

Lan-Hai Wei

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

2,237
citations

516215

16
h-index

264894

42
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59
all docs

59
docs citations

59
times ranked

2750
citing authors

#	ARTICLE	IF	CITATIONS
1	Northern gene flow into southeastern East Asians inferred from genome-wide array genotyping. <i>Journal of Systematics and Evolution</i> , 2023, 61, 179-197.	1.6	9
2	Reconstructing the genetic admixture history of Tai-Kadai and Sinitic people: Insights from genome-wide SNP data from South China. <i>Journal of Systematics and Evolution</i> , 2023, 61, 157-178.	1.6	9
3	Fine-scale north-south genetic admixture profile in Shaanxi Han Chinese revealed by genome-wide demographic history reconstruction. <i>Journal of Systematics and Evolution</i> , 2022, 60, 955-972.	1.6	26
4	Genomic history and forensic characteristics of Sherpa highlanders on the Tibetan Plateau inferred from high-resolution InDel panel and genome-wide SNPs. <i>Forensic Science International: Genetics</i> , 2022, 56, 102633.	1.6	13
5	The genomic formation of Tanka people, an isolated "gypsies in water" in the coastal region of Southeast China. <i>American Journal of Biological Anthropology</i> , 2022, 178, 154-170.	0.6	4
6	Paternal origin of Tungusic-speaking populations: Insights from the updated phylogenetic tree of Y-chromosome haplogroup C2a1M86. <i>American Journal of Human Biology</i> , 2021, 33, e23462.	0.8	11
7	Genomic insight into the population history of Central Han Chinese. <i>Annals of Human Biology</i> , 2021, 48, 49-55.	0.4	3
8	Post-last glacial maximum expansion of Y-chromosome haplogroup C2a1L1373 in northern Asia and its implications for the origin of Native Americans. <i>American Journal of Physical Anthropology</i> , 2021, 174, 363-374.	2.1	11
9	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.	0.8	3
10	Genomic insights into the formation of human populations in East Asia. <i>Nature</i> , 2021, 591, 413-419.	13.7	216
11	Ancient DNA and multimethod dating confirm the late arrival of anatomically modern humans in southern China. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	49
12	Shared paternal ancestry of Han, Tai-Kadai-speaking, and Austronesian-speaking populations as revealed by the high resolution phylogeny of O1a1M119 and distribution of its sub-lineages within China. <i>American Journal of Physical Anthropology</i> , 2021, 174, 686-700.	2.1	22
13	Fine-Scale Genetic Structure and Natural Selection Signatures of Southwestern Hans Inferred From Patterns of Genome-Wide Allele, Haplotype, and Haplogroup Lineages. <i>Frontiers in Genetics</i> , 2021, 12, 727821.	1.1	15
14	Ancient Y-DNA with reconstructed phylogeny provides insights into the demographic history of paternal haplogroup N1a2-F1360. <i>Journal of Genetics and Genomics</i> , 2021, 48, 1130-1133.	1.7	5
15	Peopling History of the Tibetan Plateau and Multiple Waves of Admixture of Tibetans Inferred From Both Ancient and Modern Genome-Wide Data. <i>Frontiers in Genetics</i> , 2021, 12, 725243.	1.1	27
16	Medieval Super-Grandfather founder of Western Kazakh Clans from Haplogroup C2a1a2-M48. <i>Journal of Human Genetics</i> , 2021, 66, 707-716.	1.1	9
17	Genetic substructure and admixture of Mongolians and Kazakhs inferred from genome-wide array genotyping. <i>Annals of Human Biology</i> , 2020, 47, 620-628.	0.4	14
18	The medieval Mongolian roots of Y-chromosomal lineages from South Kazakhstan. <i>BMC Genetics</i> , 2020, 21, 87.	2.7	15

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19	Phylogenetic analysis of the Y-chromosome haplogroup C2b-F1067, a dominant paternal lineage in Eastern Eurasia. <i>Journal of Human Genetics</i> , 2020, 65, 823-829.	1.1	11
20	Y-chromosome evidence confirmed the Kerei-Abakh origin of Aksay Kazakhs. <i>Journal of Human Genetics</i> , 2020, 65, 797-803.	1.1	7
21	Forensic Features and Population Genetic Structure of Dong, Yi, Han, and Chuanqing Human Populations in Southwest China Inferred From Insertion/Deletion Markers. <i>Frontiers in Genetics</i> , 2020, 11, 360.	1.1	17
22	Genome-wide analysis of unrecognised ethnic group Chuanqing people revealing a close affinity with Southern Han Chinese. <i>Annals of Human Biology</i> , 2020, 47, 465-471.	0.4	9
23	Inferring the population history of Tai-Kadai-speaking people and southernmost Han Chinese on Hainan Island by genome-wide array genotyping. <i>European Journal of Human Genetics</i> , 2020, 28, 1111-1123.	1.4	49
24	Paternal heritage of the Han Chinese in Henan province (Central China): high diversity and evidence of <i>in situ</i> Neolithic expansions. <i>Annals of Human Biology</i> , 2020, 47, 294-299.	0.4	2
25	Phylogeography of Y-chromosome haplogroup Q1a1a-M120, a paternal lineage connecting populations in Siberia and East Asia. <i>Annals of Human Biology</i> , 2019, 46, 261-266.	0.4	14
26	Relating Clans Ao and Aisin Gioro from northeast China by whole Y-chromosome sequencing. <i>Journal of Human Genetics</i> , 2019, 64, 775-780.	1.1	4
27	Molecular genealogy of Tusi Lu's family reveals their paternal relationship with Jochi, Genghis Khan's eldest son. <i>Journal of Human Genetics</i> , 2019, 64, 815-820.	1.1	11
28	Paternal Y chromosomal genotyping reveals multiple large-scale admixtures in the formation of Lolo-Burmese-speaking populations in southwest China. <i>Annals of Human Biology</i> , 2019, 46, 581-588.	0.4	3
29	Uniparental Genetic Analyses Reveal the Major Origin of Fujian Tanka from Ancient Indigenous Daic Populations. <i>Human Biology</i> , 2019, 91, 257.	0.4	6
30	The genetic assimilation in language borrowing inferred from Jing People. <i>American Journal of Physical Anthropology</i> , 2018, 166, 638-648.	2.1	15
31	Genetic analysis of 17 Y-STR loci from 1026 individuals of Han populations in Jilin Province, Northeast China. <i>International Journal of Legal Medicine</i> , 2018, 132, 1309-1311.	1.2	6
32	Whole-sequence analysis indicates that the Y chromosome C2*-Star Cluster traces back to ordinary Mongols, rather than Genghis Khan. <i>European Journal of Human Genetics</i> , 2018, 26, 230-237.	1.4	32
33	Whole sequence analysis indicates a recent southern origin of Mongolian Y-chromosome C2c1a1a1-M407. <i>Molecular Genetics and Genomics</i> , 2018, 293, 657-663.	1.0	16
34	Dispersals of the Siberian Y-chromosome haplogroup Q in Eurasia. <i>Molecular Genetics and Genomics</i> , 2018, 293, 107-117.	1.0	26
35	China's tuberculosis epidemic stems from historical expansion of four strains of <i>Mycobacterium tuberculosis</i> . <i>Nature Ecology and Evolution</i> , 2018, 2, 1982-1992.	3.4	83
36	Paternal origin of Paleo-Indians in Siberia: insights from Y-chromosome sequences. <i>European Journal of Human Genetics</i> , 2018, 26, 1687-1696.	1.4	21

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37	Reconstruction of Y-chromosome phylogeny reveals two neolithic expansions of Tibeto-Burman populations. <i>Molecular Genetics and Genomics</i> , 2018, 293, 1293-1300.	1.0	46
38	Fuyan human of 120â€“80 kya cannot challenge the Out-of-Africa theory for modern human dispersal. <i>Science Bulletin</i> , 2017, 62, 316-318.	4.3	0
39	Genetic Perspective on Language Replacement in Siberia. , 2017, , 37-53.		2
40	Phylogeny of Y-chromosome haplogroup C3b-F1756, an important paternal lineage in Altaic-speaking populations. <i>Journal of Human Genetics</i> , 2017, 62, 915-918.	1.1	20
41	Genetic trail for the early migrations of Aisin Gioro, the imperial house of the Qing dynasty. <i>Journal of Human Genetics</i> , 2017, 62, 407-411.	1.1	11
42	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.	1.1	16
43	Genetic analysis of 17 Y-STR loci in Han and Korean populations from Jilin Province, Northeast China. <i>Forensic Science International: Genetics</i> , 2016, 22, 8-10.	1.6	21
44	Genetic analysis of 17 Y-STR loci in Han population from Shandong Province in East China. <i>Forensic Science International: Genetics</i> , 2016, 22, e15-e17.	1.6	14
45	Southern East Asian origin and coexpansion of <i>Mycobacterium tuberculosis</i> Beijing family with Han Chinese. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8136-8141.	3.3	142
46	A late Neolithic expansion of Y chromosomal haplogroup O2a1â€“M95 from east to west. <i>Journal of Systematics and Evolution</i> , 2015, 53, 546-560.	1.6	14
47	Y chromosome of Aisin Gioro, the imperial house of the Qing dynasty. <i>Journal of Human Genetics</i> , 2015, 60, 295-298.	1.1	10
48	Y Chromosomes of 40% Chinese Descend from Three Neolithic Super-Grandfathers. <i>PLoS ONE</i> , 2014, 9, e105691.	1.1	82
49	Out-of-Africa migration and Neolithic coexpansion of <i>Mycobacterium tuberculosis</i> with modern humans. <i>Nature Genetics</i> , 2013, 45, 1176-1182.	9.4	900
50	Late Neolithic expansion of ancient Chinese revealed by Y chromosome haplogroup O3a1câ€“002611. <i>Journal of Systematics and Evolution</i> , 2013, 51, 280-286.	1.6	29
51	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.	1.1	75
52	Genomic Insights Into the Demographic History of the Southern Chinese. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	13