Urmas Saarma

List of Publications by Year
in descending order

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46 papers	3,172 citations	126907 33 h-index	223800 46 g-index
46 all docs	46 docs citations	46 times ranked	3431 citing authors

#	Article	IF	Citations
1	Revealing the History of Sheep Domestication Using Retrovirus Integrations. Science, 2009, 324, 532-536.	12.6	402
2	The Effect of Inappropriate Calibration: Three Case Studies in Molecular Ecology. PLoS ONE, 2008, 3, e1615.	2.5	201
3	A novel phylogeny for the genus Echinococcus, based on nuclear data, challenges relationships based on mitochondrial evidence. Parasitology, 2009, 136, 317-328.	1.5	146
4	Late-Quaternary biogeographic scenarios for the brown bear (Ursus arctos), a wild mammal model species. Quaternary Science Reviews, 2011, 30, 418-430.	3.0	143
5	Partial genomic survival of cave bears in living brown bears. Nature Ecology and Evolution, 2018, 2, 1563-1570.	7.8	132
6	Wolf population genetics in <scp>E</scp>urope: a systematic review, metaâ€analysis and suggestions for conservation and management. Biological Reviews, 2017, 92, 1601-1629.	10.4	131
7	Phylogenetic relationships within Echinococcus and Taenia tapeworms (Cestoda: Taeniidae): An inference from nuclear protein-coding genes. Molecular Phylogenetics and Evolution, 2011, 61, 628-638.	2.7	121
8	Sudden expansion of a single brown bear maternal lineage across northern continental Eurasia after the last ice age: a general demographic model for mammals?. Molecular Ecology, 2009, 18, 1963-1979.	3.9	119
9	Mitogenetic structure of brown bears (Ursus arctos L.) in northeastern Europe and a new time frame for the formation of European brown bear lineages. Molecular Ecology, 2006, 16, 401-413.	3.9	118
10	New mitogenome and nuclear evidence on the phylogeny and taxonomy of the highly zoonotic tapeworm Echinococcus granulosus sensu stricto. Infection, Genetics and Evolution, 2017, 52, 52-58.	2.3	102
11	First report of Echinococcus granulosus G8 in Eurasia and a reappraisal of the phylogenetic relationships of â€˜genotypesâ€™ G5-G10. Parasitology, 2008, 135, 647-654.	1.5	99
12	Carnivory is Positively Correlated with Latitude among Omnivorous Mammals: Evidence from Brown Bears, Badgers and Pine Martens. Annales Zoologici Fennici, 2009, 46, 395-415.	0.6	92
13	Genetic structure in large, continuous mammal populations: the example of brown bears in northwestern Eurasia. Molecular Ecology, 2010, 19, 5359-5370.	3.9	88
14	HELMINTHOLOGIC SURVEY OF THE WOLF (CANIS LUPUS) IN ESTONIA, WITH AN EMPHASIS ON ECHINOCOCCUS GRANULOSUS. Journal of Wildlife Diseases, 2006, 42, 359-365.	0.8	81
15	Bucking the Trend in Wolf-Dog Hybridization: First Evidence from Europe of Hybridization between Female Dogs and Male Wolves. PLoS ONE, 2012, 7, e46465.	2.5	80
16	Global phylogeography and genetic diversity of the zoonotic tapeworm Echinococcus granulosus sensu stricto genotype G1. International Journal for Parasitology, 2018, 48, 729-742.	3.1	77
17	Complete mitochondrial genomes and a novel spatial genetic method reveal cryptic phylogeographical structure and migration patterns among brown bears in northâ€western Eurasia. Journal of Biogeography, 2013, 40, 915-927.	3.0	73
18	Europeâ€wide biogeographical patterns in the diet of an ecologically and epidemiologically important mesopredator, the red fox Vulpes vulpes: a quantitative review. Mammal Review, 2017, 47, 198-211.	4.8	71

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19	Molecular phylogeny based on six nuclear genes suggests that Echinococcus granulosus sensu lato genotypes G6/G7 and G8/G10 can be regarded as two distinct species. Parasitology, 2018, 145, 1929-1937.	1.5	69
20	A Multiplex PCR for the Simultaneous Detection and Genotyping of the Echinococcus granulosus Complex. PLoS Neglected Tropical Diseases, 2013, 7, e2017.	3.0	67
21	Rapid Urbanization of Red Foxes in Estonia: Distribution, Behaviour, Attacks on Domestic Animals, and Health-Risks Related to Zoonotic Diseases. PLoS ONE, 2014, 9, e115124.	2.5	64
22	Largeâ€scale migrations of brown bears in Eurasia and to North America during the Late Pleistocene. Journal of Biogeography, 2018, 45, 394-405.	3.0	59
23	Distinguishing Echinococcus granulosus sensu stricto genotypes G1 and G3 with confidence: A practical guide. Infection, Genetics and Evolution, 2018, 64, 178-184.	2.3	54
24	The benefits of analysing complete mitochondrial genomes: Deep insights into the phylogeny and population structure of Echinococcus granulosus sensu lato genotypes G6 and G7. Infection, Genetics and Evolution, 2018, 64, 85-94.	2.3	52
25	Echinococcus multilocularisin Estonia. Emerging Infectious Diseases, 2005, 11, 1973-1974.	4.3	52
26	Alien species and their zoonotic parasites in native and introduced ranges: The raccoon dog example. Veterinary Parasitology, 2016, 219, 24-33.	1.8	43
27	Genetic diversity and phylogeography of the elusive, but epidemiologically importantEchinococcus granulosussensu stricto genotype G3. Parasitology, 2018, 145, 1613-1622.	1.5	41
28	An Invasive Vector of Zoonotic Disease Sustained by Anthropogenic Resources: The Raccoon Dog in Northern Europe. PLoS ONE, 2014, 9, e96358.	2.5	40
29	Genetic diversity and phylogeography of highly zoonotic Echinococcus granulosus genotype G1 in the Americas (Argentina, Brazil, Chile and Mexico) based on 8279 bp of mtDNA. Infection, Genetics and Evolution, 2016, 45, 290-296.	2.3	37
30	Echinococcus granulosus genotype G1 dominated in cattle and sheep during 2003â€“2006 in Buenos Aires province, an endemic area for cystic echinococcosis in Argentina. Acta Tropica, 2013, 127, 136-142.	2.0	35
31	First report of highly pathogenic Echinococcus granulosus genotype G1 in dogs in a European urban environment. Parasites and Vectors, 2015, 8, 182.	2.5	35
32	Non-invasive genetics outperforms morphological methods in faecal dietary analysis, revealing wild boar as a considerable conservation concern for ground-nesting birds. PLoS ONE, 2017, 12, e0179463.	2.5	35
33	Molecular epidemiology of Aleutian mink disease virus (AMDV) in Estonia, and a global phylogeny of AMDV. Virus Research, 2015, 199, 56-61.	2.2	33
34	First report of the zoonotic tapeworm Echinococcus multilocularis in raccoon dogs in Estonia, and comparisons with other countries in Europe. Veterinary Parasitology, 2015, 212, 200-205.	1.8	33
35	Spatial Genetic Analyses Reveal Cryptic Population Structure and Migration Patterns in a Continuously Harvested Grey Wolf (Canis lupus) Population in North-Eastern Europe. PLoS ONE, 2013, 8, e75765.	2.5	24
36	Maternal and paternal genetic diversity of ancient sheep in Estonia from the Late Bronze Age to the postâ€medieval period and comparison with other regions in Eurasia. Animal Genetics, 2016, 47, 208-218.	1.7	22

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37	Three Thousand Years of Continuity in the Maternal Lineages of Ancient Sheep (Ovis aries) in Estonia. PLoS ONE, 2016, 11, e0163676.	2.5	19
38	Assessing the roles of wolves and dogs in livestock predation with suggestions for mitigating humanâ€“wildlife conflict and conservation of wolves. Conservation Genetics, 2018, 19, 665-672.	1.5	16
39	Analysis of nad2 and nad5 enables reliable identification of genotypes G6 and G7 within the species complex Echinococcus granulosus sensu lato. Infection, Genetics and Evolution, 2019, 74, 103941.	2.3	16
40	First detection of zoonotic tapeworm Echinococcus granulosus sensu lato genotype G7 in continental Italy. Parasitology Research, 2019, 118, 2193-2201.	1.6	15
41	Cystic echinococcosis in sheep and goats of Lebanon. Parasitology, 2021, 148, 871-878.	1.5	13
42	Wolves Recolonizing Islands: Genetic Consequences and Implications for Conservation and Management. PLoS ONE, 2016, 11, e0158911.	2.5	8
43	Severe impact of sarcoptic mange on the movements and space use for one of its most important vector species, the raccoon dog. Veterinary Parasitology, 2017, 243, 67-70.	1.8	8
44	Free-ranging rural dogs are highly infected with helminths, contaminating environment nine times more than urban dogs. Journal of Helminthology, 2022, 96, e19.	1.0	3
45	Cultural influences on the castration age of cattle in the northern Baltic Sea region during the medieval and post-medieval periods. Journal of Archaeological Science, 2022, 137, 105517.	2.4	2
46	Ongoing recovery of a brown bear population from a century-old severe bottleneck: insights from population genetic and spatially explicit analyses. Conservation Genetics, 2020, 21, 27-40.	1.5	1