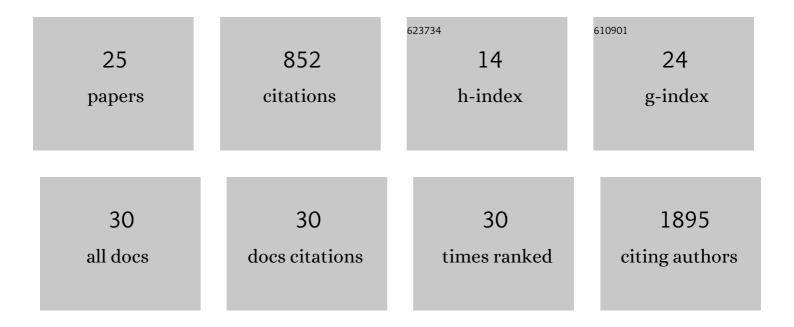
Pavel Dobrynin

List of Publications by Year in descending order

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PAVEL DORDVNIN

#	Article	IF	CITATIONS
1	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	8.8	167
2	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. Current Biology, 2015, 25, 2158-2165.	3.9	156
3	Pangolin genomes and the evolution of mammalian scales and immunity. Genome Research, 2016, 26, 1312-1322.	5.5	95
4	Chromosomer: a reference-based genome arrangement tool for producing draft chromosome sequences. GigaScience, 2016, 5, 38.	6.4	68
5	Whole-genome analysis of giraffe supports four distinct species. Current Biology, 2021, 31, 2929-2938.e5.	3.9	49
6	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. GigaScience, 2020, 9, .	6.4	48
7	Annotated features of domestic cat – Felis catus genome. GigaScience, 2014, 3, 13.	6.4	30
8	Conservation Genetics of the Cheetah: Lessons Learned and New Opportunities. Journal of Heredity, 2017, 108, 671-677.	2.4	28
9	Robust forensic matching of confiscated horns to individual poached African rhinoceros. Current Biology, 2018, 28, R13-R14.	3.9	27
10	Chromosomalâ€level genome assembly of the scimitarâ€horned oryx: Insights into diversity and demography of a species extinct in the wild. Molecular Ecology Resources, 2020, 20, 1668-1681.	4.8	26
11	The Novelty of Human Cancer/Testis Antigen Encoding Genes in Evolution. International Journal of Genomics, 2013, 2013, 1-7.	1.6	25
12	Genome-wide sequence analyses of ethnic populations across Russia. Genomics, 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. G3: Genes, Genomes, Genetics, 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. Evolutionary Applications, 2020, 13, 2143-2154.	3.1	18
15	Innovative assembly strategy contributes to understanding the evolution and conservation genetics of the endangered Solenodon paradoxus from the island of Hispaniola. GigaScience, 2018, 7, .	6.4	12
16	Mitogenomic sequences support a north–south subspecies subdivision within Solenodon paradoxus. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 662-670.	0.7	9
17	Multiple types of genomic variation contribute to adaptive traits in the mustelid subfamily Guloninae. Molecular Ecology, 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. PLoS ONE, 2018, 13, e0200423.	2.5	7

PAVEL DOBRYNIN

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