

Klaus-Peter Koepfli

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

60
papers

6,609
citations

28
h-index

73
g-index

73
ext. papers

8,362
ext. citations

8.6
avg, IF

4.83
L-index

#	Paper	IF	Citations
60	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005 , 438, 803-19	50.4	1809
59	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014 , 346, 1320-31	33.3	1182
58	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011 , 479, 359-64	50.4	483
57	Complete mitochondrial genomes of ancient canids suggest a European origin of domestic dogs. <i>Science</i> , 2013 , 342, 871-4	33.3	328
56	Broad host range of SARS-CoV-2 predicted by comparative and structural analysis of ACE2 in vertebrates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22311-22322	11.5	267
55	The Genome 10K Project: a way forward. <i>Annual Review of Animal Biosciences</i> , 2015 , 3, 57-111	13.7	223
54	Multigene phylogeny of the Mustelidae: resolving relationships, tempo and biogeographic history of a mammalian adaptive radiation. <i>BMC Biology</i> , 2008 , 6, 10	7.3	207
53	Pattern and timing of diversification of the mammalian order Carnivora inferred from multiple nuclear gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 2010 , 56, 49-63	4.1	173
52	A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships. <i>Molecular Phylogenetics and Evolution</i> , 2003 , 28, 225-40	4.1	168
51	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021 , 592, 737-746	56.4	161
50	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013 , 4, 2433	17.4	147
49	Extensive population genetic structure in the giraffe. <i>BMC Biology</i> , 2007 , 5, 57	7.3	138
48	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015 , 25, 2158-65	6.3	118
47	Phylogeny of the Procyonidae (Mammalia: Carnivora): molecules, morphology and the Great American Interchange. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 43, 1076-95	4.1	103
46	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015 , 16, 277	18.3	99
45	Phylogenetic relationships of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome b sequences. <i>Journal of Zoology</i> , 1998 , 246, 401-416	2	89
44	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018 , 2, 1479-1491	12.3	74

43	Molecular systematics of the Hyaenidae: relationships of a relictual lineage resolved by a molecular supermatrix. <i>Molecular Phylogenetics and Evolution</i> , 2006 , 38, 603-20	4.1	74
42	Type I STS markers are more informative than cytochrome B in phylogenetic reconstruction of the Mustelidae (Mammalia: Carnivora). <i>Systematic Biology</i> , 2003 , 52, 571-93	8.4	61
41	Sex identification of the Eurasian otter <i>Lutra lutra</i> by PCR typing of spraints. <i>Conservation Genetics</i> , 2000 , 1, 181-183	2.6	60
40	Evolution of a major drug metabolizing enzyme defect in the domestic cat and other felidae: phylogenetic timing and the role of hypercarnivory. <i>PLoS ONE</i> , 2011 , 6, e18046	3.7	59
39	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018 , 28, 3441-3449.e5.3		58
38	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016 , 26, 1312-1322	9.7	54
37	Broad Host Range of SARS-CoV-2 Predicted by Comparative and Structural Analysis of ACE2 in Vertebrates 2020 ,		39
36	Towards complete and error-free genome assemblies of all vertebrate species		38
35	The evolutionary history of extinct and living lions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 10927-10934	11.5	31
34	Evolutionary history of the Falklands wolf. <i>Current Biology</i> , 2009 , 19, R937-8	6.3	29
33	Establishing the foundation for an applied molecular taxonomy of otters in Southeast Asia. <i>Conservation Genetics</i> , 2008 , 9, 1589-1604	2.6	29
32	Aquatic Adaptation and Depleted Diversity: A Deep Dive into the Genomes of the Sea Otter and Giant Otter. <i>Molecular Biology and Evolution</i> , 2019 , 36, 2631-2655	8.3	26
31	Annotated features of domestic cat - <i>Felis catus</i> genome. <i>GigaScience</i> , 2014 , 3, 13	7.6	26
30	Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018 , 28, R13-R14	6.3	20
29	Taxonomic revision of the genus <i>Galictis</i> (Carnivora: Mustelidae): species delimitation, morphological diagnosis, and refined mapping of geographical distribution. <i>Zoological Journal of the Linnean Society</i> , 2013 , 167, 449-472	2.4	20
28	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, <i>Homotherium latidens</i> . <i>Current Biology</i> , 2020 , 30, 5018-5025.e5	6.3	18
27	Phylogeography and demographic history of the neotropical otter (<i>Lontra longicaudis</i>). <i>Journal of Heredity</i> , 2012 , 103, 479-92	2.4	17
26	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020 , 9,	7.6	16

25	Comparative genomics provides new insights into the remarkable adaptations of the African wild dog (<i>Lycaon pictus</i>). <i>Scientific Reports</i> , 2019 , 9, 8329	4.9	15
24	Population Genomic Analysis of North American Eastern Wolves (<i>Canis lycaon</i>) Supports Their Conservation Priority Status. <i>Genes</i> , 2018 , 9,	4.2	15
23	Whole Genome Sequencing and Re-sequencing of the Sable Antelope (<i>Oryx capensis</i>): A Resource for Monitoring Diversity in and Populations. <i>G3: Genes, Genomes, Genetics</i> , 2019 , 9, 1785-1793	3.2	14
22	Improving draft genome contiguity with reference-derived in silico mate-pair libraries. <i>GigaScience</i> , 2018 , 7,	7.6	14
21	The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016 , 107, 104-14	2.4	14
20	Breeding Centers, Private Ranches, and Genomics for Creating Sustainable Wildlife Populations. <i>BioScience</i> , 2019 , 69, 928-943	5.7	13
19	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	8.4	10
18	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016 , 6, 28199	4.9	9
17	Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020 , 13, e12754	6.9	8
16	Phylogeographic and diversification patterns of the white-nosed coati (<i>Nasua narica</i>): Evidence for south-to-north colonization of North America. <i>Molecular Phylogenetics and Evolution</i> , 2019 , 131, 149-163	4.1	8
15	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021 , 31, 2929-2938.e56.3	5.3	8
14	Cryptic phylogeographic history sheds light on the generation of species diversity in sky-island mountains. <i>Journal of Biogeography</i> , 2019 , 46, 2232-2247	4.1	6
13	Comparison of genomic diversity and structure of sable antelope (<i>Oryx capensis</i>) in zoos, conservation centers, and private ranches in North America. <i>Evolutionary Applications</i> , 2020 , 13, 2143-2154	4.8	5
12	Towards resolving taxonomic uncertainties in wolf, dog and jackal lineages of Africa, Eurasia and Australasia. <i>Journal of Zoology</i> , 2022 , 316, 155-168	2	5
11	Genetic analysis of Turkish martens: Do two species of the genus <i>Martes</i> occur in Anatolia?. <i>Zoologica Scripta</i> , 2018 , 47, 390-403	2.5	4
10	Characteristics of the complete mitochondrial genome of the monotypic genus (<i>Viverridae</i>) and its phylogenetic implications. <i>PeerJ</i> , 2019 , 7, e8033	3.1	3
9	Expanding the conservation genomics toolbox: Incorporating structural variants to enhance genomic studies for species of conservation concern. <i>Molecular Ecology</i> , 2021 , 30, 5949-5965	5.7	3
8	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020 , 7, 126	8.2	2

7	Chromosomal-level genome assembly of the scimitar-horned oryx: insights into diversity and demography of a species extinct in the wild		1
6	Diversity and Paleodemography of the Addax (<i>Oryx capensis</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021 , 12,	4.2	1
5	Insights from the rescue and breeding management of Cuvier's gazelle (<i>Gazelle gazelle</i>) through whole-genome sequencing.. <i>Evolutionary Applications</i> , 2022 , 15, 351-364	4.8	0
4	Applying genomics to metapopulation management in North American insurance populations of southern sable antelope (<i>Hippotragus niger niger</i>) and addra gazelle (<i>Nanger dama ruficollis</i>). <i>Global Ecology and Conservation</i> , 2022 , 33, e01969	2.8	0
3	Draft de novo Genome Assembly of the Elusive Jaguarundi, <i>Puma yagouaroundi</i> . <i>Journal of Heredity</i> , 2021 , 112, 540-548	2.4	0
2	A collective statement in support of saving pangolins.. <i>Science of the Total Environment</i> , 2022 , 153666	10.2	0
1	Evolution: a new cat species emerges. <i>Current Biology</i> , 2013 , 23, R1103-5	6.3	