

Klaus-Peter Koepfli

List of Publications by Year in descending order

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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 | Genomic analyses reveal range-wide devastation of sea otter populations. <i>Molecular Ecology</i> , 2023, 32, 281-298. | 3.9 | 12 |
| 2 | 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 |
| 3 | 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 |
| 4 | 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 |
| 5 | 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 |
| 6 | A collective statement in support of saving pangolins. <i>Science of the Total Environment</i> , 2022, 824, 153666. | 8.0 | 6 |
| 7 | 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 |
| 8 | Phylogenomics of the world's otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4. | 3.9 | 14 |
| 9 | Molecular Phylogeny and Evolution of Amazon Parrots in the Greater Antilles. <i>Genes</i> , 2021, 12, 608. | 2.4 | 2 |
| 10 | Towards complete and error-free genome assemblies of all vertebrate species. <i>Nature</i> , 2021, 592, 737-746. | 27.8 | 1,139 |
| 11 | Draft de novo Genome Assembly of the Elusive Jaguarundi, Puma yagouaroundi. <i>Journal of Heredity</i> , 2021, 112, 540-548. | 2.4 | 5 |
| 12 | Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5. | 3.9 | 49 |
| 13 | Chromosome-Level Genome Assemblies Expand Capabilities of Genomics for Conservation Biology. <i>Genes</i> , 2021, 12, 1336. | 2.4 | 12 |
| 14 | 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 |
| 15 | 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 |
| 16 | De novo whole-genome assembly and resequencing resources for the roan (<i>Hippotragus</i>) | 1.8 | 4 |
| 17 | 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 |
| 18 | Are pangolins scapegoats of the COVID-19 outbreak? CoV transmission and pathology evidence?. <i>Conservation Letters</i> , 2020, 13, e12754. | 5.7 | 17 |

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|----|---|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | 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 |
| 22 | GADMA: Genetic algorithm for inferring demographic history of multiple populations from allele frequency spectrum data. <i>GigaScience</i> , 2020, 9, . | 6.4 | 48 |
| 23 | A draft genome assembly of spotted hyena, <i>Crocuta crocuta</i> . <i>Scientific Data</i> , 2020, 7, 126. | 5.3 | 6 |
| 24 | 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 |
| 25 | Cryptic phylogeographic history sheds light on the generation of species diversity in sky-island mountains. <i>Journal of Biogeography</i> , 2019, 46, 2232-2247. | 3.0 | 31 |
| 26 | Breeding Centers, Private Ranches, and Genomics for Creating Sustainable Wildlife Populations. <i>BioScience</i> , 2019, 69, 928-943. | 4.9 | 25 |
| 27 | 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 |
| 28 | 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. | 3.3 | 23 |
| 29 | 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 |
| 30 | 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 |
| 31 | Characteristics of the complete mitochondrial genome of the monotypic genus <i>Arctictis</i> (Family: Tj ETQq1 1 0.784314 rgBT / Overloc 2.0 3 | 2.0 | 3 |
| 32 | Robust forensic matching of confiscated horns to individual poached African rhinoceros. <i>Current Biology</i> , 2018, 28, R13-R14. | 3.9 | 27 |
| 33 | Improving draft genome contiguity with reference-derived in silico mate-pair libraries. <i>GigaScience</i> , 2018, 7, . | 6.4 | 19 |
| 34 | 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 |
| 35 | Interspecific Gene Flow Shaped the Evolution of the Genus <i>Canis</i> . <i>Current Biology</i> , 2018, 28, 3441-3449.e5. | 3.9 | 110 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | 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 |
| 38 | Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322. | 5.5 | 95 |
| 39 | De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016, 6, 28199. | 3.3 | 16 |
| 40 | The Population Origins and Expansion of Feral Cats in Australia. <i>Journal of Heredity</i> , 2016, 107, 104-114. | 2.4 | 21 |
| 41 | Genomic legacy of the African cheetah, <i>Acinonyx jubatus</i> . <i>Genome Biology</i> , 2015, 16, 277. | 8.8 | 167 |
| 42 | The Genome 10K Project: A Way Forward. <i>Annual Review of Animal Biosciences</i> , 2015, 3, 57-111. | 7.4 | 294 |
| 43 | Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. <i>Current Biology</i> , 2015, 25, 2158-2165. | 3.9 | 156 |
| 44 | 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 |
| 45 | Annotated features of domestic cat "Felis catus" genome. <i>GigaScience</i> , 2014, 3, 13. | 6.4 | 30 |
| 46 | Complete Mitochondrial Genomes of Ancient Canids Suggest a European Origin of Domestic Dogs. <i>Science</i> , 2013, 342, 871-874. | 12.6 | 438 |
| 47 | Evolution: A New Cat Species Emerges. <i>Current Biology</i> , 2013, 23, R1103-R1105. | 3.9 | 0 |
| 48 | 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 |
| 49 | The tiger genome and comparative analysis with lion and snow leopard genomes. <i>Nature Communications</i> , 2013, 4, 2433. | 12.8 | 217 |
| 50 | Phylogeography and Demographic History of the Neotropical Otter (<i>Lontra longicaudis</i>). <i>Journal of Heredity</i> , 2012, 103, 479-492. | 2.4 | 22 |
| 51 | Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364. | 27.8 | 586 |
| 52 | 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 |
| 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. | 2.7 | 206 |
| 54 | Evolutionary history of the Falklands wolf. <i>Current Biology</i> , 2009, 19, R937-R938. | 3.9 | 33 |

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|----|---|------|-----------|
| 55 | Establishing the foundation for an applied molecular taxonomy of otters in Southeast Asia. <i>Conservation Genetics</i> , 2008, 9, 1589-1604. | 1.5 | 33 |
| 56 | 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 |
| 57 | 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 |
| 58 | Extensive population genetic structure in the giraffe. <i>BMC Biology</i> , 2007, 5, 57. | 3.8 | 163 |
| 59 | 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 |
| 60 | Genome sequence, comparative analysis and haplotype structure of the domestic dog. <i>Nature</i> , 2005, 438, 803-819. | 27.8 | 2,215 |
| 61 | 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 |
| 62 | 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 |
| 63 | 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 |
| 64 | Phylogenetic relationships of otters (Carnivora: Mustelidae) based on mitochondrial cytochrome b sequences. <i>Journal of Zoology</i> , 1998, 246, 401-416. | 1.7 | 99 |