malaysia and Singapore and implications for association studies. Human Genomics, 2015, 9, 16.	1.4	8
119	A genome-wide association study of facial morphology identifies novel genetic loci in Han Chinese. Journal of Genetics and Genomics, 2021, 48, 198-207.	1.7	8
120	Assessing genome-wide copy number variation in the Han Chinese population. Journal of Medical Genetics, 2017, 54, 685-692.	1.5	7
121	Natural Selection and Functional Potentials of Human Noncoding Elements Revealed by Analysis of Next Generation Sequencing Data. PLoS ONE, 2015, 10, e0129023.	1.1	7
122	Identification of Two Maternal Transmission Ratio Distortion Loci in Pedigrees of the Framingham Heart Study. Scientific Reports, 2013, 3, 2147.	1.6	6
123	A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. Heredity, 2018, 120, 83-89.	1.2	6
124	Detecting archaic introgression and modeling multiple-wave admixture with ArchaicSeeker 2.0. STAR Protocols, 2022, 3, 101314.	0.5	6
125	Chromosome-Wide Haplotype Sharing: A Measure Integrating Recombination Information to Reconstruct the Phylogeny of Human Populations. Annals of Human Genetics, 2011, 75, 694-706.	0.3	5
126	RET compound inheritance in Chinese patients with Hirschsprung disease: lack of penetrance from insufficient gene dysfunction. Human Genetics, 2021, 140, 813-825.	1.8	5

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127	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. Journal of Medical Genetics, 2013, 50, 534-542.	1.5	4
128	AdmixSim: A Forward-Time Simulator for Various Complex Scenarios of Population Admixture. Frontiers in Genetics, 2020, 11, 601439.	1.1	4
129	Convergent adaptive evolution—how common, or how rare?. National Science Review, 2020, 7, 945-946.	4.6	4
130	Reply to Lack of evidence for a role of PIWIL1 variants in human male infertility. Cell, 2021, 184, 1943-1944.	13.5	4
131	Complete sequence data support lack of balancing selection on PRNP in a natural Chinese population. Journal of Human Genetics, 2006, 51, 451-454.	1.1	3
132	A Probabilistic Method for Estimating the Sharing of Identity by Descent for Populations with Migration. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 281-290.	1.9	3
133	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. BMC Genomics, 2019, 20, 842.	1.2	3
134	Paternal gene pool of Malays in Southeast Asia and its applications for the early expansion of Austronesians. American Journal of Human Biology, 2021, 33, e23486.	0.8	3
135	Improved NGS variant calling tool for the *PRSS1–PRSS2* locus. Gut, 2023, 72, 210-212.	6.1	3
136	A comparative analysis of genetic diversity of candidate genes associated with type 2 diabetes in worldwide populations. Yi Chuan = Hereditas / Zhongguo Yi Chuan Xue Hui Bian Ji, 2016, 38, 543-559.	0.1	3
137	A protocol for applying a population-specific reference genome assembly to population genetics and medical studies. STAR Protocols, 2022, 3, 101440.	0.5	3
138	Reply to Denham and Donohue: Asian-Papuan genetic admixture is in excellent agreement with Austronesian dispersal in eastern Indonesia. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2578-E2578.	3.3	2
139	Large-scale genome-wide scans do not support petaloid toenail as a Mendelian trait. Journal of Genetics and Genomics, 2016, 43, 702-704.	1.7	2
140	Shared Signature of Recent Positive Selection on the *TSBP1–BTNL2–HLA-DRA* Genes in Five Native Populations from North Borneo. Genome Biology and Evolution, 2020, 12, 2245-2257.	1.1	2
141	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. Journal of Genetics and Genomics, 2021, 48, 972-983.	1.7	2
142	AdmixSim 2: a forward-time simulator for modeling complex population admixture. BMC Bioinformatics, 2021, 22, 506.	1.2	2
143	Genetic Connections and Convergent Evolution of Tropical Indigenous Peoples in Asia. Molecular Biology and Evolution, 2022, 39, .	3.5	2
144	Lineage-specific positive selection on *ACE2* contributes to the genetic susceptibility of COVID-19. National Science Review, 2022, 9, .	4.6	2

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145	CNVbase: Batch identification of novel and rare copy number variations based on multi-ethnic population data. Journal of Genetics and Genomics, 2017, 44, 367-370.	1.7	1
146	The Peopling and Migration History of the Natives in Peninsular Malaysia and Borneo: A Glimpse on the Studies Over the Past 100 years. Frontiers in Genetics, 2022, 13, 767018.	1.1	1
147	A mechanism of nitric oxide regulation in high-altitude Tibetans. National Science Review, 2018, 5, 531-531.	4.6	0
148	Population Genomics of High-Altitude Adaptation. Evolutionary Studies, 2021, , 67-100.	0.2	0
149	Population Genetics in the Genomic Era. , 0, , .		0
150	Novel Genetic Loci Affecting Facial Shape Variation in Humans. SSRN Electronic Journal, 0, , .	0.4	0