

Hua Chen

List of Publications by Year in descending order

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Version: 2024-02-01

52
papers

3,744
citations

279798

23
h-index

182427

51
g-index

61
all docs

61
docs citations

61
times ranked

6041
citing authors

#	ARTICLE	IF	CITATIONS
1	The distinct morphological phenotypes of Southeast Asian aborigines are shaped by novel mechanisms for adaptation to tropical rainforests. <i>National Science Review</i> , 2022, 9, nwab072.	9.5	3
2	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2022. <i>Nucleic Acids Research</i> , 2022, 50, D27-D38.	14.5	364
3	Origin, loss, and regain of self-incompatibility in angiosperms. <i>Plant Cell</i> , 2022, 34, 579-596.	6.6	30
4	Dosage sensitivity and exon shuffling shape the landscape of polymorphic duplicates in <i>Drosophila</i> and humans. <i>Nature Ecology and Evolution</i> , 2022, 6, 273-287.	7.8	12
5	Pinpointing the animal origins of SARS-CoV-2: a genomic approach. <i>Journal of Genetics and Genomics</i> , 2022, 49, 900-902.	3.9	1
6	Ongoing Positive Selection Drives the Evolution of SARS-CoV-2 Genomes. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 1214-1223.	6.9	9
7	Variation in the life history strategy underlies functional diversity of tumors. <i>National Science Review</i> , 2021, 8, nwaa124.	9.5	7
8	Database Resources of the National Genomics Data Center, China National Center for Bioinformatics in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D18-D28.	14.5	168
9	Will the large-scale vaccination succeed in containing the COVID-19 pandemic and how soon?. <i>Quantitative Biology</i> , 2021, 9, 304-316.	0.5	3
10	DNA transposons mediate duplications via transposition-independent and -dependent mechanisms in metazoans. <i>Nature Communications</i> , 2021, 12, 4280.	12.8	9
11	Current Progress in Evolutionary Comparative Genomics of Great Apes. <i>Frontiers in Genetics</i> , 2021, 12, 657468.	2.3	7
12	Tracing the origins of SARS-CoV-2: lessons learned from the past. <i>Cell Research</i> , 2021, 31, 1139-1141.	12.0	25
13	Genomic Epidemiology of SARS-CoV-2 in Pakistan. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 727-740.	6.9	8
14	Metagenomic evidence for the co-existence of SARS and H1N1 in patients from 2007-2012 flu seasons in France. <i>Biosafety and Health</i> , 2021, 3, 307-307.	2.7	0
15	Population Genetics of SARS-CoV-2: Disentangling Effects of Sampling Bias and Infection Clusters. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 640-647.	6.9	44
16	Modeling the epidemic dynamics and control of COVID-19 outbreak in China. <i>Quantitative Biology</i> , 2020, 8, 11-19.	0.5	249
17	Ancient familial Mediterranean fever mutations in human pyrin and resistance to <i>Yersinia pestis</i> . <i>Nature Immunology</i> , 2020, 21, 857-867.	14.5	90
18	Neo-functionalization of a Teosinte branched 1 homologue mediates adaptations of upland rice. <i>Nature Communications</i> , 2020, 11, 725.	12.8	40

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19	The Global Landscape of SARS-CoV-2 Genomes, Variants, and Haplotypes in 2019nCoV. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 749-759.	6.9	88
20	eGPS 1.0: comprehensive software for multi-omic and evolutionary analyses. <i>National Science Review</i> , 2019, 6, 867-869.	9.5	29
21	Whole Genome Analyses of Chinese Population and De Novo Assembly of A Northern Han Genome. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 229-247.	6.9	42
22	Ancestry informative SNP panels for discriminating the major East Asian populations: Han Chinese, Japanese and Korean. <i>Annals of Human Genetics</i> , 2019, 83, 348-354.	0.8	12
23	Identifying Lineage-Specific Targets of Natural Selection by a Bayesian Analysis of Genomic Polymorphisms and Divergence from Multiple Species. <i>Molecular Biology and Evolution</i> , 2019, 36, 1302-1315.	8.9	21
24	GenTree, an integrated resource for analyzing the evolution and function of primate-specific coding genes. <i>Genome Research</i> , 2019, 29, 682-696.	5.5	67
25	A Computational Approach for Modeling the Allele Frequency Spectrum of Populations with Arbitrarily Varying Size. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 635-644.	6.9	2
26	AIM-SNPtag: A computationally efficient approach for developing ancestry-informative SNP panels. <i>Forensic Science International: Genetics</i> , 2019, 38, 245-253.	3.1	15
27	Inferring Chinese surnames with Y-STR profiles. <i>Forensic Science International: Genetics</i> , 2018, 33, 66-71.	3.1	12
28	Darwinian Positive Selection on the Pleiotropic Effects of KITLG Explain Skin Pigmentation and Winter Temperature Adaptation in Eurasians. <i>Molecular Biology and Evolution</i> , 2018, 35, 2272-2283.	8.9	27
29	An intercross population study reveals genes associated with body size and plumage color in ducks. <i>Nature Communications</i> , 2018, 9, 2648.	12.8	167
30	Down-Regulation of <i>EPAS1</i> Transcription and Genetic Adaptation of Tibetans to High-Altitude Hypoxia. <i>Molecular Biology and Evolution</i> , 2017, 34, msw280.	8.9	87
31	The caterpillar fungus, <i>Ophiocordyceps sinensis</i> , genome provides insights into highland adaptation of fungal pathogenicity. <i>Scientific Reports</i> , 2017, 7, 1806.	3.3	49
32	Regional selection of the brain size regulating gene <i>CASC5</i> provides new insight into human brain evolution. <i>Human Genetics</i> , 2017, 136, 193-204.	3.8	14
33	EP300 ^Δ promotes the transcription of <i>EPAS1</i> and genetic adaptation of Tibetans to high-altitude hypoxia. <i>Zoological Research</i> , 2017, 38, 163-172.	2.1	14
34	GCH1 ^Δ promotes the transcription of <i>EPAS1</i> and genetic adaptation of Tibetans to high-altitude hypoxia. <i>Zoological Research</i> , 2017, 38, 155-162.	2.1	14
35	<i>HMOX2</i> Functions as a Modifier Gene for High-Altitude Adaptation in Tibetans. <i>Human Mutation</i> , 2016, 37, 216-223.	2.5	40
36	Base-Biased Evolution of Disease-Associated Mutations in the Human Genome. <i>Human Mutation</i> , 2016, 37, 1209-1214.	2.5	5

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37	A Genetic Mechanism for Convergent Skin Lightening during Recent Human Evolution. <i>Molecular Biology and Evolution</i> , 2016, 33, 1177-1187.	8.9	43
38	Inferring Very Recent Population Growth Rate from Population-Scale Sequencing Data: Using a Large-Sample Coalescent Estimator. <i>Molecular Biology and Evolution</i> , 2015, 32, 2996-3011.	8.9	11
39	A hidden Markov model for investigating recent positive selection through haplotype structure. <i>Theoretical Population Biology</i> , 2015, 99, 18-30.	1.1	41
40	Population genetic studies in the genomic sequencing era. <i>Zoological Research</i> , 2015, 36, 223-32.	0.6	6
41	Tracing Pastoralist Migrations to Southern Africa with Lactase Persistence Alleles. <i>Current Biology</i> , 2014, 24, 875-879.	3.9	166
42	The Interplay between Natural Selection and Susceptibility to Melanoma on Allele 374F of SLC45A2 Gene in a South European Population. <i>PLoS ONE</i> , 2014, 9, e104367.	2.5	20
43	Genetic Evidence of Paleolithic Colonization and Neolithic Expansion of Modern Humans on the Tibetan Plateau. <i>Molecular Biology and Evolution</i> , 2013, 30, 1761-1778.	8.9	194
44	Modeling Recent Human Evolution in Mice by Expression of a Selected EDAR Variant. <i>Cell</i> , 2013, 152, 691-702.	28.9	250
45	Inferring Selection Intensity and Allele Age from Multilocus Haplotype Structure. <i>G3: Genes, Genomes, Genetics</i> , 2013, 3, 1429-1442.	1.8	26
46	Identification of a Tibetan-Specific Mutation in the Hypoxic Gene EGLN1 and Its Contribution to High-Altitude Adaptation. <i>Molecular Biology and Evolution</i> , 2013, 30, 1889-1898.	8.9	151
47	Asymptotic Distributions of Coalescence Times and Ancestral Lineage Numbers for Populations with Temporally Varying Size. <i>Genetics</i> , 2013, 194, 721-736.	2.9	31
48	Intercoalescence Time Distribution of Incomplete Gene Genealogies in Temporally Varying Populations, and Applications in Population Genetic Inference. <i>Annals of Human Genetics</i> , 2013, 77, 158-173.	0.8	7
49	The joint allele frequency spectrum of multiple populations: A coalescent theory approach. <i>Theoretical Population Biology</i> , 2012, 81, 179-195.	1.1	49
50	Genetic Variations in Tibetan Populations and High-Altitude Adaptation at the Himalayas. <i>Molecular Biology and Evolution</i> , 2011, 28, 1075-1081.	8.9	327
51	Population differentiation as a test for selective sweeps. <i>Genome Research</i> , 2010, 20, 393-402.	5.5	600
52	The Joint Allele-Frequency Spectrum in Closely Related Species. <i>Genetics</i> , 2007, 177, 387-398.	2.9	28