

Robert Ekblom

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

4,297
citations

257450

24
h-index

361022

35
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39
docs citations

39
times ranked

6908
citing authors

#	ARTICLE	IF	CITATIONS
1	Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (<sc>EBVs</sc>) for genetic composition. <i>Biological Reviews</i> , 2022, 97, 1511-1538.	10.4	73
2	Bringing together approaches to reporting on within species genetic diversity. <i>Journal of Applied Ecology</i> , 2022, 59, 2227-2233.	4.0	24
3	Sample identification and pedigree reconstruction in Wolverine (<i>Gulo gulo</i>) using SNP genotyping of non-invasive samples. <i>Conservation Genetics Resources</i> , 2021, 13, 261-274.	0.8	7
4	Extreme altitude changes between night and day during marathon flights of great snipes. <i>Current Biology</i> , 2021, 31, 3433-3439.e3.	3.9	29
5	Genetic diversity is considered important but interpreted narrowly in country reports to the Convention on Biological Diversity: Current actions and indicators are insufficient. <i>Biological Conservation</i> , 2021, 261, 109233.	4.1	65
6	Review of the diet specialisation of the Blue-cheeked bee-eater (<i>Merops persicus</i>). <i>Journal of Ornithology</i> , 2019, 160, 275-279.	1.1	0
7	Genome sequencing and conservation genomics in the Scandinavian wolverine population. <i>Conservation Biology</i> , 2018, 32, 1301-1312.	4.7	49
8	Winter recovery in Sweden of a Dutch Blackcap <i>Sylvia atricapilla</i> . <i>Ornis Svecica</i> , 2018, 28, .	0.1	0
9	Blood transcriptomes and de novo identification of candidate loci for mating success in lekking great snipe (<i>Gallinago media</i>). <i>Molecular Ecology</i> , 2017, 26, 3458-3471.	3.9	8
10	Development of transcriptome genetic markers for the great snipe (<i>Gallinago media</i>). <i>Conservation Genetics Resources</i> , 2017, 9, 643-645.	0.8	1
11	A bird's eye view of a deleterious recessive allele. <i>Journal of Animal Ecology</i> , 2016, 85, 855-856.	2.8	1
12	The migration of the great snipe <i>Gallinago media</i>: intriguing variations on a grand theme. <i>Journal of Avian Biology</i> , 2016, 47, 321-334.	1.2	34
13	Reply to Garner et al.. <i>Trends in Ecology and Evolution</i> , 2016, 31, 83-84.	8.7	24
14	Genomics and the challenging translation into conservation practice. <i>Trends in Ecology and Evolution</i> , 2015, 30, 78-87.	8.7	469
15	Whole genome sequencing of the black grouse (<i>Tetrao tetrix</i>): reference guided assembly suggests faster-Z and MHC evolution. <i>BMC Genomics</i> , 2014, 15, 180.	2.8	36
16	Patterns of sequencing coverage bias revealed by ultra-deep sequencing of vertebrate mitochondria. <i>BMC Genomics</i> , 2014, 15, 467.	2.8	55
17	A field guide to whole-genome sequencing, assembly and annotation. <i>Evolutionary Applications</i> , 2014, 7, 1026-1042.	3.1	296
18	Characterization of the house sparrow (<i>P</i>asser domesticus</i>) transcriptome: a resource for molecular ecology and immunogenetics. <i>Molecular Ecology Resources</i> , 2014, 14, 636-646.	4.8	14

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19	High-utility conserved avian microsatellite markers enable parentage and population studies across a wide range of species. <i>BMC Genomics</i> , 2013, 14, 176.	2.8	68
20	Comparison between Normalised and Unnormalised 454-Sequencing Libraries for Small-Scale RNA-Seq Studies. <i>Comparative and Functional Genomics</i> , 2012, 2012, 1-8.	2.0	18
21	Transcriptome sequencing of black grouse (<i>Tetrao tetrix</i>) for immune gene discovery and microsatellite development. <i>Open Biology</i> , 2012, 2, 120054.	3.6	26
22	Gene expression divergence and nucleotide differentiation between males of different color morphs and mating strategies in the ruff. <i>Ecology and Evolution</i> , 2012, 2, 2485-2505.	1.9	20
23	Sequencing of the core MHC region of black grouse (<i>Tetrao tetrix</i>) and comparative genomics of the galliform MHC. <i>BMC Genomics</i> , 2012, 13, 553.	2.8	29
24	Applications of next generation sequencing in molecular ecology of non-model organisms. <i>Heredity</i> , 2011, 107, 1-15.	2.6	930
25	Genetic mapping of the major histocompatibility complex in the zebra finch (<i>Taeniopygia guttata</i>). <i>Immunogenetics</i> , 2011, 63, 523-530.	2.4	35
26	Balancing selection, sexual selection and geographic structure in MHC genes of Great Snipe. <i>Genetica</i> , 2010, 138, 453-461.	1.1	19
27	Digital gene expression analysis of the zebra finch genome. <i>BMC Genomics</i> , 2010, 11, 219.	2.8	41
28	Gene duplication and fragmentation in the zebra finch major histocompatibility complex. <i>BMC Biology</i> , 2010, 8, 29.	3.8	121
29	The genome of a songbird. <i>Nature</i> , 2010, 464, 757-762.	27.8	770
30	Evolutionary Analysis and Expression Profiling of Zebra Finch Immune Genes. <i>Genome Biology and Evolution</i> , 2010, 2, 781-790.	2.5	38
31	Evolution of a cluster of innate immune genes (β -defensins) along the ancestral lines of chicken and zebra finch. <i>Immunome Research</i> , 2010, 6, 3.	0.1	54
32	Adaptation genomics: the next generation. <i>Trends in Ecology and Evolution</i> , 2010, 25, 705-712.	8.7	589
33	Spatial pattern of MHC class II variation in the great snipe (<i>Gallinago media</i>). <i>Molecular Ecology</i> , 2007, 16, 1439-1451.	3.9	149
34	Female choice and male humoral immune response in the lekking great snipe (<i>Gallinago media</i>). <i>Behavioral Ecology</i> , 2005, 16, 346-351.	2.2	12
35	Direct and Indirect Mate Choice on Leks. <i>American Naturalist</i> , 2005, 166, 145-157.	2.1	33
36	Major histocompatibility complex variation and mate choice in a lekking bird, the great snipe (<i>Gallinago media</i>). <i>Molecular Ecology</i> , 2004, 13, 3821-3828.	3.9	110

#	ARTICLE	IF	CITATIONS
37	Patterns of polymorphism in the MHC class II of a non-passerine bird, the great snipe (<i>Gallinago media</i>). Immunogenetics, 2003, 54, 734-741.	2.4	45