

Dong-Dong Wu

List of Publications by Year in descending order

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Version: 2024-02-01

71
papers

2,748
citations

236612

25
h-index

205818

48
g-index

80
all docs

80
docs citations

80
times ranked

4138
citing authors

#	ARTICLE	IF	CITATIONS
1	Long-read genome sequencing provides molecular insights into scavenging and societal complexity in spotted hyena <i>Crocuta crocuta</i> . <i>Molecular Biology and Evolution</i> , 2022, , .	3.5	1
2	Initiation of the Primate Genome Project. <i>Zoological Research</i> , 2022, 43, 147-149.	0.9	7
3	Genomic Analysis Revealed a Convergent Evolution of LINE-1 in Coat Color: A Case Study in Water Buffaloes (<i>Bubalus bubalis</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 1122-1136.	3.5	32
4	Population Genomics Reveals Incipient Speciation, Introgression, and Adaptation in the African Mona Monkey (<i>Cercopithecus mona</i>). <i>Molecular Biology and Evolution</i> , 2021, 38, 876-890.	3.5	15
5	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. <i>Zoological Research</i> , 2021, 42, 450-460.	0.9	9
6	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 787-799.	3.0	7
7	Variation in predicted COVID-19 risk among lemurs and lorises. <i>American Journal of Primatology</i> , 2021, 83, e23255.	0.8	7
8	Large-scale genomic analysis reveals the genetic cost of chicken domestication. <i>BMC Biology</i> , 2021, 19, 118.	1.7	22
9	Finding unknown species in the genomes of extant species. <i>Journal of Genetics and Genomics</i> , 2021, 48, 867-871.	1.7	2
10	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. <i>Molecular Biology and Evolution</i> , 2020, 37, 134-148.	3.5	23
11	Convergent genomic signatures of high-altitude adaptation among domestic mammals. <i>National Science Review</i> , 2020, 7, 952-963.	4.6	52
12	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 489-500.	3.0	5
13	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. <i>BMC Genomics</i> , 2020, 21, 496.	1.2	14
14	Donkey genomes provide new insights into domestication and selection for coat color. <i>Nature Communications</i> , 2020, 11, 6014.	5.8	63
15	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. <i>Molecular Biology and Evolution</i> , 2020, 37, 2616-2629.	3.5	46
16	Genome and single-cell RNA-sequencing of the earthworm <i>Eisenia andrei</i> identifies cellular mechanisms underlying regeneration. <i>Nature Communications</i> , 2020, 11, 2656.	5.8	43
17	Evolution and transition of expression trajectory during human brain development. <i>BMC Evolutionary Biology</i> , 2020, 20, 72.	3.2	10
18	863 genomes reveal the origin and domestication of chicken. <i>Cell Research</i> , 2020, 30, 693-701.	5.7	144

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19	Identification of a Zeb1 expressing basal stem cell subpopulation in the prostate. <i>Nature Communications</i> , 2020, 11, 706.	5.8	42
20	The genome of Shaw's sea snake (<i>Hydrophis curtus</i>) reveals secondary adaptation to its marine environment. <i>Molecular Biology and Evolution</i> , 2020, 37, 1744-1760.	3.5	28
21	The wild species genome ancestry of domestic chickens. <i>BMC Biology</i> , 2020, 18, 13.	1.7	61
22	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. <i>Nature Communications</i> , 2019, 10, 4892.	5.8	256
23	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. <i>Genome Biology</i> , 2019, 20, 79.	3.8	81
24	Complete mitochondrial genome sequence for the <i>Cercopithecus erythrotis camerunensis</i> (Primate:). <i>Tj ETQq0 0 0 ggBT /Overlock 10 Tf</i>	0.2	1
25	547 transcriptomes from 44 brain areas reveal features of the aging brain in non-human primates. <i>Genome Biology</i> , 2019, 20, 258.	3.8	26
26	Conserved sequences identify the closest living relatives of primates. <i>Zoological Research</i> , 2019, 40, 532-540.	0.9	8
27	Chromosomal level assembly and population sequencing of the Chinese tree shrew genome. <i>Zoological Research</i> , 2019, 40, 506-521.	0.9	43
28	Does the Genetic Feature of the Chinese Tree Shrew (<i>Tupaia belangeri chinensis</i>) Support Its Potential as a Viable Model for Alzheimer's Disease Research?. <i>Journal of Alzheimer's Disease</i> , 2018, 61, 1015-1028.	1.2	25
29	Origin of new genes after zygotic genome activation in vertebrate. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 139-146.	1.5	1
30	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. <i>Molecular Biology and Evolution</i> , 2018, 35, 149-158.	3.5	36
31	Detection of breed-specific copy number variations in domestic chicken genome. <i>Genome</i> , 2018, 61, 7-14.	0.9	21
32	Understanding the cryptic introgression and mixed ancestry of Red Junglefowl in India. <i>PLoS ONE</i> , 2018, 13, e0204351.	1.1	6
33	Pervasive introgression facilitated domestication and adaptation in the <i>Bos</i> species complex. <i>Nature Ecology and Evolution</i> , 2018, 2, 1139-1145.	3.4	157
34	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 8406-8411.	3.3	119
35	Evolution of Trichocyte Keratin Associated Proteins. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1054, 47-56.	0.8	10
36	A parallel mechanism underlying frizzle in domestic chickens. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 589-591.	1.5	19

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37	The RNA editome of <i>Macaca mulatta</i> and functional characterization of RNA editing in mitochondria. <i>Science Bulletin</i> , 2017, 62, 820-830.	4.3	4
38	Draft genome of the gayal, <i>Bos frontalis</i> . <i>GigaScience</i> , 2017, 6, 1-7.	3.3	23
39	An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens. <i>Molecular Biology and Evolution</i> , 2017, 34, 3081-3088.	3.5	42
40	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. <i>Molecular Biology and Evolution</i> , 2017, 34, 3148-3153.	3.5	14
41	Annotating long intergenic non-coding RNAs under artificial selection during chicken domestication. <i>BMC Evolutionary Biology</i> , 2017, 17, 192.	3.2	12
42	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant at <i>SLC39A8</i> in Europeans. <i>Schizophrenia Bulletin</i> , 2016, 42, sbv070.	2.3	35
43	Transcriptome Profiles Using Next-Generation Sequencing Reveal Liver Changes in the Early Stage of Diabetes in Tree Shrew (<i>Tupaia belangeri chinensis</i>). <i>Journal of Diabetes Research</i> , 2016, 2016, 1-15.	1.0	13
44	Functional prediction of differentially expressed lncRNAs in HSV-1 infected human foreskin fibroblasts. <i>Virology Journal</i> , 2016, 13, 137.	1.4	23
45	Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. <i>Cell Research</i> , 2016, 26, 556-573.	5.7	69
46	Olfactory genes in Tibetan wild boar. <i>Nature Genetics</i> , 2016, 48, 972-973.	9.4	6
47	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 542-552.	1.5	41
48	A molecular genome scan to identify DNA segments associated with live weight in Japanese quail. <i>Molecular Biology Reports</i> , 2016, 43, 1267-1272.	1.0	4
49	Cellular responses to HSV-1 infection are linked to specific types of alterations in the host transcriptome. <i>Scientific Reports</i> , 2016, 6, 28075.	1.6	61
50	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. <i>Genome Biology and Evolution</i> , 2016, 8, 42-50.	1.1	57
51	Transcriptomes reveal the genetic mechanisms underlying ionic regulatory adaptations to salt in the crab-eating frog. <i>Scientific Reports</i> , 2015, 5, 17551.	1.6	14
52	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1257-62.	3.3	159
53	Integrative analyses of RNA editing, alternative splicing, and expression of young genes in human brain transcriptome by deep RNA sequencing. <i>Journal of Molecular Cell Biology</i> , 2015, 7, 314-325.	1.5	12
54	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. <i>Molecular Biology and Evolution</i> , 2015, 32, 1880-1889.	3.5	193

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55	The prion protein gene polymorphisms associated with bovine spongiform encephalopathy susceptibility differ significantly between cattle and buffalo. <i>Infection, Genetics and Evolution</i> , 2015, 36, 531-538.	1.0	15
56	Accelerated evolution of constraint elements for hematophagic adaptation in mosquitoes. <i>Zoological Research</i> , 2015, 36, 320-7.	0.6	0
57	Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. <i>Genome Biology and Evolution</i> , 2014, 6, 3115-3121.	1.1	38
58	“Out of Pollen” Hypothesis for Origin of New Genes in Flowering Plants: Study from <i>Arabidopsis thaliana</i> . <i>Genome Biology and Evolution</i> , 2014, 6, 2822-2829.	1.1	28
59	Molecular evolution in the CREB1 signal pathway and a rare haplotype in CREB1 with genetic predisposition to schizophrenia. <i>Journal of Psychiatric Research</i> , 2014, 57, 84-89.	1.5	18
60	Evolution and function of de novo originated genes. <i>Molecular Phylogenetics and Evolution</i> , 2013, 67, 541-545.	1.2	27
61	Positive Selection on the Osteoarthritis-Risk and Decreased-Height Associated Variants at the GDF5 Gene in East Asians. <i>PLoS ONE</i> , 2012, 7, e42553.	1.1	24
62	Eukaryotic origin of a metabolic pathway in virus by horizontal gene transfer. <i>Genomics</i> , 2011, 98, 367-369.	1.3	8
63	Different level of population differentiation among human genes. <i>BMC Evolutionary Biology</i> , 2011, 11, 16.	3.2	24
64	Correlated Evolution among Six Gene Families in <i>Drosophila</i> Revealed by Parallel Change of Gene Numbers. <i>Genome Biology and Evolution</i> , 2011, 3, 396-400.	1.1	8
65	De Novo Origin of Human Protein-Coding Genes. <i>PLoS Genetics</i> , 2011, 7, e1002379.	1.5	153
66	Association of disease-predisposition polymorphisms of the melatonin receptors and sunshine duration in the global human populations. <i>Journal of Pineal Research</i> , 2010, 48, 133-141.	3.4	18
67	Positive selection drives population differentiation in the skeletal genes in modern humans. <i>Human Molecular Genetics</i> , 2010, 19, 2341-2346.	1.4	14
68	Evidence for Positive Selection on the Osteogenin (BMP3) Gene in Human Populations. <i>PLoS ONE</i> , 2010, 5, e10959.	1.1	9
69	A Profound Role for the Expansion of Trypsin-Like Serine Protease Family in the Evolution of Hematophagy in Mosquito. <i>Molecular Biology and Evolution</i> , 2009, 26, 2333-2341.	3.5	46
70	Positive Darwinian selection in human population: A review. <i>Science Bulletin</i> , 2008, 53, 1457-1467.	4.3	4
71	Molecular evolution of the keratin associated protein gene family in mammals, role in the evolution of mammalian hair. <i>BMC Evolutionary Biology</i> , 2008, 8, 241.	3.2	85