Hua Chen

List of Publications by Year
in descending order

52	3,744	279798	182427
papers	citations	23	51
		h-index	g-index

61	61	61	6041
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Population differentiation as a test for selective sweeps. Genome Research, 2010, 20, 393-402.	5.5	600
2	Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2022. Nucleic Acids Research, 2022, 50, D27-D38.	14.5	364
3	Genetic Variations in Tibetan Populations and High-Altitude Adaptation at the Himalayas. Molecular Biology and Evolution, 2011, 28, 1075-1081.	8.9	327
4	Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. Cell, 2013, 152, 691-702.	28.9	250
5	Modeling the epidemic dynamics and control of COVID‑19 outbreak in China. Quantitative Biology, 2020, 8, 11-19.	0.5	249
6	Genetic Evidence of Paleolithic Colonization and Neolithic Expansion of Modern Humans on the Tibetan Plateau. Molecular Biology and Evolution, 2013, 30, 1761-1778.	8.9	194
7	DatabaseÂResources of the National Genomics Data Center, China National Center for Bioinformation in 2021. Nucleic Acids Research, 2021, 49, D18-D28.	14.5	168
8	An intercross population study reveals genes associated with body size and plumage color in ducks. Nature Communications, 2018, 9, 2648.	12.8	167
9	Tracing Pastoralist Migrations to Southern Africa with Lactase Persistence Alleles. Current Biology, 2014, 24, 875-879.	3.9	166
10	Identification of a Tibetan-Specific Mutation in the Hypoxic Gene EGLN1 and Its Contribution to High-Altitude Adaptation. Molecular Biology and Evolution, 2013, 30, 1889-1898.	8.9	151
11	Ancient familial Mediterranean fever mutations in human pyrin and resistance to Yersinia pestis. Nature Immunology, 2020, 21, 857-867.	14.5	90
12	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoVR. Genomics, Proteomics and Bioinformatics, 2020, 18, 749-759.	6.9	88
13	Down-Regulation of *EPAS1* Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia. Molecular Biology and Evolution, 2017, 34, msw280.	8.9	87
14	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. Genome Research, 2019, 29, 682-696.	5.5	67
15	The joint allele frequency spectrum of multiple populations: A coalescent theory approach. Theoretical Population Biology, 2012, 81, 179-195.	1.1	49
16	The caterpillar fungus, Ophiocordyceps sinensis, genome provides insights into highland adaptation of fungal pathogenicity. Scientific Reports, 2017, 7, 1806.	3.3	49
17	Population Genetics of SARS-CoV-2: Disentangling Effects of Sampling Bias and Infection Clusters. Genomics, Proteomics and Bioinformatics, 2020, 18, 640-647.	6.9	44
18	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. Molecular Biology and Evolution, 2016, 33, 1177-1187.	8.9	43

#	Article	IF	Citations
19	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. Genomics, Proteomics and Bioinformatics, 2019, 17, 229-247.	6.9	42
20	A hidden Markov model for investigating recent positive selection through haplotype structure. Theoretical Population Biology, 2015, 99, 18-30.	1.1	41
21	*HMOX2* Functions as a Modifier Gene for High-Altitude Adaptation in Tibetans. Human Mutation, 2016, 37, 216-223.	2.5	40
22	Neo-functionalization of a Teosinte branched 1 homologue mediates adaptations of upland rice. Nature Communications, 2020, 11, 725.	12.8	40
23	Asymptotic Distributions of Coalescence Times and Ancestral Lineage Numbers for Populations with Temporally Varying Size. Genetics, 2013, 194, 721-736.	2.9	31
24	Origin, loss, and regain of self-incompatibility in angiosperms. Plant Cell, 2022, 34, 579-596.	6.6	30
25	eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. National Science Review, 2019, 6, 867-869.	9.5	29
26	The Joint Allele-Frequency Spectrum in Closely Related Species. Genetics, 2007, 177, 387-398.	2.9	28
27	Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. Molecular Biology and Evolution, 2018, 35, 2272-2283.	8.9	27
28	Inferring Selection Intensity and Allele Age from Multilocus Haplotype Structure. G3: Genes, Genomes, Genetics, 2013, 3, 1429-1442.	1.8	26
29	Tracing the origins of SARS-CoV-2: lessons learned from the past. Cell Research, 2021, 31, 1139-1141.	12.0	25
30	Identifying Lineage-Specific Targets of Natural Selection by a Bayesian Analysis of Genomic Polymorphisms and Divergence from Multiple Species. Molecular Biology and Evolution, 2019, 36, 1302-1315.	8.9	21
31	The Interplay between Natural Selection and Susceptibility to Melanoma on Allele 374F of SLC45A2 Gene in a South European Population. PLoS ONE, 2014, 9, e104367.	2.5	20
32	AIM-SNPtag: A computationally efficient approach for developing ancestry-informative SNP panels. Forensic Science International: Genetics, 2019, 38, 245-253.	3.1	15
33	Regional selection of the brain size regulating gene CASC5 provides new insight into human brain evolution. Human Genetics, 2017, 136, 193-204.	3.8	14
34	GCH1åŸ°å›åœ¨è—æ—é«˜åŽŸé€‚åº"ä¸å‰æŒ¥ä½œç""". Zoological Research, 2017, 38, 155-162.	2.1	14
35	Inferring Chinese surnames with Y-STR profiles. Forensic Science International: Genetics, 2018, 33, 66-71.	3.1	12
36	Ancestry informative SNP panels for discriminating the major East Asian populations: Han Chinese, Japanese and Korean. Annals of Human Genetics, 2019, 83, 348-354.	0.8	12

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37	Dosage sensitivity and exon shuffling shape the landscape of polymorphic duplicates in Drosophila and humans. Nature Ecology and Evolution, 2022, 6, 273-287.	7.8	12
38	Inferring Very Recent Population Growth Rate from Population-Scale Sequencing Data: Using a Large-Sample Coalescent Estimator. Molecular Biology and Evolution, 2015, 32, 2996-3011.	8.9	11
39	EP300åŸºå›é€šè¿‡è°ƒæŽ§ä¸€æ°åŒ—æ°å¸æˆâ€¸å®šˆ©è—æ—ä°°ç¾ä€€å°"é‹˜åŽŸä½½Žæ°§çŽ¯å¢ƒ. Zoological Research, 2017, 38, 163-	2.1	10
40	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. Nature Communications, 2021, 12, 4280.	12.8	9
41	Ongoing Positive Selection Drives the Evolution of SARS-CoV-2 Genomes. Genomics, Proteomics and Bioinformatics, 2022, 20, 1214-1223.	6.9	9
42	Genomic Epidemiology of SARS-CoV-2 in Pakistan. Genomics, Proteomics and Bioinformatics, 2021, 19, 727-740.	6.9	8
43	Intercoalescence Time Distribution of Incomplete Gene Genealogies in Temporally Varying Populations, and Applications in Population Genetic Inference. Annals of Human Genetics, 2013, 77, 158-173.	0.8	7
44	Variation in the life history strategy underlies functional diversity of tumors. National Science Review, 2021, 8, nwaa124.	9.5	7
45	Current Progress in Evolutionary Comparative Genomics of Great Apes. Frontiers in Genetics, 2021, 12, 657468.	2.3	7
46	Population genetic studies in the genomic sequencing era. Zoological Research, 2015, 36, 223-32.	0.6	6
47	Base-Biased Evolution of Disease-Associated Mutations in the Human Genome. Human Mutation, 2016, 37, 1209-1214.	2.5	5
48	Will the large‐scale vaccination succeed in containing the COVID‐19 pandemic and how soon?. Quantitative Biology, 2021, 9, 304-316.	0.5	3
49	The distinct morphological phenotypes of Southeast Asian aborigines are shaped by novel mechanisms for adaptation to tropical rainforests. National Science Review, 2022, 9, nwab072.	9.5	3
50	A Computational Approach for Modeling the Allele Frequency Spectrum of Populations with Arbitrarily Varying Size. Genomics, Proteomics and Bioinformatics, 2019, 17, 635-644.	6.9	2
51	Pinpointing the animal origins of SARS-CoV-2: a genomic approach. Journal of Genetics and Genomics, 2022, 49, 900-902.	3.9	1
52	Metagenomic evidence for the co-existence of SARS and H1N1 in patients from 2007-2012 flu seasons in France. Biosafety and Health, 2021, 3, 307-307.	2.7	0