

Sample order

A. Type and scope of genetic analyses

The Senckenberg Center for Wildlife Genetics supports species conservation and wildlife monitoring by providing advanced molecular genetic methods. We carry out population genetic analyses for numerous protected Central European mammals (including beaver, bison, brown bear, European hamster, hazel dormouse, garden dormouse, lynx, red deer, otter, wildcat and wolf). Multiple genetic and genome-wide analysis methods are used to answer various questions relevant to species conservation. These include determination of genetic diversity, population size, population delimitation, species and population membership as well as the degree of hybridisation. We specialize in non-invasively collected and forensic environmental samples with low DNA content (e.g., eDNA, hair, faeces, urine, bones).

If you are interested, please contact us to plan a project or analysis. Please refer to the notes and FAQs. As a research institute, we can only accept samples from private individuals in exceptional cases where there is a research interest in the results.

B. Costs

Our analyses are carried out according to strict scientific standards. The performance of several replicates, which is the case for non-invasive and forensic samples, as well as the use of high-quality chemicals creates considerable costs, which usually have to be borne by the client. Only completely performed services (no partial services) are invoiced. Negative findings represent a result and will be fully invoiced accordingly. All prices (in €) are exclusive of VAT.

Analysis	Invasive			Non-invasive		
	Urgent	Standard	Bulk order	Urgent	Standard	Bulk order
Species identification general	-	50,-	37,50	-	100,-	75,-
Individualization with previous species identification	150,-	100,-	75,-	300,-	200,-	150,-

Species identification in general: mitochondrial DNA sequencing, species identification (including haplotype)

Individualization with previous species identification: determination of the individual profile, STR or SNP, is carried out after successful confirmation of the target species. Changes to the type of analysis is not possible. If the species identification does not result in the target species, the analysis is stopped and only the costs for the species identification are incurred.

Invasive: Samples with high DNA content, no analysis replicates are needed: muscle tissue or blood samples taken from the living animal or oral cavity swabs.

Non-invasive: Samples with low DNA content, analyses are replicated at least three times: Kill swab, blood traces, faeces, hair, urine, bones, teeth, decomposed tissue, feathers, saliva residues found in the environment on different carrier material or animal components.

Urgent samples: Particularly urgent samples where species identification and genotyping are processed in parallel within a few working days. The results are usually available within one week. If, in exceptional cases, the processing time exceeds 10 working days from sample receipt, the surcharge for urgent samples will not apply. If particularly fast processing times are required, this must be agreed with us in advance.

Bulk order: Bulk discount is provided for orders of at least 50 samples. The analysis time may vary depending on the sample type and number. We recommend coordination with sufficient notice if timely processing is required.

C. Ordering & sample shipment

Please contact us by email or phone before sending samples.

Contact

Michelle Müller (scientific project manager)

Phone: +49 6051-61954-3138

Email: wildtiergenetik@senckenberg.de

Commissioning

Sample analyses can only be ordered via our online tool (www.wildtiergenetik.de). Uncommissioned samples cannot be processed. Please make sure that the details on the samples correspond to those in the order.

Sending samples

Please send the samples after ordering via the online tool to:

Senckenberg Gesellschaft für Naturforschung

Zentrum für Wildtiergenetik

Probenannahme

Clamecystraße 12

D-63571 Gelnhausen

D. Notes & FAQs

Data use The Center for Wildlife Genetics is part of the Senckenberg - Leibniz Institution for Biodiversity and Earth System Research. According to § 2 of the statutes of the Senckenberg - Leibniz Institution for Biodiversity and Earth System Research, its mission is to conduct natural history research and to make the results of this research available to the general public through publication, through teaching and through its natural history museums. Therefore, we reserve the right to scientifically exploit data that we collect in connection with your samples in the form of lectures and publications. Exceptions to this rule are to be discussed in advance. By placing an order, you agree to the scientific use of data.

Scope of analysis We receive over 4000 samples annually from about 100 different clients and cooperation partners. Of these, approx. 95% are non-invasively collected samples with critical DNA content, such as faeces or kill swabs. In order to achieve high success rates and well-validated results, each sample is treated carefully and individually. It is not uncommon for a case to be investigated with a single sample to represent a small research project of its own, in which different analytical methods are used, often commissioned one after the other. Population genetic analyses are also sometimes very complex and computationally expensive, especially when several hundred reference samples are included in the evaluations. Such analyses do not represent standardised routine examinations, such as those offered in disease diagnostics.

How reliable are my results? Methods we use have been used for years by laboratories worldwide for species identification, hybridisation detection and population assignment. We have an extensive reference database of European wild animals, which contains >10,000 individual genotypes of wild cats, wolves and other wild animals and is continuously being expanded. This, together with our experience from more than 30,000 wild animal samples, guarantees a high reliability of the results. Nevertheless, it should be noted that on non-invasive or forensic sample material, mostly taken from the environment, uncertainties can arise with regard to the interpretation of the results and also deviations between examined replicates within the same or between different laboratories are possible. This is caused, among other things, by very small and heterogeneously distributed amounts of DNA in the samples or by contamination with foreign DNA and is normal for environmental samples.

Is the analysis of sent-in samples guaranteed? As a reference center for genetic investigations of wolves and lynx, we guarantee the processing of wolf and lynx samples sent to us by the official authorities on the basis of the conditions mentioned above. Wolf and lynx samples from third parties, however, cannot be accepted for analysis. In this case, please contact the competent authorities in your federal state. The analysis of samples from other species is a voluntary offer and requires prior agreement. An order is then placed via our wildlife genetics database. This requires the creation of a password-protected user account.