Pierre Taberlet

List of Publications by Year in descending order

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252 papers	50,533 citations	1980 101 h-index	1668 214 g-index
262 all docs	262 docs citations	262 times ranked	34887 citing authors

#	Article	IF	Citations
1	Broad maternal geographic origin of domestic sheep in Anatolia and the Zagros. Animal Genetics, 2022, 53, 452-459.	0.6	3
2	Editorial 2022. Molecular Ecology, 2022, 31, 1-30.	2.0	5
3	Assessing environmental DNA metabarcoding and camera trap surveys as complementary tools for biomonitoring of remote desert water bodies. Environmental DNA, 2022, 4, 580-595.	3.1	7
4	Interspecific coprophagia by wild red foxes:<scp>DNA</scp>metabarcoding reveals a potentially widespread form of commensalism among animals. Ecology and Evolution, 2022, 12, .	0.8	6
5	Modelling technical and biological biases in macroinvertebrate community assessment from bulk preservative using multiple metabarcoding markers. Molecular Ecology, 2021, 30, 3221-3238.	2.0	30
6	Comparison of markers for the monitoring of freshwater benthic biodiversity through DNA metabarcoding. Molecular Ecology, 2021, 30, 3189-3202.	2.0	35
7	Morphological vs. DNA metabarcoding approaches for the evaluation of stream ecological status with benthic invertebrates: Testing different combinations of markers and strategies of data filtering. Molecular Ecology, 2021, 30, 3203-3220.	2.0	27
8	Environmental DNA metabarcoding for freshwater bivalves biodiversity assessment: methods and results for the Western Palearctic (European sub-region). Hydrobiologia, 2021, 848, 2931-2950.	1.0	24
9	Power and limitations of environmental DNA metabarcoding for surveying leaf litter eukaryotic communities. Environmental DNA, 2021, 3, 528-540.	3.1	4
10	How do forest management and wolf space-use affect diet composition of the wolfâ€™s main prey, the red deer versus a non-prey species, the European bison?. Forest Ecology and Management, 2021, 479, 118620.	1.4	8
11	Sharing and reporting benefits from biodiversity research. Molecular Ecology, 2021, 30, 1103-1107.	2.0	19
12	Small shrubs with large importance? Smaller deer may increase the moose-forestry conflict through feeding competition over Vaccinium shrubs in the field layer. Forest Ecology and Management, 2021, 480, 118768.	1.4	13
13	Lake Sedimentary DNA Research on Past Terrestrial and Aquatic Biodiversity: Overview and Recommendations. Quaternary, 2021, 4, 6.	1.0	121
14	eDNA metabarcoding for biodiversity assessment, generalist predators as sampling assistants. Scientific Reports, 2021, 11, 6820.	1.6	20
15	Comprehensive coverage of human last meal components revealed by a forensic DNA metabarcoding approach. Scientific Reports, 2021, 11, 8876.	1.6	5
16	Biodiversity monitoring using environmental DNA. Molecular Ecology Resources, 2021, 21, 1405-1409.	2.2	15
17	Environmental DNA for biomonitoring. Molecular Ecology, 2021, 30, 2931-2936.	2.0	38
18	Analysis of complex trophic networks reveals the signature of land-use intensification on soil communities in agroecosystems. Scientific Reports, 2021, 11, 18260.	1.6	10

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19	Assessing changes in stream macroinvertebrate communities across ecological gradients using morphological versus DNA metabarcoding approaches. Science of the Total Environment, 2021, 797, 149030.	3.9	3
20	The bear-berry connection: Ecological and management implications of brown bears' food habits in a highly touristic protected area. Biological Conservation, 2021, 264, 109376.	1.9	11
21	Latent Dirichlet Allocation reveals spatial and taxonomic structure in a DNAâ€based census of soil biodiversity from a tropical forest. Molecular Ecology Resources, 2020, 20, 371-386.	2.2	16
22	Ecological specialization and niche overlap of subterranean rodents inferred from DNA metabarcoding diet analysis. Molecular Ecology, 2020, 29, 3143-3153.	2.0	18
23	High levels of primary biogenic organic aerosols are driven by only a few plant-associated microbial taxa. Atmospheric Chemistry and Physics, 2020, 20, 5609-5628.	1.9	16
24	Advances and prospects of environmental DNA in neotropical rainforests. Advances in Ecological Research, 2020, , 331-373.	1.4	27
25	Editorial 2020. Molecular Ecology, 2020, 29, 1-19.	2.0	3
26	Variability of the Atmospheric PM10 Microbiome in Three Climatic Regions of France. Frontiers in Microbiology, 2020, 11, 576750.	1.5	6
27	Unlocking biodiversity and conservation studies in highâ€diversity environments using environmental DNA (eDNA): A test with Guianese freshwater fishes. Molecular Ecology Resources, 2019, 19, 27-46.	2.2	135
28	Foraging plasticity allows a large herbivore to persist in a sheltering forest habitat: DNA metabarcoding diet analysis of the European bison. Forest Ecology and Management, 2019, 449, 117474.	1.4	39
29	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. Molecular Ecology Resources, 2019, 19, 1497-1515.	2.2	31
30	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. Science Advances, 2019, 5, eaav8391.	4.7	218
31	DNA metabarcodingâ€"Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology, 2019, 28, 1857-1862.	2.0	300
32	Optimizing environmental DNA sampling effort for fish inventories in tropical streams and rivers. Scientific Reports, 2019, 9, 3085.	1.6	93
33	Doubting dung: eDNA reveals high rates of misidentification in diverse European ungulate communities. European Journal of Wildlife Research, 2019, 65, 1.	0.7	27
34	Last but not beast: the fall of the Alpine wolves told by historical DNA. Mammal Research, 2019, 64, 595-600.	0.6	4
35	Environmental DNA and metabarcoding for the study of amphibians and reptiles: species distribution, the microbiome, and much more. Amphibia - Reptilia, 2019, 40, 129-148.	0.1	47
36	Environmental and biotic drivers of soil microbial Î²â€diversity across spatial and phylogenetic scales. Ecography, 2019, 42, 2144-2156.	2.1	21

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37	Diet of the brown bear in Himalaya: Combining classical and molecular genetic techniques. PLoS ONE, 2019, 14, e0225698.	1.1	12
38	Body size determines soil community assembly in a tropical forest. Molecular Ecology, 2019, 28, 528-543.	2.0	129
39	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	5.8	220
40	Sheep genome functional annotation reveals proximal regulatory elements contributed to the evolution of modern breeds. Nature Communications, 2018, 9, 859.	5.8	126
41	Lack of evidence for selection favouring MHC haplotypes that combine high functional diversity. Heredity, 2018, 120, 396-406.	1.2	14
42	Preserving genetic connectivity in the European Alps protected area network. Biological Conservation, 2018, 218, 99-109.	1.9	16
43	Ancient environmental DNA reveals shifts in dominant mutualisms during the lateÂQuaternary. Nature Communications, 2018, 9, 139.	5.8	24
44	Present conditions may mediate the legacy effect of past landâ€use changes on species richness and composition of aboveâ€•and belowâ€ground assemblages. Journal of Ecology, 2018, 106, 306-318.	1.9	23
45	Environmental DNA Time Series in Ecology. Trends in Ecology and Evolution, 2018, 33, 945-957.	4.2	152
46	Metabarcoding of modern soil DNA gives a highly local vegetation signal in Svalbard tundra. Holocene, 2018, 28, 2006-2016.	0.9	52
47	Diet shifts by adult flightless dung beetles Circellium bacchus, revealed using DNA metabarcoding, reflect complex life histories. Oecologia, 2018, 188, 107-115.	0.9	19
48	Howling from the past: historical phylogeography and diversity losses in European grey wolves. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20181148.	1.2	41
49	DNA from lake sediments reveals long-term ecosystem changes after a biological invasion. Science Advances, 2018, 4, eaar4292.	4.7	73
50	Mapping the imprint of biotic interactions on Î²â€diversity. Ecology Letters, 2018, 21, 1660-1669.	3.0	40
51	Body condition, diet and ecosystem function of red deer (Cervus elaphus) in a fenced nature reserve. Global Ecology and Conservation, 2017, 11, 312-323.	1.0	18
52	Long-term changes in alpine pedogenetic processes: Effect of millennial agro-pastoralism activities (French-Italian Alps). Geoderma, 2017, 306, 217-236.	2.3	35
53	Evaluating the impact of domestication and captivity on the horse gut microbiome. Scientific Reports, 2017, 7, 15497.	1.6	112
54	6-kyr record of flood frequency and intensity in the western Mediterranean Alps â€“ Interplay of solar and temperature forcing. Quaternary Science Reviews, 2017, 170, 121-135.	1.4	53

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55	Microrefugia, Climate Change, and Conservation of Cedrus atlantica in the Rif Mountains, Morocco. Frontiers in Ecology and Evolution, 2017, 5, .	1.1	45
56	Spatial Representativeness of Environmental DNA Metabarcoding Signal for Fish Biodiversity Assessment in a Natural Freshwater System. PLoS ONE, 2016, 11, e0157366.	1.1	167
57	Oral Samples as Non-Invasive Proxies for Assessing the Composition of the Rumen Microbial Community. PLoS ONE, 2016, 11, e0151220.	1.1	70
58	The ecologist's field guide to sequenceâ€based identification of biodiversity. Methods in Ecology and Evolution, 2016, 7, 1008-1018.	2.2	316
59	Critical considerations for the application of environmental <scp>DNA</scp> methods to detect aquatic species. Methods in Ecology and Evolution, 2016, 7, 1299-1307.	2.2	684
60	Nextâ€generation monitoring of aquatic biodiversity using environmental <scp>DNA</scp> metabarcoding. Molecular Ecology, 2016, 25, 929-942.	2.0	873
61	From barcodes to genomes: extending the concept of DNA barcoding. Molecular Ecology, 2016, 25, 1423-1428.	2.0	322
62	How to limit false positives in environmental <scp>DNA</scp> and metabarcoding?. Molecular Ecology Resources, 2016, 16, 604-607.	2.2	166
63	Decades of population genetic research reveal the need for harmonization of molecular markers: the grey wolf <scp>C</scp>anis lupus as a case study. Mammal Review, 2016, 46, 44-59.	2.2	49
64	Using metabarcoding to reveal and quantify plant-pollinator interactions. Scientific Reports, 2016, 6, 27282.	1.6	118
65	Inferring neutral biodiversity parameters using environmental DNA data sets. Scientific Reports, 2016, 6, 35644.	1.6	13
66	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasiteCytinus hypocistis(Cytinaceae). Annals of Botany, 2016, 118, 885-896.	1.4	55
67	Extracellular DNA extraction is a fast, cheap and reliable alternative for multi-taxa surveys based on soil DNA. Soil Biology and Biochemistry, 2016, 96, 16-19.	4.2	71
68	<scp>obitools</scp>: a <scp>unix</scp>â€inspired software package for <scp>DNA</scp> metabarcoding. Molecular Ecology Resources, 2016, 16, 176-182.	2.2	765
69	Detection of Invasive Mosquito Vectors Using Environmental DNA (eDNA) from Water Samples. PLoS ONE, 2016, 11, e0162493.	1.1	83
70	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966.	0.9	111
71	Spatio-temporal monitoring of deep-sea communities using metabarcoding of sediment DNA and RNA. PeerJ, 2016, 4, e2807.	0.9	103
72	Metagenome skimming for phylogenetic community ecology: a new era in biodiversity research. Molecular Ecology, 2015, 24, 3515-3517.	2.0	34

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73	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. BMC Genomics, 2015, 16, 1115.	1.2	56
74	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. Frontiers in Genetics, 2015, 6, 107.	1.1	108
75	Highly Overlapping Winter Diet in Two Sympatric Lemming Species Revealed by DNA Metabarcoding. PLoS ONE, 2015, 10, e0115335.	1.1	125
76	Landscape-scale distribution patterns of earthworms inferred from soil DNA. Soil Biology and Biochemistry, 2015, 83, 100-105.	4.2	29
77	Upscaling the niche variation hypothesis from the intra- to the inter-specific level. Oecologia, 2015, 179, 835-842.	0.9	35
78	Reconstructing longâ€term human impacts on plant communities: an ecological approach based on lake sediment <scp>DNA</scp>. Molecular Ecology, 2015, 24, 1485-1498.	2.0	109
79	Long-lasting modification of soil fungal diversity associated with the introduction of rabbits to a remote sub-Antarctic archipelago. Biology Letters, 2015, 11, 20150408.	1.0	19
80	Replication levels, false presences and the estimation of the presence/absence from <scp>eDNA</scp> metabarcoding data. Molecular Ecology Resources, 2015, 15, 543-556.	2.2	517
81	Forest without prey: livestock sustain a leopard Panthera pardus population in Pakistan. Oryx, 2015, 49, 248-253.	0.5	53
82	Deep-Sea, Deep-Sequencing: Metabarcoding Extracellular DNA from Sediments of Marine Canyons. PLoS ONE, 2015, 10, e0139633.	1.1	163
83	No Evidence for the Effect of MHC on Male Mating Success in the Brown Bear. PLoS ONE, 2014, 9, e113414.	1.1	8
84	Long livestock farming history and human landscape shaping revealed by lake sediment DNA. Nature Communications, 2014, 5, 3211.	5.8	297
85	Fifty thousand years of Arctic vegetation and megafaunal diet. Nature, 2014, 506, 47-51.	13.7	505
86	Do Scandinavian brown bears approach settlements to obtain high-quality food?. Biological Conservation, 2014, 178, 128-135.	1.9	80
87	DNA metabarcoding and the cytochrome c oxidase subunit I marker: not a perfect match. Biology Letters, 2014, 10, 20140562.	1.0	445
88	Effect of DNA extraction and sample preservation method on rumen bacterial population. Anaerobe, 2014, 29, 80-84.	1.0	81
89	Fast and efficient DNA-based method for winter diet analysis from stools of three cervids: moose, red deer, and roe deer. Acta Theriologica, 2013, 58, 379-386.	1.1	34
90	Genetic roadmap of the Arctic: plant dispersal highways, traffic barriers and capitals of diversity. New Phytologist, 2013, 200, 898-910.	3.5	122

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91	Plant functional traits reveal the relative contribution of habitat and food preferences to the diet of grasshoppers. Oecologia, 2013, 173, 1459-1470.	0.9	69
92	An outlier locus relevant in habitat-mediated selection in an alpine plant across independent regional replicates. Evolutionary Ecology, 2013, 27, 285-300.	0.5	14
93	Fungal palaeodiversity revealed using highâ€throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. Environmental Microbiology, 2013, 15, 1176-1189.	1.8	115
94	Unveiling the Diet of Elusive Rainforest Herbivores in Next Generation Sequencing Era? The Tapir as a Case Study. PLoS ONE, 2013, 8, e60799.	1.1	60
95	A DNA Metabarcoding Study of a Primate Dietary Diversity and Plasticity across Its Entire Fragmented Range. PLoS ONE, 2013, 8, e58971.	1.1	89
96	Who is who in litter decomposition? Metaproteomics reveals major microbial players and their biogeochemical functions. ISME Journal, 2012, 6, 1749-1762.	4.4	537
97	Genetic diversity in widespread species is not congruent with species richness in alpine plant communities. Ecology Letters, 2012, 15, 1439-1448.	3.0	135
98	Evolution of major histocompatibility complex class I and class II genes in the brown bear. BMC Evolutionary Biology, 2012, 12, 197.	3.2	63
99	Glacial Survival of Boreal Trees in Northern Scandinavia. Science, 2012, 335, 1083-1086.	6.0	287
100	Genetic consequences of climate change for northern plants. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2042-2051.	1.2	162
101	Major histocompatibility complex class II compatibility, but not class I, predicts mate choice in a bird with highly developed olfaction. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 4457-4463.	1.2	87
102	Assessment of the Food Habits of the Moroccan Dorcas Gazelle in Mâ€™Sabih Talaa, West Central Morocco, Using the trnL Approach. PLoS ONE, 2012, 7, e35643.	1.1	56
103	Two Methods to Easily Obtain Nucleotide Sequences from AFLP Loci of Interest. Methods in Molecular Biology, 2012, 888, 91-108.	0.4	6
104	A Dig into the Past Mitochondrial Diversity of Corsican Goats Reveals the Influence of Secular Herding Practices. PLoS ONE, 2012, 7, e30272.	1.1	10
105	Prey Preference of Snow Leopard (Panthera uncia) in South Gobi, Mongolia. PLoS ONE, 2012, 7, e32104.	1.1	110
106	Improved detection of an alien invasive species through environmental DNA barcoding: the example of the American bullfrog Lithobates catesbeianus. Journal of Applied Ecology, 2012, 49, 953-959.	1.9	447
107	A universal method for the detection and identification of Aphidiinae parasitoids within their aphid hosts. Molecular Ecology Resources, 2012, 12, 634-645.	2.2	37
108	Molecular tools and analytical approaches for the characterization of farm animal genetic diversity. Animal Genetics, 2012, 43, 483-502.	0.6	104

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109	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA Metaâ€barcoding. Molecular Ecology, 2012, 21, 1980-1988.	2.0	67
110	A comparative study of ancient sedimentary DNA, pollen and macrofossils from permafrost sediments of northern Siberia reveals longâ€term vegetational stability. Molecular Ecology, 2012, 21, 1989-2003.	2.0	144
111	Soil sampling and isolation of extracellular DNA from large amount of starting material suitable for metabarcoding studies. Molecular Ecology, 2012, 21, 1816-1820.	2.0	264
112	AFLP markers reveal high clonal diversity and extreme longevity in four key arcticâ€alpine species. Molecular Ecology, 2012, 21, 1081-1097.	2.0	75
113	Who is eating what: diet assessment using next generation sequencing. Molecular Ecology, 2012, 21, 1931-1950.	2.0	913
114	Tracking earthworm communities from soil DNA. Molecular Ecology, 2012, 21, 2017-2030.	2.0	109
115	Carnivore diet analysis based on nextâ€generation sequencing: application to the leopard cat (Prionailurus bengalensis) in Pakistan. Molecular Ecology, 2012, 21, 1951-1965.	2.0	244
116	Towards nextâ€generation biodiversity assessment using DNA metabarcoding. Molecular Ecology, 2012, 21, 2045-2050.	2.0	1,253
117	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. Molecular Ecology, 2012, 21, 1821-1833.	2.0	259
118	Forecasting changes in population genetic structure of alpine plants in response to global warming. Molecular Ecology, 2012, 21, 2354-2368.	2.0	127
119	Environmental DNA. Molecular Ecology, 2012, 21, 1789-1793.	2.0	926
120	DNA from soil mirrors plant taxonomic and growth form diversity. Molecular Ecology, 2012, 21, 3647-3655.	2.0	262
121	Broadâ€scale adaptive genetic variation in alpine plants is driven by temperature and precipitation. Molecular Ecology, 2012, 21, 3729-3738.	2.0	161
122	Estimating population size and trends of the Swedish brown bear Ursus arctos population. Wildlife Biology, 2011, 17, 114-123.	0.6	152
123	ecoPrimers: inference of new DNA barcode markers from whole genome sequence analysis. Nucleic Acids Research, 2011, 39, e145-e145.	6.5	416
124	Conservation genetics of cattle, sheep, and goats. Comptes Rendus - Biologies, 2011, 334, 247-254.	0.1	137
125	Influence of management practices on large herbivore dietâ€"Case of European bison in BiaÅ‚owieÅ¼a Primeval Forest (Poland). Forest Ecology and Management, 2011, 261, 821-828.	1.4	154
126	Break zones in the distributions of alleles and species in alpine plants. Journal of Biogeography, 2011, 38, 772-782.	1.4	77

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127	Genetics and conservation of European brown bears Ursus arctos. Mammal Review, 2011, 41, 87-98.	2.2	92
128	Mitochondrial DNA polymorphism in Moroccan goats. Small Ruminant Research, 2011, 98, 201-205.	0.6	13
129	New insights on diet variability revealed by DNA barcoding and highâ€throughput pyrosequencing: chamois diet in autumn as a case study. Ecological Research, 2011, 26, 265-276.	0.7	64
130	Promoting collaboration between livestock and wildlife conservation genetics communities. Conservation Genetics Resources, 2011, 3, 785-788.	0.4	32
131	Persistence of Environmental DNA in Freshwater Ecosystems. PLoS ONE, 2011, 6, e23398.	1.1	507
132	ITS as an environmental DNA barcode for fungi: an in silico approach reveals potential PCR biases. BMC Microbiology, 2010, 10, 189.	1.3	792
133	Applications of landscape genetics in conservation biology: concepts and challenges. Conservation Genetics, 2010, 11, 375-385.	0.8	356
134	An In silico approach for the evaluation of DNA barcodes. BMC Genomics, 2010, 11, 434.	1.2	370
135	Evolution and taxonomy of the wild species of the genus Ovis (Mammalia, Artiodactyla, Bovidae). Molecular Phylogenetics and Evolution, 2010, 54, 315-326.	1.2	124
136	Importance of Accounting for Detection Heterogeneity When Estimating Abundance: the Case of French Wolves. Conservation Biology, 2010, 24, 621-626.	2.4	104
137	Tracking genes of ecological relevance using a genome scan in two independent regional population samples of Arabis alpina. Molecular Ecology, 2010, 19, 2896-2907.	2.0	136
138	Nuclear and mitochondrial phylogenies provide evidence for four species of Eurasian badgers (Carnivora). Zoologica Scripta, 2010, 39, 415-425.	0.7	36
139	DNA Barcoding for Honey Biodiversity. Diversity, 2010, 2, 610-617.	0.7	90
140	Using nextâ€generation sequencing for molecular reconstruction of past Arctic vegetation and climate. Molecular Ecology Resources, 2010, 10, 1009-1018.	2.2	196
141	Selection criteria for scoring amplified fragment length polymorphisms (AFLPs) positively affect the reliability of population genetic parameter estimates. Genome, 2010, 53, 302-310.	0.9	44
142	A system for sex determination from degraded DNA: a useful tool for palaeogenetics and conservation genetics of ursids. Conservation Genetics, 2009, 10, 897-907.	0.8	29
143	Analysing diet of small herbivores: the efficiency of DNA barcoding coupled with high-throughput pyrosequencing for deciphering the composition of complex plant mixtures. Frontiers in Zoology, 2009, 6, 16.	0.9	233
144	Genetic diversity of European cattle breeds highlights the conservation value of traditional unselected breeds with high effective population size. Molecular Ecology, 2009, 18, 3394-3410.	2.0	83

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145	History or ecology? Substrate type as a major driver of patial genetic structure in Alpine plants. Ecology Letters, 2009, 12, 632-640.	3.0	167
146	Effects of species traits on the genetic diversity of highâ€mountain plants: a multiâ€species study across the Alps and the Carpathians. Global Ecology and Biogeography, 2009, 18, 78-87.	2.7	62
147	Combining genetic and ecological data to assess the conservation status of the endangered Ethiopian walia ibex. Animal Conservation, 2009, 12, 89-100.	1.5	59
148	Frontiers in identifying conservation units: from neutral markers to adaptive genetic variation. Animal Conservation, 2009, 12, 107-109.	1.5	40
149	DNA barcoding for ecologists. Trends in Ecology and Evolution, 2009, 24, 110-117.	4.2	803
150	Universal DNA-Based Methods for Assessing the Diet of Grazing Livestock and Wildlife from Feces. Journal of Agricultural and Food Chemistry, 2009, 57, 5700-5706.	2.4	80
151	New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the trnL approach. Molecular Ecology Resources, 2009, 9, 51-60.	2.2	358
152	New generation sequencers as a tool for genotyping of highly polymorphic multilocus MHC system. Molecular Ecology Resources, 2009, 9, 713-719.	2.2	133
153	Exonuclease activity of proofreading DNA polymerases is at the origin of artifacts in molecular profiling studies. Electrophoresis, 2008, 29, 2437-2444.	1.3	12
154	No positive correlation between species and genetic diversity in European alpine grasslands dominated by Carex curvula. Diversity and Distributions, 2008, 14, 852-861.	1.9	40
155	Are cattle, sheep, and goats endangered species?. Molecular Ecology, 2008, 17, 275-284.	2.0	217
156	Low Genotyping Error Rates and Noninvasive Sampling in Bighorn Sheep. Journal of Wildlife Management, 2008, 72, 299-304.	0.7	31
157	Species detection using environmental DNA from water samples. Biology Letters, 2008, 4, 423-425.	1.0	1,216
158	Relationships among levels of biodiversity and the relevance of intraspecific diversity in conservation â€“ a project synopsis. Perspectives in Plant Ecology, Evolution and Systematics, 2008, 10, 259-281.	1.1	77
159	Distinguishing dung from blue, red and yellowâ€backed duikers through noninvasive genetic techniques. African Journal of Ecology, 2008, 46, 411-417.	0.4	41
160	The goat domestication process inferred from large-scale mitochondrial DNA analysis of wild and domestic individuals. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 17659-17664.	3.3	279
161	Land ahead: using genome scans to identify molecular markers of adaptive relevance. Plant Ecology and Diversity, 2008, 1, 273-283.	1.0	94
162	Frequent Long-Distance Plant Colonization in the Changing Arctic. Science, 2007, 316, 1606-1609.	6.0	300

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163	Genetic tracking of the brown bear in northern Pakistan and implications for conservation. Biological Conservation, 2007, 134, 537-547.	1.9	47
164	Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. Nucleic Acids Research, 2007, 35, e14-e14.	6.5	842
165	Ancient Biomolecules from Deep Ice Cores Reveal a Forested Southern Greenland. Science, 2007, 317, 111-114.	6.0	393
166	Large-Scale Mitochondrial DNA Analysis of the Domestic Goat Reveals Six Haplogroups with High Diversity. PLoS ONE, 2007, 2, e1012.	1.1	185
167	Phylogeography and conservation genetics of a giant lobelia (Lobelia giberroa) in Ethiopian and Tropical East African mountains. Molecular Ecology, 2007, 16, 1233-1243.	2.0	74
168	From the Apennines to the Alps: colonization genetics of the naturally expanding Italian wolf (Canis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	2.0	143
169	A new individual-based spatial approach for identifying genetic discontinuities in natural populations. Molecular Ecology, 2007, 16, 2031-2043.	2.0	72
170	Genetic estimates of annual reproductive success in male brown bears: the effects of body size, age, internal relatedness and population density. Journal of Animal Ecology, 2007, 76, 368-375.	1.3	117
171	Genetic structure of Hypochaeris uniflora (Asteraceae) suggests vicariance in the Carpathians and rapid postâ€glacial colonization of the Alps from an eastern Alpine refugium. Journal of Biogeography, 2007, 34, 2100-2114.	1.4	90
172	Population Adaptive Index: a New Method to Help Measure Intraspecific Genetic Diversity and Prioritize Populations for Conservation. Conservation Biology, 2007, 21, 697-708.	2.4	186
173	Improvements of Polymerase Chain Reaction and Capillary Electrophoresis Single-Strand Conformation Polymorphism Methods in Microbial Ecology: Toward a High-throughput Method for Microbial Diversity Studies in Soil. Microbial Ecology, 2007, 54, 203-216.	1.4	35
174	Phylogeography of the capercaillie in Eurasia: what is the conservation status in the Pyrenees and Cantabrian Mounts?. Conservation Genetics, 2007, 8, 513-526.	0.8	43
175	Integrating Population Genetics with Landscape Ecology to Infer Spatio-temporal Processes. Landscape Series, 2007, , 145-156.	0.1	7
176	An evaluation of field and non-invasive genetic methods to estimate brown bear (Ursus arctos) population size. Biological Conservation, 2006, 128, 158-168.	1.9	174
177	Mating Strategies in Relation to Sexually Selected Infanticide in a Non-Social Carnivore: the Brown Bear.. Ethology, 2006, 112, 238-246.	0.5	136
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