

Pavel Dobrynin

List of Publications by Year in descending order

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Version: 2024-02-01

25
papers

852
citations

623734

14
h-index

610901

24
g-index

30
all docs

30
docs citations

30
times ranked

1895
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	8.8	167
2	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015, 25, 2158-2165.	3.9	156
3	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	5.5	95
4	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. <i>GigaScience</i> , 2016, 5, 38.	6.4	68
5	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5.	3.9	49
6	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020, 9, .	6.4	48
7	Annotated features of domestic cat “ <i>Felis catus</i> ” genome. <i>GigaScience</i> , 2014, 3, 13.	6.4	30
8	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. <i>Journal of Heredity</i> , 2017, 108, 671-677.	2.4	28
9	Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018, 28, R13-R14.	3.9	27
10	Chromosomal-level genome assembly of the scimitar-horned oryx: Insights into diversity and demography of a species extinct in the wild. <i>Molecular Ecology Resources</i> , 2020, 20, 1668-1681.	4.8	26
11	The Novelty of Human Cancer/Testis Antigen Encoding Genes in Evolution. <i>International Journal of Genomics</i> , 2013, 2013, 1-7.	1.6	25
12	Genome-wide sequence analyses of ethnic populations across Russia. <i>Genomics</i> , 2020, 112, 442-458.	2.9	19
13	Whole Genome Sequencing and Re-sequencing of the Sable Antelope (<i>Hippotragus niger</i>): A Resource for Monitoring Diversity in <i>ex Situ</i> and <i>in Situ</i> Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 1785-1793.	1.8	18
14	Comparison of genomic diversity and structure of sable antelope (<i>Hippotragus niger</i>) in zoos, conservation centers, and private ranches in North America. <i>Evolutionary Applications</i> , 2020, 13, 2143-2154.	3.1	18
15	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered <i>Solenodon paradoxus</i> from the island of Hispaniola. <i>GigaScience</i> , 2018, 7, .	6.4	12
16	Mitogenomic sequences support a north-south subspecies subdivision within <i>Solenodon paradoxus</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2017, 28, 662-670.	0.7	9
17	Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae. <i>Molecular Ecology</i> , 2022, 31, 2898-2919.	3.9	8
18	Analytical “bake-off” of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. <i>PLoS ONE</i> , 2018, 13, e0200423.	2.5	7

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19	GWATCH: a web platform for automated gene association discovery analysis. <i>GigaScience</i> , 2014, 3, 18.	6.4	5
20	PGD: a pangolin genome hub for the research community. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw063.	3.0	5
21	Draft de novo Genome Assembly of the Elusive Jaguarundi, <i>Puma yagouaroundi</i> . <i>Journal of Heredity</i> , 2021, 112, 540-548.	2.4	5
22	Response to Comment by Faurby, Werdelin and Svenning. <i>Genome Biology</i> , 2016, 17, 90.	8.8	2
23	Insights from the rescue and breeding management of Cuvier's gazelle (<i>Gazella cuvieri</i>) through whole-genome sequencing. <i>Evolutionary Applications</i> , 2022, 15, 351-364.	3.1	2
24	The complete mitochondrial genome of the parthenogenetic Caucasian rock lizard <i>Darevskia unisexualis</i> (<i>Squamata</i> : <i>lacertidae</i>) contains long tandem repeat formed by 59bp monomer. <i>Mitochondrial DNA Part B: Resources</i> , 2016, 1, 875-877.	0.4	1
25	141 Gene Discovery and Data Sharing in Genome Wide Association Analyses. <i>Journal of Acquired Immune Deficiency Syndromes</i> (1999), 2014, 65, 59.	2.1	0