John P Pollinger

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Natural re-colonization and admixture of wolves (Canis lupus) in the US Pacific Northwest: challenges for the protection and management of rare and endangered taxa. Heredity, 2019, 122, 133-149.	1.2	13
2	Admixture mapping identifies introgressed genomic regions in North American canids. Molecular Ecology, 2016, 25, 2443-2453.	2.0	79
3	Interactions between demography, genetics, and landscape connectivity increase extinction probability for a small population of large carnivores in a major metropolitan area. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160957.	1.2	65
4	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. Science Advances, 2016, 2, e1501714.	4.7	150
5	Worldwide patterns of genomic variation and admixture in gray wolves. Genome Research, 2016, 26, 163-173.	2.4	160
6	Genome-wide Evidence Reveals that African and Eurasian Golden Jackals Are Distinct Species. Current Biology, 2015, 25, 2158-2165.	1.8	156
7	Optimization of RNA isolation and leukocyte viability in canid RNA expression studies. Conservation Genetics Resources, 2012, 4, 27-29.	0.4	2
8	A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids. Genome Research, 2011, 21, 1294-1305.	2.4	266
9	Fine-scale genetic structure in Ethiopian wolves imposed by sociality, migration, and population bottlenecks. Conservation Genetics, 2010, 11, 89-101.	0.8	25
10	A novel assessment of population structure and gene flow in grey wolf populations of the Northern Rocky Mountains of the United States. Molecular Ecology, 2010, 19, 4412-4427.	2.0	80
11	The genealogy and genetic viability of reintroduced Yellowstone grey wolves. Molecular Ecology, 2008, 17, 252-274.	2.0	177
12	Genetic evidence for the persistence of the critically endangered Sierra Nevada red fox in California. Conservation Genetics, 2007, 8, 1083-1095.	0.8	53
13	Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature, 2005, 438, 803-819.	13.7	2,215
14	Selective sweep mapping of genes with large phenotypic effects. Genome Research, 2005, 15, 1809-1819.	2.4	102