

Shuhua Xu

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.

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	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> , 2022 , 13, 767018	4.5	0
150	Genomic diversity and post-admixture adaptation in the Uyghurs.. <i>National Science Review</i> , 2022 , 9, nwab1124	11.24	3
149	Haplotype-resolved de novo assembly of a Tujia genome suggests the necessity for high-quality population-specific genome references.. <i>Cell Systems</i> , 2022 ,	10.6	3
148	Improved NGS variant calling tool for the locus.. <i>Gut</i> , 2022 ,	19.2	0
147	Mapping genomic loci implicates genes and synaptic biology in schizophrenia.. <i>Nature</i> , 2022 ,	50.4	35
146	Detecting archaic introgression and modeling multiple-wave admixture with ArchaicSeeker 2.0.. <i>STAR Protocols</i> , 2022 , 3, 101314	1.4	0
145	A protocol for applying a population-specific reference genome assembly to population genetics and medical studies. <i>STAR Protocols</i> , 2022 , 3, 101440	1.4	
144	Genetic connections and convergent evolution of tropical indigenous peoples in Asia.. <i>Molecular Biology and Evolution</i> , 2021 ,	8.3	1
143	AdmixSim 2: a forward-time simulator for modeling complex population admixture. <i>BMC Bioinformatics</i> , 2021 , 22, 506	3.6	1
142	Refining models of archaic admixture in Eurasia with ArchaicSeeker 2.0. <i>Nature Communications</i> , 2021 , 12, 6232	17.4	2
141	Y-LineageTracker: a high-throughput analysis framework for Y-chromosomal next-generation sequencing data. <i>BMC Bioinformatics</i> , 2021 , 22, 114	3.6	2
140	Reply to Lack of evidence for a role of PIWIL1 variants in human male infertility. <i>Cell</i> , 2021 , 184, 1943-1944	46.2	0
139	Genetic Origins and Sex-Biased Admixture of the Huis. <i>Molecular Biology and Evolution</i> , 2021 , 38, 3804-3819	11.9	4
138	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> , 2021 , 118,	11.5	12
137	A genome-wide association study of facial morphology identifies novel genetic loci in Han Chinese. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 198-207	4	1
136	Paternal gene pool of Malays in Southeast Asia and its applications for the early expansion of Austronesians. <i>American Journal of Human Biology</i> , 2021 , 33, e23486	2.7	1
135	RET compound inheritance in Chinese patients with Hirschsprung disease: lack of penetrance from insufficient gene dysfunction. <i>Human Genetics</i> , 2021 , 140, 813-825	6.3	1

134	Population Genomics of High-Altitude Adaptation. <i>Evolutionary Studies</i> , 2021 , 67-100	2.5	
133	The HuaBiao project: whole-exome sequencing of 5000 Han Chinese individuals. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 1032-1035	4	2
132	Micro-coevolution of host genetics with gut microbiome in three Chinese ethnic groups. <i>Journal of Genetics and Genomics</i> , 2021 , 48, 972-983	4	1
131	Population genomics of East Asian ethnic groups. <i>Hereditas</i> , 2020 , 157, 49	2.4	4
130	Convergent adaptive evolution-how common, or how rare?. <i>National Science Review</i> , 2020 , 7, 945-946	10.8	2
129	Database Resources of the National Genomics Data Center in 2020. <i>Nucleic Acids Research</i> , 2020 , 48, D24-D33	20.1	119
128	Triose Kinase Controls the Lipogenic Potential of Fructose and Dietary Tolerance. <i>Cell Metabolism</i> , 2020 , 32, 605-618.e7	24.6	13
127	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> , 2020 , 12, 2245-2257	3.9	2
126	AdmixSim: A Forward-Time Simulator for Various Complex Scenarios of Population Admixture. <i>Frontiers in Genetics</i> , 2020 , 11, 601439	4.5	3
125	PGG.Han: the Han Chinese genome database and analysis platform. <i>Nucleic Acids Research</i> , 2020 , 48, D971-D976	20.1	31
124	assembly of a Tibetan genome and identification of novel structural variants associated with high-altitude adaptation. <i>National Science Review</i> , 2020 , 7, 391-402	10.8	11
123	PGG.SNV: understanding the evolutionary and medical implications of human single nucleotide variations in diverse populations. <i>Genome Biology</i> , 2019 , 20, 215	18.3	11
122	Prioritizing natural-selection signals from the deep-sequencing genomic data suggests multi-variant adaptation in Tibetan highlanders. <i>National Science Review</i> , 2019 , 6, 1201-1222	10.8	15
121	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. <i>Nature Communications</i> , 2019 , 10, 4892	17.4	140
120	Novel genetic loci affecting facial shape variation in humans. <i>ELife</i> , 2019 , 8,	8.9	22
119	Comparative genetic architectures of schizophrenia in East Asian and European populations. <i>Nature Genetics</i> , 2019 , 51, 1670-1678	36.3	185
118	Analysis of five deep-sequenced trio-genomes of the Peninsular Malaysia Orang Asli and North Borneo populations. <i>BMC Genomics</i> , 2019 , 20, 842	4.5	0
117	Trio deep-sequencing does not reveal unexpected off-target and on-target mutations in Cas9-edited rhesus monkeys. <i>Nature Communications</i> , 2019 , 10, 5525	17.4	15

116	MultiWaver 2.0: modeling discrete and continuous gene flow to reconstruct complex population admixtures. <i>European Journal of Human Genetics</i> , 2019 , 27, 133-139	5.3	13
115	A genome-wide characterization of copy number variations in native populations of Peninsular Malaysia. <i>European Journal of Human Genetics</i> , 2018 , 26, 886-897	5.3	6
114	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> , 2018 , 82, 216-226	2.2	6
113	PGG.Population: a database for understanding the genomic diversity and genetic ancestry of human populations. <i>Nucleic Acids Research</i> , 2018 , 46, D984-D993	20.1	7
112	Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. <i>Human Genetics</i> , 2018 , 137, 161-173	6.3	15
111	Genome-wide comparison of allele-specific gene expression between African and European populations. <i>Human Molecular Genetics</i> , 2018 , 27, 1067-1077	5.6	8
110	Inference of multiple-wave admixtures by length distribution of ancestral tracks. <i>Heredity</i> , 2018 , 121, 52-63	3.6	11
109	Meta-analysis of genome-wide association studies identifies 8 novel loci involved in shape variation of human head hair. <i>Human Molecular Genetics</i> , 2018 , 27, 559-575	5.6	33
108	Genetic structure, divergence and admixture of Han Chinese, Japanese and Korean populations. <i>Hereditas</i> , 2018 , 155, 19	2.4	48
107	A mechanism of nitric oxide regulation in high-altitude Tibetans. <i>National Science Review</i> , 2018 , 5, 531-538	1.8	8
106	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. <i>European Journal of Human Genetics</i> , 2018 , 26, 1687-1696	5.3	12
105	Adaptation of human skin color in various populations. <i>Hereditas</i> , 2018 , 155, 1	2.4	34
104	Nomogram to predict lymph node metastasis in patients with early oesophageal squamous cell carcinoma. <i>British Journal of Surgery</i> , 2018 , 105, 1464-1470	5.3	12
103	Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations. <i>Molecular Genetics and Genomics</i> , 2018 , 293, 1293-1300	3.1	23
102	A missense point mutation in COL10A1 identified with whole-genome deep sequencing in a 7-generation Pakistan dwarf family. <i>Heredity</i> , 2018 , 120, 83-89	3.6	6
101	A metagenomic approach to dissect the genetic composition of enterotypes in Han Chinese and two Muslim groups. <i>Systematic and Applied Microbiology</i> , 2018 , 41, 1-12	4.2	13
100	AncestryPainter: A Graphic Program for Displaying Ancestry Composition of Populations and Individuals. <i>Genomics, Proteomics and Bioinformatics</i> , 2018 , 16, 382-385	6.5	10
99	Genome-wide association studies and CRISPR/Cas9-mediated gene editing identify regulatory variants influencing eyebrow thickness in humans. <i>PLoS Genetics</i> , 2018 , 14, e1007640	6	14

98	Towards broadening Forensic DNA Phenotyping beyond pigmentation: Improving the prediction of head hair shape from DNA. <i>Forensic Science International: Genetics</i> , 2018 , 37, 241-251	4.3	24
97	Genome-wide variants of Eurasian facial shape differentiation and a prospective model of DNA based face prediction. <i>Journal of Genetics and Genomics</i> , 2018 , 45, 419-432	4	16
96	Characterising private and shared signatures of positive selection in 37 Asian populations. <i>European Journal of Human Genetics</i> , 2017 , 25, 499-508	5.3	15
95	Down-Regulation of EPAS1 Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia. <i>Molecular Biology and Evolution</i> , 2017 , 34, 818-830	8.3	58
94	Inference of multiple-wave population admixture by modeling decay of linkage disequilibrium with polynomial functions. <i>Heredity</i> , 2017 , 118, 503-510	3.6	9
93	Genetic History of Xinjiang's Uyghurs Suggests Bronze Age Multiple-Way Contacts in Eurasia. <i>Molecular Biology and Evolution</i> , 2017 , 34, 2572-2582	8.3	38
92	Modeling Continuous Admixture Using Admixture-Induced Linkage Disequilibrium. <i>Scientific Reports</i> , 2017 , 7, 43054	4.9	9
91	Phylogeography of Y-chromosome haplogroup O3a2b2-N6 reveals patrilineal traces of Austronesian populations on the eastern coastal regions of Asia. <i>PLoS ONE</i> , 2017 , 12, e0175080	3.7	12
90	The fine-scale genetic structure and evolution of the Japanese population. <i>PLoS ONE</i> , 2017 , 12, e0185487	3.7	21
89	contributes to high-altitude adaptation in Tibetans by regulating nitric oxide production. <i>Zoological Research</i> , 2017 , 38, 163-170	3.4	5
88	Homozygous p.Ser267Phe in SLC10A1 is associated with a new type of hypercholanemia and implications for personalized medicine. <i>Scientific Reports</i> , 2017 , 7, 9214	4.9	23
87	Models, methods and tools for ancestry inference and admixture analysis. <i>Quantitative Biology</i> , 2017 , 5, 236-250	3.9	6
86	CNVbase: Batch identification of novel and rare copy number variations based on multi-ethnic population data. <i>Journal of Genetics and Genomics</i> , 2017 , 44, 367-370	4	1
85	Assessing genome-wide copy number variation in the Han Chinese population. <i>Journal of Medical Genetics</i> , 2017 , 54, 685-692	5.8	5
84	Differentiated demographic histories and local adaptations between Sherpas and Tibetans. <i>Genome Biology</i> , 2017 , 18, 115	18.3	40
83	plays a role in the high-altitude adaptation of Tibetans. <i>Zoological Research</i> , 2017 , 38, 155-162	3.4	9
82	Ancestral Origins and Genetic History of Tibetan Highlanders. <i>American Journal of Human Genetics</i> , 2016 , 99, 580-594	11	124
81	Precision Medicine: What Challenges Are We Facing?. <i>Genomics, Proteomics and Bioinformatics</i> , 2016 , 14, 253-261	6.5	9

80	Genetic diversity and natural selection footprints of the glycine amidinotransferase gene in various human populations. <i>Scientific Reports</i> , 2016 , 6, 18755	4.9	6
79	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. <i>Molecular Biology and Evolution</i> , 2016 , 33, 1177-87	8.3	28
78	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> , 2016 , 13, 281-90	3	1
77	Pooled analysis of genome-wide association studies of cervical intraepithelial neoplasia 3 (CIN3) identifies a new susceptibility locus. <i>Oncotarget</i> , 2016 , 7, 42216-42224	3.3	16
76	Ancestry variation and footprints of natural selection along the genome in Latin American populations. <i>Scientific Reports</i> , 2016 , 6, 21766	4.9	17
75	Length Distribution of Ancestral Tracks under a General Admixture Model and Its Applications in Population History Inference. <i>Scientific Reports</i> , 2016 , 6, 20048	4.9	15
74	Large-scale genome-wide scans do not support petaloid toenail as a Mendelian trait. <i>Journal of Genetics and Genomics</i> , 2016 , 43, 702-704	4	0
73	EDARV370A associated facial characteristics in Uyghur population revealing further pleiotropic effects. <i>Human Genetics</i> , 2016 , 135, 99-108	6.3	15
72	Genome-wide scans reveal variants at EDAR predominantly affecting hair straightness in Han Chinese and Uyghur populations. <i>Human Genetics</i> , 2016 , 135, 1279-1286	6.3	18
71	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> , 2016 , 38, 543-559	1.4	3
70	Differential Natural Selection of Human Zinc Transporter Genes between African and Non-African Populations. <i>Scientific Reports</i> , 2015 , 5, 9658	4.9	14
69	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> , 2015 , 290, 1741-52	3.1	7
68	Reintroduction of a Homocysteine Level-Associated Allele into East Asians by Neanderthal Introgression. <i>Molecular Biology and Evolution</i> , 2015 , 32, 3108-13	8.3	8
67	Quantitating and dating recent gene flow between European and East Asian populations. <i>Scientific Reports</i> , 2015 , 5, 9500	4.9	20
66	A probabilistic method for testing and estimating selection differences between populations. <i>Genome Research</i> , 2015 , 25, 1903-9	9.7	8
65	The p.Ser267Phe variant in SLC10A1 is associated with resistance to chronic hepatitis B. <i>Hepatology</i> , 2015 , 61, 1251-60	11.2	59
64	Dissecting the genetic structure and admixture of four geographical Malay populations. <i>Scientific Reports</i> , 2015 , 5, 14375	4.9	17
63	Gossypium barbadense genome sequence provides insight into the evolution of extra-long staple fiber and specialized metabolites. <i>Scientific Reports</i> , 2015 , 5, 14139	4.9	165

62	Fine-scale population structure of Malays in Peninsular Malaysia and Singapore and implications for association studies. <i>Human Genomics</i> , 2015 , 9, 16	6.8	7
61	HIF2A Variants Were Associated with Different Levels of High-Altitude Hypoxia among Native Tibetans. <i>PLoS ONE</i> , 2015 , 10, e0137956	3.7	11
60	Copy number variations and genetic admixtures in three Xinjiang ethnic minority groups. <i>European Journal of Human Genetics</i> , 2015 , 23, 536-42	5.3	18
59	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> , 2015 , 97, 54-66	11	40
58	Differential positive selection of malaria resistance genes in three indigenous populations of Peninsular Malaysia. <i>Human Genetics</i> , 2015 , 134, 375-92	6.3	17
57	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> , 2015 , 5, 7960	4.9	12
56	Natural Selection and Functional Potentials of Human Noncoding Elements Revealed by Analysis of Next Generation Sequencing Data. <i>PLoS ONE</i> , 2015 , 10, e0129023	3.7	6
55	A new method for modeling coalescent processes with recombination. <i>BMC Bioinformatics</i> , 2014 , 15, 273	3.6	10
54	Increased genetic diversity of ADME genes in African Americans compared with their putative ancestral source populations and implications for pharmacogenomics. <i>BMC Genetics</i> , 2014 , 15, 52	2.6	11
53	Neanderthal origin of the haplotypes carrying the functional variant Val92Met in the MC1R in modern humans. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1994-2003	8.3	23
52	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> , 2014 , 22, 930-7	5.3	19
51	The population genomic landscape of human genetic structure, admixture history and local adaptation in Peninsular Malaysia. <i>Human Genetics</i> , 2014 , 133, 1169-85	6.3	23
50	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> , 2014 , 22, 248-53	5.3	31
49	Neanderthal introgression at chromosome 3p21.31 was under positive natural selection in East Asians. <i>Molecular Biology and Evolution</i> , 2014 , 31, 683-95	8.3	46
48	<i>Helicobacter pylori</i> induces increased expression of the vitamin d receptor in immune responses. <i>Helicobacter</i> , 2014 , 19, 37-47	4.9	37
47	Variation and signatures of selection on the human face. <i>Journal of Human Evolution</i> , 2014 , 75, 143-52	3.1	20
46	The influence of admixture and consanguinity on population genetic diversity in Middle East. <i>Journal of Human Genetics</i> , 2014 , 59, 615-22	4.3	11
45	Genetic architectures of ADME genes in five Eurasian admixed populations and implications for drug safety and efficacy. <i>Journal of Medical Genetics</i> , 2014 , 51, 614-22	5.8	17

44	A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. <i>The HUGO Journal</i> , 2014 , 8, 5		11
43	Towards understanding the low prevalence of <i>Helicobacter pylori</i> in Malays: genetic variants among <i>Helicobacter pylori</i> -negative ethnic Malays in the north-eastern region of Peninsular Malaysia and Han Chinese and South Indians. <i>Journal of Digestive Diseases</i> , 2013 , 14, 196-202	3.3	9
42	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> , 2013 , 112, 1361-70	4.1	8
41	Identification of well-differentiated gene expressions between Han Chinese and Japanese using genome-wide microarray data analysis. <i>Journal of Medical Genetics</i> , 2013 , 50, 534-42	5.8	4
40	Identification of two maternal transmission ratio distortion loci in pedigrees of the Framingham heart study. <i>Scientific Reports</i> , 2013 , 3, 2147	4.9	6
39	Genome-wide landscapes of human local adaptation in Asia. <i>PLoS ONE</i> , 2013 , 8, e54224	3.7	17
38	Identification of functional mutations in GATA4 in patients with congenital heart disease. <i>PLoS ONE</i> , 2013 , 8, e62138	3.7	38
37	Principal component analysis reveals the 1000 Genomes Project does not sufficiently cover the human genetic diversity in Asia. <i>Frontiers in Genetics</i> , 2013 , 4, 127	4.5	26
36	Gastric precancerous lesions are associated with gene variants in <i>Helicobacter pylori</i> -susceptible ethnic Malays. <i>World Journal of Gastroenterology</i> , 2013 , 19, 3615-22	5.6	18
35	Deleted in Colorectal Cancer (DCC) gene polymorphism is associated with <i>H. pylori</i> infection among susceptible Malays from the north-eastern region of Peninsular Malaysia. <i>Hepato-Gastroenterology</i> , 2013 , 60, 124-8		8
34	Deletion of the APOBEC3B gene strongly impacts susceptibility to falciparum malaria. <i>Infection, Genetics and Evolution</i> , 2012 , 12, 142-8	4.5	25
33	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> , 2012 , 109, 4574-9	11.5	60
32	Exploring population admixture dynamics via empirical and simulated genome-wide distribution of ancestral chromosomal segments. <i>American Journal of Human Genetics</i> , 2012 , 91, 849-62	11	25
31	Genome-wide detection of natural selection in African Americans pre- and post-admixture. <i>Genome Research</i> , 2012 , 22, 519-27	9.7	60
30	Ancestry informative marker set for han chinese population. <i>G3: Genes, Genomes, Genetics</i> , 2012 , 2, 339-41	4.1	8
29	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> , 2012 , 109, E2578-E2578	11.5	0
28	A systematic characterization of genes underlying both complex and Mendelian diseases. <i>Human Molecular Genetics</i> , 2012 , 21, 1611-24	5.6	27
27	Paleolithic Contingent in Modern Japanese: Estimation and Inference using Genome-wide Data. <i>Scientific Reports</i> , 2012 , 2, 355	4.9	11

26	Human population admixture in Asia. <i>Genomics and Informatics</i> , 2012 , 10, 133-44	1.9	8
25	Population genetic structure of peninsular Malaysia Malay sub-ethnic groups. <i>PLoS ONE</i> , 2011 , 6, e18312	3.7	62
24	Human migration through bottlenecks from Southeast Asia into East Asia during Last Glacial Maximum revealed by Y chromosomes. <i>PLoS ONE</i> , 2011 , 6, e24282	3.7	58
23	A map of copy number variations in Chinese populations. <i>PLoS ONE</i> , 2011 , 6, e27341	3.7	40
22	Identification of close relatives in the HUGO Pan-Asian SNP database. <i>PLoS ONE</i> , 2011 , 6, e29502	3.7	10
21	Chromosome-wide haplotype sharing: a measure integrating recombination information to reconstruct the phylogeny of human populations. <i>Annals of Human Genetics</i> , 2011 , 75, 694-706	2.2	2
20	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> , 2011 , 19, 224-30	5.3	66
19	A genome-wide search for signals of high-altitude adaptation in Tibetans. <i>Molecular Biology and Evolution</i> , 2011 , 28, 1003-11	8.3	231
18	PanSNPdb: the Pan-Asian SNP genotyping database. <i>PLoS ONE</i> , 2011 , 6, e21451	3.7	40
17	PEAS V1.0: a package for elementary analysis of SNP data. <i>Molecular Ecology Resources</i> , 2010 , 10, 1085-88	4.4	28
16	Genetic evidence supports linguistic affinity of Mlabri—a hunter-gatherer group in Thailand. <i>BMC Genetics</i> , 2010 , 11, 18	2.6	20
15	Haplotype-sharing analysis showing Uyghurs are unlikely genetic donors. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2197-206	8.3	27
14	A design of multi-source samples as a shared control for association studies in genetically stratified populations. <i>Cell Research</i> , 2009 , 19, 913-5	24.7	2
13	Genomic dissection of population substructure of Han Chinese and its implication in association studies. <i>American Journal of Human Genetics</i> , 2009 , 85, 762-74	11	264
12	Response to Li et al.. <i>American Journal of Human Genetics</i> , 2009 , 85, 937-939	11	10
11	Mapping human genetic diversity in Asia. <i>Science</i> , 2009 , 326, 1541-5	33.3	444
10	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> , 2008 , 16, 705-17	5.3	38
9	Analysis of genomic admixture in Uyghur and its implication in mapping strategy. <i>American Journal of Human Genetics</i> , 2008 , 82, 883-94	11	142

8	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> , 2008 , 105, 10414-9	11.5	148
7	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> , 2008 , 83, 322-36	11	100
6	Dissecting linkage disequilibrium in African-American genomes: roles of markers and individuals. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2049-58	8.3	17
5	Complete sequence data support lack of balancing selection on PRNP in a natural Chinese population. <i>Journal of Human Genetics</i> , 2006 , 51, 451-454	4.3	3
4	AdmixSim: A Forward-Time Simulator for Various and Complex Scenarios of Population Admixture		2
3	The history and evolution of the Denisovan-EPAS1 haplotype in Tibetans		4
2	Trio deep-sequencing does not reveal unexpected mutations in Cas9-edited monkeys		1
1	De novo assembly of a Tibetan genome and identification of novel structural variants associated with high altitude adaptation		1