## Dong-Dong Wu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1005972/publications.pdf

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236925 206112 2,748 71 25 48 citations h-index g-index papers 80 80 80 4138 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	YTHDF1 links hypoxia adaptation and non-small cell lung cancer progression. Nature Communications, 2019, 10, 4892.	12.8	256
2	Genomic Analyses Reveal Potential Independent Adaptation to High Altitude in Tibetan Chickens. Molecular Biology and Evolution, 2015, 32, 1880-1889.	8.9	193
3	Whole-genome sequence of the Tibetan frog <i>Nanorana parkeri</i> and the comparative evolution of tetrapod genomes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E1257-62.	7.1	159
4	Pervasive introgression facilitated domestication and adaptation in the Bos species complex. Nature Ecology and Evolution, 2018, 2, 1139-1145.	7.8	157
5	De Novo Origin of Human Protein-Coding Genes. PLoS Genetics, 2011, 7, e1002379.	3.5	153
6	863 genomes reveal the origin and domestication of chicken. Cell Research, 2020, 30, 693-701.	12.0	144
7	Comparative genomic investigation of high-elevation adaptation in ectothermic snakes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 8406-8411.	7.1	119
8	Molecular evolution of the keratin associated protein gene family in mammals, role in the evolution of mammalian hair. BMC Evolutionary Biology, 2008, 8, 241.	3.2	85
9	Whole genomes and transcriptomes reveal adaptation and domestication of pistachio. Genome Biology, 2019, 20, 79.	8.8	81
10	Positive selection rather than relaxation of functional constraint drives the evolution of vision during chicken domestication. Cell Research, 2016, 26, 556-573.	12.0	69
11	Donkey genomes provide new insights into domestication and selection for coat color. Nature Communications, 2020, 11, 6014.	12.8	63
12	Cellular responses to HSV-1 infection are linked to specific types of alterations in the host transcriptome. Scientific Reports, 2016, 6, 28075.	3.3	61
13	The wild species genome ancestry of domestic chickens. BMC Biology, 2020, 18, 13.	3.8	61
14	Population Variation Reveals Independent Selection toward Small Body Size in Chinese Debao Pony. Genome Biology and Evolution, 2016, 8, 42-50.	2.5	57
15	Convergent genomic signatures of high-altitude adaptation among domestic mammals. National Science Review, 2020, 7, 952-963.	9.5	52
16	A Profound Role for the Expansion of Trypsin-Like Serine Protease Family in the Evolution of Hematophagy in Mosquito. Molecular Biology and Evolution, 2009, 26, 2333-2341.	8.9	46
17	Ancient Hybridization with an Unknown Population Facilitated High-Altitude Adaptation of Canids. Molecular Biology and Evolution, 2020, 37, 2616-2629.	8.9	46
18	Genome and single-cell RNA-sequencing of the earthworm Eisenia andrei identifies cellular mechanisms underlying regeneration. Nature Communications, 2020, 11, 2656.	12.8	43

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19	Chromosomal level assembly and population sequencing of the Chinese tree shrew genome. Zoological Research, 2019, 40, 506-521.	2.1	43
20	An Evolutionary Genomic Perspective on the Breeding of Dwarf Chickens. Molecular Biology and Evolution, 2017, 34, 3081-3088.	8.9	42
21	Identification of a Zeb1 expressing basal stem cell subpopulation in the prostate. Nature Communications, 2020, $11$ , 706.	12.8	42
22	Comparative population genomics reveals genetic basis underlying body size of domestic chickens. Journal of Molecular Cell Biology, 2016, 8, 542-552.	3.3	41
23	Domestication of the Dog from the Wolf Was Promoted by Enhanced Excitatory Synaptic Plasticity: A Hypothesis. Genome Biology and Evolution, 2014, 6, 3115-3121.	2.5	38
24	Out of Southern East Asia of the Brown Rat Revealed by Large-Scale Genome Sequencing. Molecular Biology and Evolution, 2018, 35, 149-158.	8.9	36
25	Recent Positive Selection Drives the Expansion of a Schizophrenia Risk Nonsynonymous Variant at <i>SLC39A8</i> in Europeans. Schizophrenia Bulletin, 2016, 42, sbv070.	4.3	35
26	Genomic Analysis Revealed a Convergent Evolution of LINE-1 in Coat Color: A Case Study in Water Buffaloes ( <i>Bubalis bubalis   Nolecular Biology and Evolution, 2021, 38, 1122-1136.</i>	8.9	32
27	"Out of Pollen―Hypothesis for Origin of New Genes in Flowering Plants: Study from Arabidopsis thaliana. Genome Biology and Evolution, 2014, 6, 2822-2829.	2.5	28
28	The genome of Shaw's sea snake (Hydrophis curtus) reveals secondary adaptation to its marine environment. Molecular Biology and Evolution, 2020, 37, 1744-1760.	8.9	28
29	Evolution and function of de novo originated genes. Molecular Phylogenetics and Evolution, 2013, 67, 541-545.	2.7	27
30	547 transcriptomes from 44 brain areas reveal features of the aging brain in non-human primates. Genome Biology, 2019, 20, 258.	8.8	26
31	Does the Genetic Feature of the Chinese Tree Shrew (Tupaia belangeri chinensis) Support Its Potential as a Viable Model for Alzheimer's Disease Research?. Journal of Alzheimer's Disease, 2018, 61, 1015-1028.	2.6	25
32	Different level of population differentiation among human genes. BMC Evolutionary Biology, 2011, 11, 16.	3.2	24
33	Positive Selection on the Osteoarthritis-Risk and Decreased-Height Associated Variants at the GDF5 Gene in East Asians. PLoS ONE, 2012, 7, e42553.	2.5	24
34	Functional prediction of differentially expressed lncRNAs in HSV-1 infected human foreskin fibroblasts. Virology Journal, 2016, 13, 137.	3.4	23
35	Draft genome of the gayal, Bos frontalis. GigaScience, 2017, 6, 1-7.	6.4	23
36	Genomic and Phenotypic Analyses Reveal Mechanisms Underlying Homing Ability in Pigeon. Molecular Biology and Evolution, 2020, 37, 134-148.	8.9	23

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37	Large-scale genomic analysis reveals the genetic cost of chicken domestication. BMC Biology, 2021, 19, 118.	3.8	22
38	Detection of breed-specific copy number variations in domestic chicken genome. Genome, 2018, 61, 7-14.	2.0	21
39	A parallel mechanism underlying frizzle in domestic chickens. Journal of Molecular Cell Biology, 2018, 10, 589-591.	3.3	19
40	Association of disease-predisposition polymorphisms of the melatonin receptors and sunshine duration in the global human populations. Journal of Pineal Research, 2010, 48, 133-141.	7.4	18
41	Molecular evolution in the CREB1 signal pathway and a rare haplotype in CREB1 with genetic predisposition to schizophrenia. Journal of Psychiatric Research, 2014, 57, 84-89.	3.1	18
42	The prion protein gene polymorphisms associated with bovine spongiform encephalopathy susceptibility differ significantly between cattle and buffalo. Infection, Genetics and Evolution, 2015, 36, 531-538.	2.3	15
43	Population Genomics Reveals Incipient Speciation, Introgression, and Adaptation in the African Mona Monkey ( <i>Cercopithecus mona</i> ). Molecular Biology and Evolution, 2021, 38, 876-890.	8.9	15
44	Positive selection drives population differentiation in the skeletal genes in modern humans. Human Molecular Genetics, 2010, 19, 2341-2346.	2.9	14
45	Transcriptomes reveal the genetic mechanisms underlying ionic regulatory adaptations to salt in the crab-eating frog. Scientific Reports, 2015, 5, 17551.	3.3	14
46	Rapid Evolution of Genes Involved in Learning and Energy Metabolism for Domestication of the Laboratory Rat. Molecular Biology and Evolution, 2017, 34, 3148-3153.	8.9	14
47	Comparative population genomic analysis uncovers novel genomic footprints and genes associated with small body size in Chinese pony. BMC Genomics, 2020, 21, 496.	2.8	14
48	Transcriptome Profiles Using Next-Generation Sequencing Reveal Liver Changes in the Early Stage of Diabetes in Tree Shrew ( <i>Tupaia belangeri chinensis</i> ). Journal of Diabetes Research, 2016, 2016, 1-15.	2.3	13
49	Integrative analyses of RNA editing, alternative splicing, and expression of young genes in human brain transcriptome by deep RNA sequencing. Journal of Molecular Cell Biology, 2015, 7, 314-325.	3.3	12
50	Annotating long intergenic non-coding RNAs under artificial selection during chicken domestication. BMC Evolutionary Biology, 2017, 17, 192.	3.2	12
51	Evolution of Trichocyte Keratin Associated Proteins. Advances in Experimental Medicine and Biology, 2018, 1054, 47-56.	1.6	10
52	Evolution and transition of expression trajectory during human brain development. BMC Evolutionary Biology, 2020, 20, 72.	3.2	10
53	Genomes reveal selective sweeps in kiang and donkey for high-altitude adaptation. Zoological Research, 2021, 42, 450-460.	2.1	9
54	Evidence for Positive Selection on the Osteogenin (BMP3) Gene in Human Populations. PLoS ONE, 2010, 5, e10959.	2.5	9

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55	Eukaryotic origin of a metabolic pathway in virus by horizontal gene transfer. Genomics, 2011, 98, 367-369.	2.9	8
56	Correlated Evolution among Six Gene Families in Drosophila Revealed by Parallel Change of Gene Numbers. Genome Biology and Evolution, 2011, 3, 396-400.	2.5	8
57	Conserved sequences identify the closest living relatives of primates. Zoological Research, 2019, 40, 532-540.	2.1	8
58	Integrating Genomic and Transcriptomic Data to Reveal Genetic Mechanisms Underlying Piao Chicken Rumpless Trait. Genomics, Proteomics and Bioinformatics, 2021, 19, 787-799.	6.9	7
59	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	1.7	7
60	Initiation of the Primate Genome Project. Zoological Research, 2022, 43, 147-149.	2.1	7
61	Olfactory genes in Tibetan wild boar. Nature Genetics, 2016, 48, 972-973.	21.4	6
62	Understanding the cryptic introgression and mixed ancestry of Red Junglefowl in India. PLoS ONE, 2018, 13, e0204351.	2.5	6
63	Ambient Temperature is A Strong Selective Factor Influencing Human Development and Immunity. Genomics, Proteomics and Bioinformatics, 2020, 18, 489-500.	6.9	5
64	Positive Darwinian selection in human population: A review. Science Bulletin, 2008, 53, 1457-1467.	9.0	4
65	A molecular genome scan to identify DNA segments associated with live weight in Japanese quail. Molecular Biology Reports, 2016, 43, 1267-1272.	2.3	4
66	The RNA editome of Macaca mulatta and functional characterization of RNA editing in mitochondria. Science Bulletin, 2017, 62, 820-830.	9.0	4
67	Finding unknown species in the genomes of extant species. Journal of Genetics and Genomics, 2021, 48, 867-871.	3.9	2
68	Origin of new genes after zygotic genome activation in vertebrate. Journal of Molecular Cell Biology, 2018, 10, 139-146.	3.3	1
69	Complete mitochondrial genome sequence for the Cercopithecus erythrotis camerunensis (Primate:) Tj ETQq $1\ 1$	0.784314	rgBT /Overlo
70	Long-read genome sequencing provides molecular insights into scavenging and societal complexity in spotted hyena Crocuta crocuta. Molecular Biology and Evolution, 2022, , .	8.9	1
71	Accelerated evolution of constraint elements for hematophagic adaptation in mosquitoes. Zoological Research, 2015, 36, 320-7.	0.6	O