

Klaus-Peter Koepfli

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1091755/publications.pdf>

Version: 2024-02-01

64
papers

9,900
citations

159585

30
h-index

106344

65
g-index

73
all docs

73
docs citations

73
times ranked

13180
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819.	27.8	2,215
2	Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.	12.6	1,583
3	Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746.	27.8	1,139
4	Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.	27.8	586
5	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.	7.1	517
6	Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs. <i>Science</i> , 2013, 342, 871-874.	12.6	438
7	The Genome 10K Project: A Way Forward. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 57-111.	7.4	294
8	Multigene phylogeny of the Mustelidae: Resolving relationships, tempo and biogeographic history of a mammalian adaptive radiation. <i>BMC Biology</i> , 2008, 6, 10.	3.8	258
9	The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433.	12.8	217
10	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.	2.7	206
11	A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 225-240.	2.7	183
12	Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277.	8.8	167
13	Extensive population genetic structure in the giraffe. <i>BMC Biology</i> , 2007, 5, 57.	3.8	163
14	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015, 25, 2158-2165.	3.9	156
15	Phylogeny of the Procyonidae (Mammalia: Carnivora): Molecules, morphology and the Great American Interchange. <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 1076-1095.	2.7	116
16	Red fox genome assembly identifies genomic regions associated with tame and aggressive behaviours. <i>Nature Ecology and Evolution</i> , 2018, 2, 1479-1491.	7.8	113
17	Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5.	3.9	110
18	Phylogenetic relationships of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome b sequences. <i>Journal of Zoology</i> , 1998, 246, 401-416.	1.7	99

#	ARTICLE	IF	CITATIONS
19	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	5.5	95
20	Molecular systematics of the Hyaenidae: Relationships of a relictual lineage resolved by a molecular supermatrix. <i>Molecular Phylogenetics and Evolution</i> , 2006, 38, 603-620.	2.7	92
21	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.	2.5	71
22	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.	7.1	70
23	Type I Sts Markers Are More Informative than Cytochrome b in Phylogenetic Reconstruction of the Mustelidae (Mammalia: Carnivora). <i>Systematic Biology</i> , 2003, 52, 571-593.	5.6	68
24	Sex identification of the Eurasian otter <i>Lutra lutra</i> by PCR typing of spraints. <i>Conservation Genetics</i> , 2000, 1, 181-183.	1.5	66
25	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5.	3.9	49
26	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.	8.9	48
27	GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020, 9, .	6.4	48
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.	3.9	34
29	Establishing the foundation for an applied molecular taxonomy of otters in Southeast Asia. <i>Conservation Genetics</i> , 2008, 9, 1589-1604.	1.5	33
30	Evolutionary history of the Falklands wolf. <i>Current Biology</i> , 2009, 19, R937-R938.	3.9	33
31	Population Genomic Analysis of North American Eastern Wolves (<i>Canis lycaon</i>) Supports Their Conservation Priority Status. <i>Genes</i> , 2018, 9, 606.	2.4	32
32	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.	2.3	31
33	Cryptic phylogeographic history sheds light on the generation of species diversity in skyâ€island mountains. <i>Journal of Biogeography</i> , 2019, 46, 2232-2247.	3.0	31
34	Annotated features of domestic cat â€ Felis catus genome. <i>GigaScience</i> , 2014, 3, 13.	6.4	30
35	Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018, 28, R13-R14.	3.9	27
36	Chromosomalâ€level genome assembly of the scimitarâ€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

#	ARTICLE	IF	CITATIONS
37	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.	3.9	26
38	Breeding Centers, Private Ranches, and Genomics for Creating Sustainable Wildlife Populations. <i>BioScience</i> , 2019, 69, 928-943.	4.9	25
39	Comparative genomics provides new insights into the remarkable adaptations of the African wild dog (<i>Lycan pictus</i>). <i>Scientific Reports</i> , 2019, 9, 8329.	3.3	23
40	Phylogeography and Demographic History of the Neotropical Otter (<i>Lontra longicaudis</i>). <i>Journal of Heredity</i> , 2012, 103, 479-492.	2.4	22
41	The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016, 107, 104-114.	2.4	21
42	Improving draft genome contiguity with reference-derived in silico mate-pair libraries. <i>GigaScience</i> , 2018, 7, .	6.4	19
43	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
44	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
45	Are pangolins scapegoats of the COVID-19 outbreak? CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020, 13, e12754.	5.7	17
46	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016, 6, 28199.	3.3	16
47	Towards resolving taxonomic uncertainties in wolf, dog and jackal lineages of Africa, Eurasia and Australasia. <i>Journal of Zoology</i> , 2022, 316, 155-168.	1.7	15
48	Phylogenomics of the world's otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4.	3.9	14
49	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.	2.7	12
50	Chromosome-Level Genome Assemblies Expand Capabilities of Genomics for Conservation Biology. <i>Genes</i> , 2021, 12, 1336.	2.4	12
51	Genomic analyses reveal range-wide devastation of sea otter populations. <i>Molecular Ecology</i> , 2023, 32, 281-298.	3.9	12
52	Diversity and Paleodemography of the Addax (<i>Addax nasomaculatus</i>), a Saharan Antelope on the Verge of Extinction. <i>Genes</i> , 2021, 12, 1236.	2.4	8
53	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
54	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.	1.7	7

#	ARTICLE	IF	CITATIONS
55	A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020, 7, 126.	5.3	6
56	A collective statement in support of saving pangolins. <i>Science of the Total Environment</i> , 2022, 824, 153666.	8.0	6
57	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
58	Genome Sequencing of a Gray Wolf from Peninsular India Provides New Insights into the Evolution and Hybridization of Gray Wolves. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	5
59	<i>De novo</i> whole-genome assembly and resequencing resources for the roan (<i>Hippotragus</i>) Tj ETQq1 1 0.784314 rgBT /Overlock 1.8 4	1.8	4
60	Characteristics of the complete mitochondrial genome of the monotypic genus <i>Arctictis</i> (Family:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 3 2.0	2.0	3
61	Molecular Phylogeny and Evolution of Amazon Parrots in the Greater Antilles. <i>Genes</i> , 2021, 12, 608.	2.4	2
62	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.	2.1	2
63	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
64	Evolution: A New Cat Species Emerges. <i>Current Biology</i> , 2013, 23, R1103-R1105.	3.9	0