Linnéa Smeds

List of Publications by Year in descending order

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361413 642732 4,717 23 20 23 citations h-index g-index papers 23 23 23 6349 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Wholeâ€genome analyses provide no evidence for dog introgression in Fennoscandian wolf populations. Evolutionary Applications, 2021, 14, 721-734.	3.1	19
2	Genomic inference of contemporary effective population size in a large island population of collared flycatchers (<i>Ficedula albicollis</i>). Molecular Ecology, 2021, 30, 3965-3973.	3.9	17
3	The evolutionary history of grey wolf Y chromosomes. Molecular Ecology, 2019, 28, 2173-2191.	3.9	14
4	Abundant recent activity of retrovirusâ€like retrotransposons within and among flycatcher species implies a rich source of structural variation in songbird genomes. Molecular Ecology, 2018, 27, 99-111.	3.9	59
5	Genome sequencing and conservation genomics in the Scandinavian wolverine population. Conservation Biology, 2018, 32, 1301-1312.	4.7	49
6	Sexâ€biased gene expression, sexual antagonism and levels of genetic diversity in the collared flycatcher (<i>Ficedula albicollis</i>) genome. Molecular Ecology, 2018, 27, 3572-3581.	3.9	51
7	Wholeâ€genome patterns of linkage disequilibrium across flycatcher populations clarify the causes and consequences of fineâ€scale recombination rate variation in birds. Molecular Ecology, 2017, 26, 4158-4172.	3.9	87
8	<scp>PSMC</scp> analysis of effective population sizes in molecular ecology and its application to blackâ€andâ€white <i>Ficedula</i> flycatchers. Molecular Ecology, 2016, 25, 1058-1072.	3.9	225
9	Direct estimate of the rate of germline mutation in a bird. Genome Research, 2016, 26, 1211-1218.	5.5	190
10	High-Resolution Mapping of Crossover and Non-crossover Recombination Events by Whole-Genome Re-sequencing of an Avian Pedigree. PLoS Genetics, 2016, 12, e1006044.	3.5	85
11	Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of <i>Ficedula</i> flycatchers. Genome Research, 2015, 25, 1656-1665.	5.5	385
12	Resolving Evolutionary Relationships in Closely Related Species with Whole-Genome Sequencing Data. Systematic Biology, 2015, 64, 1000-1017.	5.6	102
13	Evolutionary analysis of the female-specific avian W chromosome. Nature Communications, 2015, 6, 7330.	12.8	121
14	Temporal Dynamics of Avian Populations during Pleistocene Revealed by Whole-Genome Sequences. Current Biology, 2015, 25, 1375-1380.	3.9	243
15	Genome-wide association mapping in a wild avian population identifies a link between genetic and phenotypic variation in a life-history trait. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20150156.	2.6	45
16	The Dynamics of Incomplete Lineage Sorting across the Ancient Adaptive Radiation of Neoavian Birds. PLoS Biology, 2015, 13, e1002224.	5.6	223
17	A Transcriptome Derived Female-Specific Marker from the Invasive Western Mosquitofish (Gambusia) Tj ETQq $1\ 1$	1 0.784314 	4 rgBT /Ove <mark>rlo</mark>
18	Genomic identification and characterization of the pseudoautosomal region in highly differentiated avian sex chromosomes. Nature Communications, 2014, 5, 5448.	12.8	44

#	Article	IF	CITATIONS
19	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	12.6	1,583
20	A highâ€density linkage map enables a secondâ€generation collared flycatcher genome assembly and reveals the patterns of avian recombination rate variation and chromosomal evolution. Molecular Ecology, 2014, 23, 4035-4058.	3.9	220
21	Demographic Divergence History of Pied Flycatcher and Collared Flycatcher Inferred from Whole-Genome Re-sequencing Data. PLoS Genetics, 2013, 9, e1003942.	3.5	124
22	The genomic landscape of species divergence in Ficedula flycatchers. Nature, 2012, 491, 756-760.	27.8	589
23	ConDeTri - A Content Dependent Read Trimmer for Illumina Data. PLoS ONE, 2011, 6, e26314.	2.5	216