Yin-Qiu Cui

List of Publications by Year in descending order

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38
papers ci

1,551 citations

430442 18 h-index 36 g-index

41 all docs

41 docs citations

41 times ranked 1880 citing authors

#	Article	IF	CITATIONS
1	Postâ€last glacial maximum expansion of Yâ€chromosome haplogroup <scp>C2aâ€L1373</scp> in northern Asia and its implications for the origin of Native Americans. American Journal of Physical Anthropology, 2021, 174, 363-374.	2.1	11
2	The Baigetuobie cemetery: New discovery and human genetic features of Andronovo community's diffusion to the Eastern Tianshan Mountains (1800–1500 BC). Holocene, 2021, 31, 217-229.	0.9	5
3	Ancient Y-DNA with reconstructed phylogeny provides insights into the demographic history of paternal haplogroup N1a2-F1360. Journal of Genetics and Genomics, 2021, 48, 1130-1133.	1.7	5
4	Ancient Mitochondrial Genomes Reveal Extensive Genetic Influence of the Steppe Pastoralists in Western Xinjiang. Frontiers in Genetics, 2021, 12, 740167.	1.1	6
5	A 3,000-year-old, basal S. enterica lineage from Bronze Age Xinjiang suggests spread along the Proto-Silk Road. PLoS Pathogens, 2021, 17, e1009886.	2.1	7
6	Ancient genome analyses shed light on kinship organization and mating practice of Late Neolithic society in China. IScience, 2021, 24, 103352.	1.9	10
7	The genomic origins of the Bronze Age Tarim Basin mummies. Nature, 2021, 599, 256-261.	13.7	65
8	Triangulation supports agricultural spread of the Transeurasian languages. Nature, 2021, 599, 616-621.	13.7	58
9	Bioarchaeological perspective on the expansion of Transeurasian languages in Neolithic Amur River basin. Evolutionary Human Sciences, 2020, 2, .	0.9	6
10	Ancient genomes from northern China suggest links between subsistence changes and human migration. Nature Communications, 2020, 11 , 2700.	5.8	133
11	Ancient DNA indicates human population shifts and admixture in northern and southern China. Science, 2020, 369, 282-288.	6.0	214
12	Study on the burial practice of tomb M13 of the Yangshao culture at Baligang site in Dengzhou City. Chinese Archaeology, 2020, 20, 132-138.	0.1	1
13	Ancient Genomes Reveal Yamnaya-Related Ancestry and a Potential Source of Indo-European Speakers in Iron Age Tianshan. Current Biology, 2019, 29, 2526-2532.e4.	1.8	64
14	G9a and histone deacetylases are crucial for Snail2â€mediated Eâ€cadherin repression and metastasis in hepatocellular carcinoma. Cancer Science, 2019, 110, 3442-3452.	1.7	40
15	Different maternal lineages revealed by ancient mitochondrial genome of <i>Camelus bactrianus</i> from China. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2019, 30, 786-793.	0.7	4
16	Phylogenetic and population structural inference from genomic ancestry maintained in presentâ€day common wheat Chinese landraces. Plant Journal, 2019, 99, 201-215.	2.8	5
17	Mitochondrial Genome of an 8,400-Year-Old Individual from Northern China Reveals a Novel Subclade under C5d. Human Biology, 2019, 91, 21.	0.4	1
18	Ancient mitochondrial genome reveals trace of prehistoric migration in the east Pamir by pastoralists. Journal of Human Genetics, 2016, 61, 103-108.	1.1	8

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19	Refined phylogenetic structure of an abundant East Asian Y-chromosomal haplogroup O*-M134. European Journal of Human Genetics, 2016, 24, 307-309.	1.4	14
20	Size-dependent filtration of nanoparticles on porous films composed by polystyrene microsphere monolayers and applications in site-selective deposition of nanoparticles. Journal of Nanoparticle Research, 2015, 17, 1.	0.8	1
21	Fabrication of periodical Ag–Au compound nanostructure films with controllable Ag nanoparticle aggregate patterns: a study on surfaceâ€enhanced Raman scattering. Journal of Raman Spectroscopy, 2015, 46, 1117-1123.	1.2	7
22	Low Mitochondrial DNA Diversity in an Ancient Population from China: Insight into Social Organization at the Fujia Site. Human Biology, 2015, 87, 71.	0.4	30
23	Ancient <scp>DNA</scp> reveals a migration of the ancient <scp>D</scp> iâ€qiang populations into <scp>X</scp> injiang as early as the early <scp>B</scp> ronze <scp>A</scp> ge. American Journal of Physical Anthropology, 2015, 157, 71-80.	2.1	39
24	Comparative and population mitogenomic analyses of Madagascar's extinct, giant â€~subfossil' lemurs. Journal of Human Evolution, 2015, 79, 45-54.	1.3	86
25	A potential signature of eight long non-coding RNAs predicts survival in patients with non-small cell lung cancer. Journal of Translational Medicine, 2015, 13, 231.	1.8	207
26	Identification of kinship and occupant status in Mongolian noble burials of the Yuan Dynasty through a multidisciplinary approach. Philosophical Transactions of the Royal Society B: Biological Sciences, 2015, 370, 20130378.	1.8	22
27	Submicron patterns obtained by thermal-induced reconstruction of self-assembled monolayer of Ag nanoparticles and their application in SERS. Applied Surface Science, 2014, 309, 295-299.	3.1	9
28	Y Chromosome analysis of prehistoric human populations in the West Liao River Valley, Northeast China. BMC Evolutionary Biology, 2013, 13, 216.	3.2	33
29	Ancient DNA Analysis of Mid-Holocene Individuals from the Northwest Coast of North America Reveals Different Evolutionary Paths for Mitogenomes. PLoS ONE, 2013, 8, e66948.	1.1	56
30	Ancient DNA analysis of desiccated wheat grains excavated from a Bronze Age cemetery in Xinjiang. Journal of Archaeological Science, 2011, 38, 115-119.	1.2	55
31	Genetic characteristics and migration history of a bronze culture population in the West Liao-River valley revealed by ancient DNA. Journal of Human Genetics, 2011, 56, 815-822.	1.1	32
32	Early Eurasian migration traces in the Tarim Basin revealed by mtDNA polymorphisms. American Journal of Physical Anthropology, 2010, 142, 558-564.	2.1	23
33	Evidence that a West-East admixed population lived in the Tarim Basin as early as the early Bronze Age. BMC Biology, 2010, 8, 15.	1.7	101
34	Analysis of the matrilineal genetic structure of population in the early Iron Age from Tarim Basin, Xinjiang, China. Science Bulletin, 2009, 54, 3916-3923.	1.7	11
35	Mitochondrial DNA analysis of human remains from the Yuansha site in Xinjiang, China. Science in China Series C: Life Sciences, 2008, 51, 205-213.	1.3	16
36	Molecular genetic analysis of Dongzhou-period ancient human of Helingeer in Inner Mongolia, China. Frontiers of Biology in China: Selected Publications From Chinese Universities, 2008, 3, 9-12.	0.2	0

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37	Molecular genetic analysis of Wanggu remains, Inner Mongolia, China. American Journal of Physical Anthropology, 2007, 132, 285-291.	2.1	13
38	An enzyme-coupled continuous spectrophotometric assay for S-adenosylmethionine-dependent methyltransferases. Analytical Biochemistry, 2006, 350, 249-255.	1.1	139