

Genetic tagging of humpback whales

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Review of DNA-based census and effective population size estimators. <i>Animal Conservation</i> , 1998, 1, 293-299.	1.5	120
2	Molecular analysis of the efficiency of sloughed skin sampling in whale population genetics. <i>Molecular Ecology</i> , 1998, 7, 1419-1422.	2.0	26
3	Genetic estimates of population structure and gene flow: Limitations, lessons and new directions. <i>Trends in Ecology and Evolution</i> , 1998, 13, 202-206.	4.2	503
4	Aerial surveys of cetaceans in the Gulf of St. Lawrence in 1995 and 1996. <i>Canadian Journal of Zoology</i> , 1998, 76, 1529-1550.	0.4	42
5	Chapter 10 The organization and regulation of non-NMDA receptors in neurons. <i>Progress in Brain Research</i> , 1998, 116, 133-152.	0.9	13
6	Culture and Genetic Evolution in Whales. <i>Science</i> , 1999, 284, 2055a-2055.	6.0	32
7	Baleen whales: conservation issues and the status of the most endangered populations. <i>Mammal Review</i> , 1999, 29, 37-62.	2.2	271
8	Characterization and isolation of microsatellite loci from the endangered North Atlantic right whale. <i>Molecular Ecology</i> , 1999, 8, 1763-1765.	2.0	43
9	A Quantitative Approach to Endangered Species Act Classification of Long-Lived Vertebrates: Application to the North Pacific Humpback Whale. <i>Conservation Biology</i> , 1999, 13, 1203-1214.	2.4	33
10	Genetic tagging: contemporary molecular ecology. <i>Biological Journal of the Linnean Society</i> , 1999, 68, 3-22.	0.7	91
11	AN OCEAN-BASIN-WIDE MARK-RECAPTURE STUDY OF THE NORTH ATLANTIC HUMPBACK WHALE (MEGAPTERA) Tj ETQq0 0 0 rgBT /Ove	0.9	154
12	Single-Locus Tests of Microsatellite Evolution: Multi-Step Mutations and Constraints on Allele Size. <i>Molecular Phylogenetics and Evolution</i> , 1999, 11, 477-484.	1.2	26
13	Sex-biased dispersal in sperm whales: contrasting mitochondrial and nuclear genetic structure of global populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 347-354.	1.2	132
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15	Estimating Animal Abundance: Review III. <i>Statistical Science</i> , 1999, 14, 427.	1.6	383
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17	Biases associated with population estimation using molecular tagging. <i>Animal Conservation</i> , 2000, 3, 191-199.	1.5	150
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20	ESTIMATING ANIMAL ABUNDANCE USING NONINVASIVE DNA SAMPLING: PROMISE AND PITFALLS. , 2000, 10, 283-294.		328
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25	A genetic analogue of “mark-recapture” methods for estimating population size: an approach based on molecular parentage assessments. <i>Molecular Ecology</i> , 2001, 10, 2711-2718.	2.0	52
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37	Wombat coprogenetics: enumerating a common wombat population by microsatellite analysis of faecal DNA. <i>Australian Journal of Zoology</i> , 2002, 50, 193.	0.6	54

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43	A NOVEL BEHAVIOR OBSERVED IN HUMPBACK WHALES ON WINTERING GROUNDS AT ABROLHOS BANK (BRAZIL). <i>Marine Mammal Science</i> , 2003, 19, 694-707.	0.9	15
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60	Abundance, genetic diversity and conservation of Louisiana black bears (<i>Ursus americanus luteolus</i>) as detected through noninvasive sampling. <i>Conservation Genetics</i> , 2004, 5, 647-659.	0.8	27
61	Beyond FST: Analysis of population genetic data for conservation. <i>Conservation Genetics</i> , 2004, 5, 585-602.	0.8	223
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