



**DNA Bank**

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**DNA BANK BEST PRACTICE MANUALS**

**IMPORT OF SAMPLE DATA TO COREMA  
AVIAN SAMPLES**

**PREAMBLE**

To be registered in the DNA Bank, all available information for the samples should be entered in one of the import template files available at [https://wiki.uio.no/nhm/skf/best-practices/index.php/DNA\\_Bank](https://wiki.uio.no/nhm/skf/best-practices/index.php/DNA_Bank). The current document provides guidelines on how to fill in the import template file for avian samples.

**BASIC COLLECTION DATA – LOCALITY, DATES, COLLECTOR ETC.**

Data common to all items originating from the same “sampling event” should be entered in the yellow (taxon), green (“collection event”, individual data) and orange (locality) columns. Try to fill in as much information as possible, but at least the shaded columns should be filled in.

For many of the columns (fields) hints and comments on how to fill them in are included as comments to the header cells (indicated by the small red triangle in the upper right corner of the cells). You should also read the information in the *Info* sheet before you start filling in your data.

**DATA ON PHYSICAL SAMPLES – SAMPLE TYPE, STORAGE MEDIA ETC.**

The actual, physical samples should be registered as items belonging to a specific accession. Given that an accession typically corresponds to one sampling event of one individual, e.g. a blood sample, a sperm sample and a sperm motility recording sampled from the same bird during one sampling event would all be registered as separate items under the same accession. If, on the other hand, the same bird was recaptured later the same or some other day, that would typically represent a new sampling event and thus also a new accession with new items.

The import template is by default set up for four items. To register more items, just select all the blue columns for one of the items (e.g. all columns ending with “...\_1”) and add as many copies of these as needed before the *Associated documents* column. Make sure to change the trailing number (e.g. “...\_1”) to “...\_4”, “...\_5” etc. in BOTH header rows (row 1 and 2) for the newly added columns.

You don’t have to have the same number of items for all accessions, and you may use any of the four item columns. When imported the items will be numbered consecutively from left to right (1 to 4).

**SOME COMMENTS ON DATA ENTRY:**

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- Remember to fill in the status of the samples (hopefully mostly “OK” but still...)
- Fill in the date and collector (person) columns also for the items (typically the same as filled in for the accession in the green fields)
- Remember to indicate type of tube/container and medium in which the sample is stored
- Remember to fill in any relevant restrictions on use of the samples – if none apply use the “None” option!

**ITEM TYPES ACCEPTED**

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The following item types can currently be registered (contact the Corema administrator if you need to register other types of samples):

- Blood
- Tissue
- DNA extract
- Sperm
- Sperm morphology slide
- Sperm motility recording
- Testes
- Seminal glomera
- Preserved specimens (skins etc.)
- Feather
- Eggshell
- Ectoparasite