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# BIOSCAN Manifest

# Standard Operating Procedure (SOP) V3

# Release date: August 2023

Correct and comprehensive recording of sample metadata is critical to the long-term utility of the work we do. Metadata will link the sequence data we generate to their origins.

**Please read this Standard Operating Procedure (SOP) in full. This will help you accurately record metadata in the** [**Sample Manifest**](https://docs.google.com/spreadsheets/d/1-iMh6Vn6iudwsonsWKEAtNoNzT6-86EkQX6jHV0CzRw/edit?usp=sharing). Please also watch this [**training video**](https://youtu.be/yrZAEg6FgWA) to assist you in filling in the manifest rapidly and correctly. Please note that some things have changed since the training video was produced – the table below highlights where the video is incorrect. Always follow the guidance in the Partner Pack and this SOP over the videos.

| **Time in video (mm:ss)** | **Correction** |
| --- | --- |
| 0:54 | Manifest V3 |
| 01:40 | Swarm plating instructions have changed. |
| 3:45 | TAB 3 now has G12 highlighted yellow and different options for the plate level only input. |
| 3:50 5:18 18:05 | G12 also highlighted yellow. |
| 6:40 | CATCH\_SOLUTION is now column G and a required field. |
| 10:20 | SPECIMEN\_IDENTITY\_RISK only fill this in if you filled in PREDICTED\_SCIENTIFIC\_NAME and if you are confident there is no identification risk (put N). Otherwise leave empty. |
| 10:58 | AMOUNT\_OF\_CATCH\_PLATED is now column AC and important to fill in. |
| 15:27 | G12 is treated the same as H12 now. |
| 16:50 | PLATE\_ONLY term is now either “PLATE\_ONLY\_1\_BLANK” or “PLATE\_ONLY\_2\_BLANKS” while we transition from 1 empty well to 2 empty wells per plate. |
| 20:36 | All other plates should contain 94 specimens and 2 blank wells. |

## OVERVIEW

This document contains column by column instructions for capturing metadata at a single sample level (a sample can be a whole insect in a microtiter plate well, or a part of an insect in a well). To accomplish this, the manifest contains two data entry tabs:

**TAB 1**: “Contributors” records the information for all people who contributed to the batch of samples recorded in the manifest, for example, the collection, identification, and/or preservation of samples.

**TAB 2**: “Metadata Entry” records information on each individual sample / specimen.

There are also three further tabs:

**TAB 3**: “Well IDs (for copy / paste)” contains the well numbers on a plate so this does not need to be manually entered but can be copy / pasted into TAB 2 in the “TUBE\_OR\_WELL\_ID” column for each submitted plate. If entering data at plate level only, the correct term can be copy / pasted from column B in this tab (i.e. “*PLATE\_ONLY\_2\_BLANKS*”).

**TAB 4**: “Data Validation” is solely for populating drop down menus and cannot be modified by partners without seeking confirmation from [bioscan.info@sanger.ac.uk](mailto:bioscan.info@sanger.ac.uk). It is possible to see all fixed term options in advance of adding metadata by viewing this tab. This tab has been locked for editing on Google Sheets, however when this is downloaded as an excel file, it is no longer locked. If using Excel, please be careful not to change any terms in this tab otherwise it will affect the drop down menus in TAB 2.

**TAB 5**: “Example Metadata Entry” is for illustrative purposes only and shows an example dataset for three plates that represent three trap collection events made over three months that are ready for shipping to Sanger. To help illustrate potential uses with the manifest, each 96-well plate is highlighted in a different colour and each trap collection event is separated by a black line to demonstrate that a plate will often have specimens from more than one collection event. The first plate has plate-level only data and only requires one row in the manifest as all metadata for the specimens contained in that plate is identical (row highlighted in blue). Our manifest validation process will expand this one row to 96 rows so you do not have to, but this option can only be used when the entire plate is full (except G12 and H12) and all metadata is identical for each specimen (e.g. nothing was identified to Order, or all specimens have the same Order). The second plate (rows highlighted in yellow) and third plate (rows highlighted in green) need to be filled in at well level because metadata are different for some of the specimens (e.g. the first two specimens in plate 2 are from a different catch). Note that we allow one partially filled plate per shipment batch so that all specimens in the latest collection event can be processed and analysed together.

**Orange** metadata fields (i.e. columns) are mandatory – we must have meaningful information to proceed with sample processing. **Purple** columnsare strongly recommended if the data have been collected. If the information was not collected the entry can be left empty. **White**  columns are not validated and mostly allow descriptive text relating to the specimen that you feel is important to record, and we encourage data entry if the data have been collected.

After sequencing, all raw sequence data will be submitted to an open access repository linked to a specimen identifier (SPECIMEN\_ID) that will be assigned to each specimen after manifest validation. You will receive the SPECIMEN\_ID for each specimen in the post-validation manifest as an additional column.

## 1. Contributions

Each time a manifest is filled in, all people who hold primary responsibility for your samples and anyone who contributes to individual collections at a level warranting authorship to resulting publications should have their names added to “TAB 1 Contributors”. These fields are mandatory, highlighted in **orange** .

## 2. Manifest submission guidelines

**Every time you start a new manifest, always download or make a copy of the Google Sheet linked to at the top of this document .** This will ensure you are always working with the latest version. You can make a copy of the Google Sheet (File > Make a copy) and work there online or offline (File > Make available offline), or download it as an Excel file (File > Download > Microsoft Excel (.xlsx)). It is important to save the manifest with its original formatting (i.e., not as a .txt or .csv file) otherwise you will lose the drop down menu terms. You may have some issues if you are working on the Google Sheet directly in a browser other than Chrome.

**Please always name your manifest using the format:**

**[PARTNER CODE]\_[YYMM]\_BIOSCAN\_Manifest\_V3.xslx**

PARTNERCODE is a four letter site code assigned during partner onboarding, and the date you should use will be the year and month of your manifest submission to [bioscan.info@sanger.ac.uk](mailto:bioscan.info@sanger.ac.uk), rather than the timing of the collection or shipment (you will not know your manifest submission date until you are ready to send the manifest). So for example, if the Partner CAMP was submitting a manifest in July 2023, the manifest would be renamed as CAMP\_2307\_BIOSCAN\_Manifest\_V3.xslx. Manifests not following this naming convention will not be accepted.

Note that if you copy / paste, you will overwrite any data validation and the error flags that pop up to let you know you have entered data incorrectly will no longer occur, so please be careful when you use copy / paste to enter metadata to ensure that your entries meet the requirements (e.g. “*FEMALE”*, not “*F”* or “*fem”*). We recommend first doing a manual entry of several specimens so that you can take advantage of the data validation and identify where there are likely to be issues when using copy / paste.

Before we are able to accept any samples you need to fill in a TOL Collector Onboarding Form (TOL COF) as instructed in the BIOSCAN Partner Pack, then your completed manifest must go through a “validation” process. Please send the manifest (as a link to a Google Sheet or as an Excel file) to [bioscan.info@sanger.ac.uk](mailto:bioscan.info@sanger.ac.uk) for validation.The validation ensures that all fields are complete and interpretable for every submitted sample. If any issues with the information provided are identified (e.g., missing mandatory entries, duplicate rows, incorrect date formats) the sample manifest will be returned to you along with a list of detected issues and you must resubmit your manifest once you have resolved these issues. Please carefully read the guidance in this SOP for each field, and attempt to get your submitted manifests as close to the guidance as possible to avoid many iterations of validation. ***NOTE****: This validation process is due to change when our partner validation portal is live.*

## 3. Sample submission

We can only accept samples in the 96 well microtiter plates that we provide to you as part of the project. Specimens (in ethanol or lysis buffer) should be shipped in skirted plates (ThermoFisher Scientific P/N AB2800) with strip caps (Fisherbrand Domed 8-Cap Strips P/N 14-230-231) properly sealed with a sealing tool to prevent evaporation.

### 3.1. Plating Specimens/samples



When you are ready to begin plating out your catch, stick a barcode label to the short edge of the plate closest to the lettering (image left) and record this plate name in your manifest before you begin plating.

1. Before plating, ensure your plate is in the correct orientation (e.g. first well in upper left is labelled A1) and the name of the first plate has been recorded in the manifest. Then pour out the catch in the catch bottle into the white tray for sorting, and immediately put 5-10 mL of the ethanol back into your labelled Catch Lot tube using the pipette. Plate insects in a vertical direction in 96-well plates working down columns (e.g A1 -> H1 followed by A2 -> H2 and so on, see figure below). Please ensure every well of the plate is filled with a specimen apart from G12 and H12 (circled in red below), which serve as controls in sequencing. Thus, each plate should have 94 insect specimens and only positions G12 and H12 should be left empty. Plates should be sealed with tightly fitting 8-strip caps as soon as the column is filled with arthropods and before you then repeat this procedure with the next plate (recording the name in the manifest, plating specimens, sealing the plate, etc).



1. Plates can comprise specimens from more than one trap collection event – this is much preferred to submitting partial plates. Please endeavour to fill plates completely. Partial plates are acceptable for the final collection event before a shipment to Sanger.
2. Some insects will be too large to be plated in a microtiter plate well and in these cases, leg(s) should be put into the well and the remainder of the specimen should be preserved as deemed appropriate by the partner depending on longer term plans (see below). The body part that has been plated should be recorded in the ORGANISM\_PART column. For large insects (e.g. a bumblebee), place a piece of a single leg in the well. For smaller insects (e.g. a Marmalade hoverfly), place 1-3 legs in the well, preferably all from one side of the organism so that the voucher specimen keeps a representative of each leg type. The remaining tissue that has not been plated can either:
3. remain with the Partner and it will be up to them as to how and where to store them, including linking the specimen (use the VOUCHER\_ID field for this, see *Section 6*, column AG) with the SPECIMEN\_ID (provided after validation of the manifest) of the ORGANISM\_PART. This can also be pre-arranged with the sample repository of choice (e.g. a museum).
4. be placed back into the original 50 mL Catch Lot tube. These tubes and their contents are returned to Sanger and may be used for R&D studies and not necessarily returned to partners.
5. Every submitted plate should contain exactly 94 samples, unless otherwise instructed. **Please always leave the final two wells (G12 and H12) empty of specimens –** these wells must contain the PRESERVATIVE\_SOLUTION but no biological material. The only fields that must have entries for the empty wells are SERIES, CATCH\_LOT, RACK\_OR\_PLATE\_ID, TUBE\_OR\_WELL\_ID, PRESERVATIVE\_SOLUTION (which should be the same as the rest of plate), and ORGANISM\_PART (select “NOT\_APPLICABLE”). If your last plate in the shipment is partially filled, this should be done for every empty well on the plate, though as mentioned above, endeavour to always fill plates with 94 specimens.

### 3.2. Metadata entry

1. If a plate represents one catch lot and all well-level data is identical (i.e. all specimens are WHOLE\_ORGANISM, no specimens have taxonomic identifications, no wells are empty apart from G12 and H12, and the entire plate contains samples from a single catch), then this can be submitted in one row of the manifest avoiding the need to copy the same information across 94 rows. If a single entry for an entire plate is possible, then the TUBE\_OR\_WELL\_ID column must be filled with the term “PLATE\_ONLY\_2\_BLANKS” to make this clear. If any of these conditions are not met, please follow the guidance and submit 96 rows of metadata per plate.
2. The manifest has drop-down menus in some fields. If you discover a missing term in the drop-down menus, new terms can be suggested by contacting us. Please only request new terms if the absence of the term is likely to affect many samples.
3. **Information must be entered for all fields below with orange highlighted names** [in the Google Sheet version of the manifest, these fields are represented by cells with an orange fill]. The fill will go white when an entry has been made to help you identify which mandatory fields still require data. All fields with orange highlighted namesare mandatory and must be filled with the appropriate information. For all other fields, if you have collected the information, please add it. If not, you may leave these fields empty. It is permitted to add information for a subset of specimens on a plate.
4. **All dates in the manifest must be formatted consistently as YYYY-MM-DD** (ISO 8601). If only year or year/month are known, use **YYYY** or **YYYY-MM**, respectively.

**3.3. Submitting your samples**

When you have a batch of plates ready to submit, please fill in the [**TOL Collector Onboarding Form (ToL COF)**](https://docs.google.com/forms/u/0/d/e/1FAIpQLSd1-YXfjpChUtKkhdcpbRPtv_n2HiB1s9r2DX7uN1HCb27C6Q/viewform?pli=1) as described in ‘Stage 4. Submission - Manifest’ in the Partner Pack before you email your manifest or send a link to the BIOSCAN team at[bioscan.info@sanger.ac.uk](mailto:bioscan.info@sanger.ac.uk).

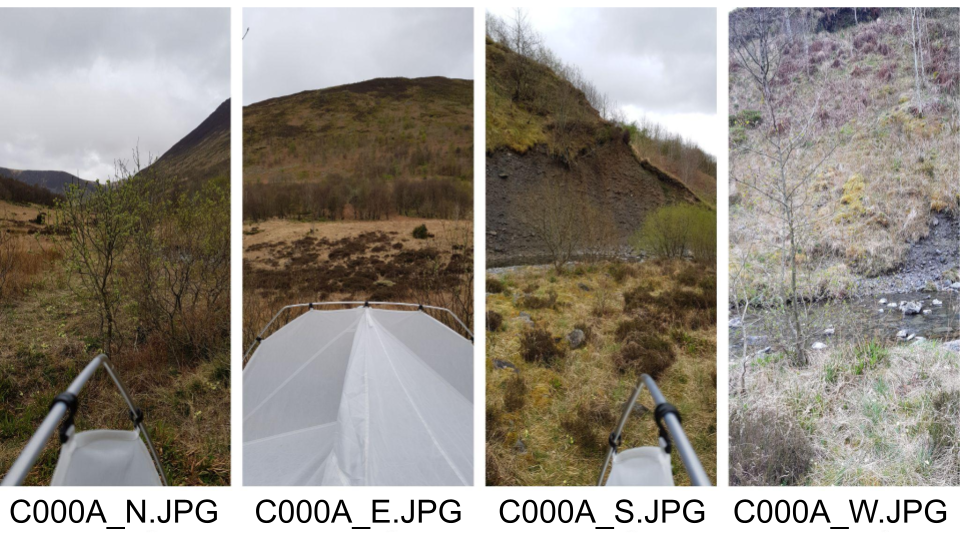
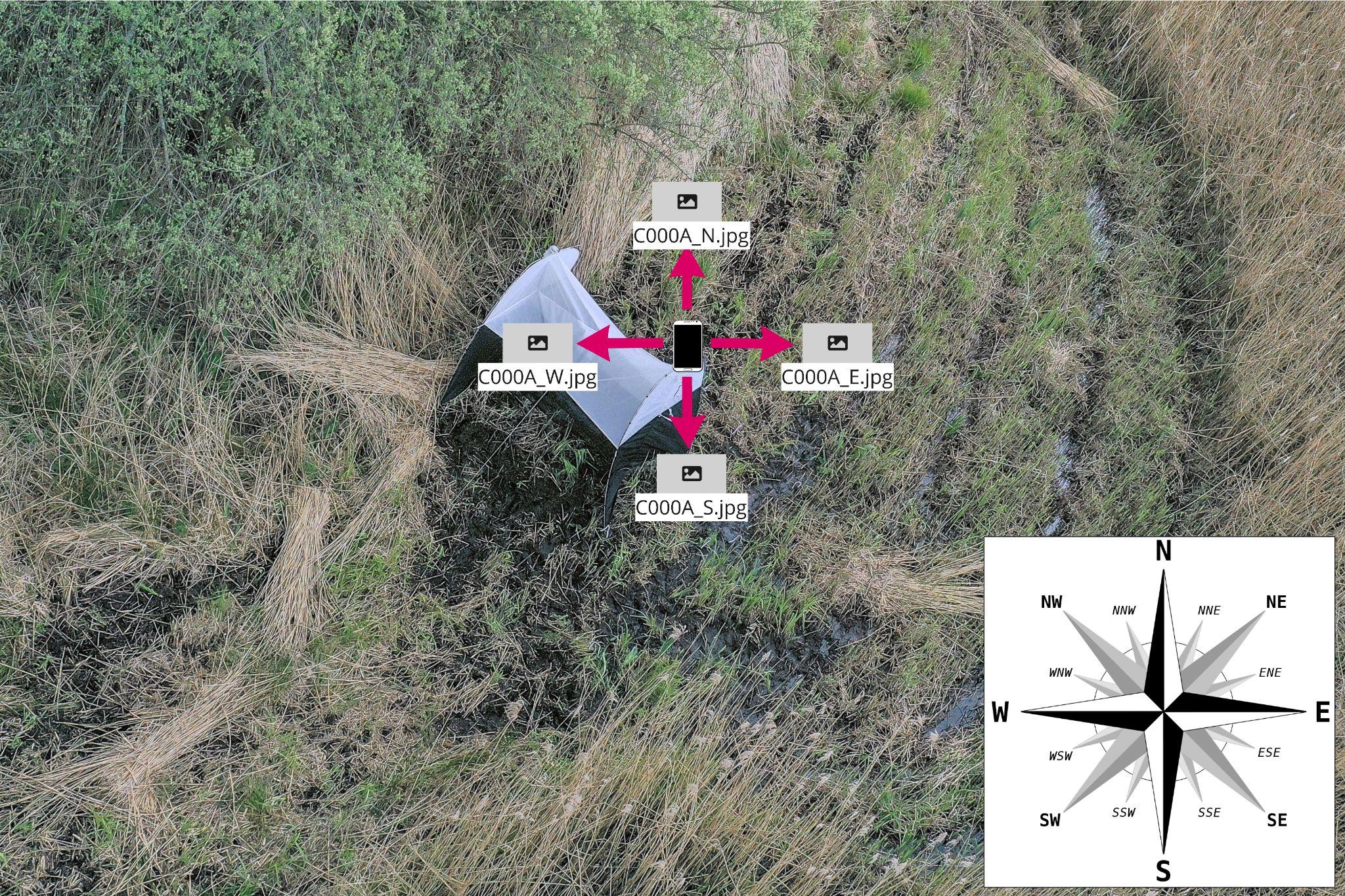
**Once invited to send your manifest for validation, please name your manifest as described above.**When your manifest has passed validation, a copy will be sent to you which will include additional columns required for our sample tracking system. *NOTE: This validation process will change when our partner validation portal is live.*

# 4. A note regarding photographs

There are three categories of photographs recommended or required for each collection event, 1) Site, 2) Catch and, 3) Specimen Plate with barcode label. Please upload photos after each collection event to the folder containing your partner code at [this link](https://drive.google.com/drive/folders/1HJLUo7_V2lyh31xJA-l0-2qqCK0AoN4V?usp=sharing). Further guidance on the photographs can be found below:

For instructions on how to access your photo folder please refer to the [BIOSCAN photo folder and upload guide](https://docs.google.com/document/u/0/d/1uM6rBXp2ayyu4ZOdCR_TN9YXpLCzCyYP7aLFbtFNGVQ/edit).

1. **Site photographs (recommended)**: To capture the habitat and conditions at each Malaise trap per monthly catch period, take four photographs from the top of a trap bottle in the directions of the four cardinal points, starting with North, then rotating the camera 90° in a clockwise direction until you have taken four photographs in the order: North, East, South, West. Take a photo of each cardinal point direction from the top of the malaise trap catch bottle (choose one bottle to do this from for migratory, 2-bottle Malaise traps). Label each photo with the CATCH\_LOT code (either CATCH\_LOT code is fine for migratory, 2-bottle Malaise traps) followed by an underscore (\_) and the cardinal point direction of the photo (e.g. C000A\_N; C000A\_E; C000A\_S; C000A\_W). Upload all site photos in this section.



1. **Catch photographs (recommended)**: After the 24 hour trapping period, when specimens have been tipped out of the trap bottle and into the sorting tray, please take one photo of the catch in the tray from directly above, please include the 50 mL Catch Lot tube in the photograph so that the label is visible in the photo. Label the photo with CATCH\_LOT code, followed by an underscore and “tray”, e.g. C000A\_tray.



**C000A\_tray.JPG**

1. **Specimen Plate photograph (required)**: Once the specimens have been plated, please take one photo of each plate from the underside at an angle so that specimens and barcode are both visible. These are useful to us for quality control checks on receipt of the specimen plates. Label the photos with the human readable barcode on the plate (e.g. the photo of this plate would be renamed RRNW\_010.jpg).

**Either of these images is fine – we just need to be able to read the Partner code and Plate number (e.g. RRNW\_010) and see the plate’s density of insects.** 

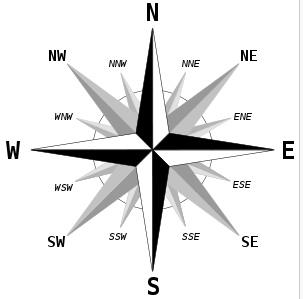
# 5. TAB 1: Contributors

All contributors to the sample collection and the overall study should have their names and affiliations listed in this tab. Please list all people who contributed at a level warranting authorship to samples contained within TAB 2. This may include people who are responsible for the collection, identification, preservation of samples or have overall responsibility for the project.

1. **SURNAME**: First letter capitalised, rest lower case (e.g., Darwin)
2. **FIRST\_NAME**: First letter capitalised, rest lower case (e.g., Charles). If middle initials should be included, please add these here (e.g. Charles R. ).
3. **PRIMARY\_AFFILIATION**: Add the primary affiliation for each individual. For those without an official affiliation (e.g. volunteers), partners should discuss the use of their affiliation as the work was done on their behalf. Additional affiliations and complete addresses will be requested at the time of publication by emailing everyone on the Contributors Tab.
4. **EMAIL\_ADDRESS**: Add a reliable email address as this is the primary route by which we will contact you for authorship queries.
5. **CONTRIBUTION:** List the contribution(s) made by the individual (e.g., collected specimens). Please list “Primary Contact” as an entry here for the person responsible for answering queries on the specimens. For contributors that identify to species level, re-enter your name in TAB 2, column IDENTIFIED\_BY, for any specimens you ID confidently to species level.
6. **CONFIRMATION:** For every shipment, the primary investigator leading the project must confirm that all samples contained within the shipment have been collected with local permissions and under local ethical guidelines. Please write “YES” in this column to confirm that these standards have been met and that the necessary regulatory compliance documents have been obtained and are available to you, only once is necessary, and in the same row as the primary investigator’s details. We are not able to accept samples that do not meet these standards. These may include landowner permission, veterinary pathogen sampling permissions, and / or Nagoya compliance. This is an important check that ensures that permissions were granted to collect and transfer the specimen for this research purpose. The sample provider should ensure this documentation is obtained.

# 6. TAB 2: Column by column instructions

* 1. **SERIES:** This field is simply a series of numbers that should reflect the total number of wells submitted, e.g., if 10 plates are submitted, each with 94 samples (and two blank sample wells), then the series will begin at 1 and end at 960.
  2. **CATCH\_LOT:** One 50 mL falcon tube containing 100% ethanol is used per trap bottle for each Malaise trap collection event. That is, for a bidirectional Malaise trap, two 50 mL tubes will be used, one for each trap bottle during the catch period. Each 50 mL tube has an alphanumeric label QR set up as C###[A-Z], e.g. C001A. Any leftover or excess insects remaining after plating should be returned to the same 50 mL falcon tube along with the required 5-10 mL ethanol from the trap. If the specimens have been caught en masse but using a different system than BIOSCAN QR codes, please confirm your CATCH\_LOT equivalent codes are viable with the BIOSCAN team and then record them here. If the specimens are not part of a CATCH\_LOT, enter “NOT\_APPLICABLE” here (e.g. they have been hand caught).
  3. **RACK\_OR\_PLATE\_ID:** Each plate must be labelled with a sticker that has a human readable label and a scannable barcode. The human readable label will contain your Partner Code, assigned to you by BIOSCAN, and a numeric plate identifier (e.g. CAMP\_001 would represent the first plate from the CAMPUS site). We will provide you with the stickers to label your own plates.
  4. **TUBE\_OR\_WELL\_ID:** This field should have a record for each well in a plate. This column can be populated by copy / pasting from the first column in TAB 3, the Well IDs tab. From the same TAB, when plate level only metadata is being entered please copy / paste “PLATE\_ONLY\_1\_BLANK” if only H12 is empty, or “PLATE\_ONLY\_2\_BLANKS” if G12 and H12 are empty and use only one row to capture the metadata for the whole plate. Use this only if a plate represents all identical metadata (i.e. one catch lot, all specimens are WHOLE\_ORGANISM, either taxonomic identifications are blank or all the same, no blank samples other than the designated blank wells, and all specimens are from one catch lot). Otherwise please follow previous guidance and submit 96 rows of metadata.
  5. **ORGANISM\_PART:** A description of the exact tissue(s) in the tube or well. This field has a controlled vocabulary: use the drop-down menu. For empty wells that contain only preservative solution, select “NOT\_APPLICABLE” (G12 and H12 on every plate plus any other wells with no specimen). Refer to *3.1. Plating Specimens/samples section III* for guidance on how to plate larger insects. If multiple parts must be submitted within a well, combine tissues by typing in multiple terms from the list using the | (vertical pipe) symbol to separate them (e.g. if you put a head and abdomen of an insect into a well enter “HEAD | ABDOMEN”). If a specimen is damaged but largely complete (e.g., missing some legs or wings), then select “WHOLE\_ORGANISM”.
  6. **PRESERVATIVE\_SOLUTION:** This is the suspension liquid used to preserve each sample in the 96 well plate, which should typically be “100%\_ETHANOL”. This field has a controlled vocabulary: select the correct option from the drop down menu for the first entry, then in order to fill multiple samples, click on the cell containing the data entry and then click on the little blue square that will appear at the lower right corner of the cell (in Google Sheets) and drag the square down to fill any remaining cells with the same information. This field is also required for wells that contain no specimen. If a different percentage of ethanol has been used, select “V%\_ETHANOL” and add the percentage (e.g. 85% ethanol) to the field PRESERVATION\_APPROACH. If none of the drop-down terms are suitable, select “OTHER” and add information to PRESERVATION\_APPROACH.
  7. **CATCH\_SOLUTION:** Suspension liquid used in the catch bottle, which should typically be “100%\_ETHANOL” for BIOSCAN Malaise trap catches. However this may vary for other trap methods such as pan traps or historical collections (contact the BIOSCAN team if you are planning to use other trap methods or provide historical samples). This field has a controlled vocabulary, select the correct option from the drop down menu. If none of the drop-down terms are suitable, select “OTHER” and add information to PRESERVATION\_APPROACH.
  8. **BOTTLE\_DIRECTION:** When the catch comes from a Malaise trap, please put the direction the bottle end of the trap was oriented towards using the one (N,S,W,E), two (NE,SE,NW,SW), or three letter codes as below. If using a two-bottle trap then label each bottle with the corresponding compass point so you know which bottle has each catch when you remove them for plating. Leave this field empty if the specimen is not from a Malaise trap.



* 1. **DATE\_OF\_COLLECTION:** The date of the sample collection, with year, month and day specified in this order using hyphens (YYYY-MM-DD). It is important to provide the complete date, but if only the year or the year and month are known, then enter YYYY or YYYY-MM, respectively. If the collection spans multiple days (as Malaise catches set for 24 hours will), we request that the **end** date is entered here rather than the start date. If your collection ends precisely at midnight, we consider midnight to be the first minute of the day (00:00 as opposed to 24:00) and thus the end date should reflect this.
  2. **COUNTRY\_OF\_COLLECTION:** This must use the accepted country name, which can be looked up here <https://www.insdc.org/country>.
  3. **COLLECTION\_LOCATION:** Where possible, this should use your country’s administrative districts to as fine of a resolution as you can provide ranging from least to most specific and separated by | character, e.g. “*England | East of England | Cambridgeshire | Hinxton | Wellcome Genome Campus | East Pond*”. It is important to give the name of the specific collection site whenever possible. If the specimen is from a laboratory colony, give the current location (e.g. Imperial College London) rather than information on the original collection, but indicate original collection location in OTHER\_INFORMATION.
  4. **DECIMAL\_LATITUDE:** In decimal degrees, between -90 and 90. We advise that locations are specified to at least 4 decimal places (<https://en.wikipedia.org/wiki/Decimal_degrees>) giving 11 m resolution to the location from which the Malaise catch was collected. If GPS coordinates were not taken at the time of collection, this is easy to retrospectively collect by dropping a pin in google maps or grid reference finder for UK sites (<https://gridreferencefinder.com/>) and clicking on the pin to reveal coordinates.
  5. **DECIMAL\_LONGITUDE:** guidance same as latitude, except that range is from -180 to 180.
  6. **WHAT\_3\_WORDS:** This column can be left blank. This information is for geolocating the sample area to a 3 m square, mapped by what3words.com (see guidance at <https://what3words.com/how-to-use-the-what3words-app/>), this can also be found using site <https://gridreferencefinder.com/>. This gives a more precise resolution to where the Malaise trap was set up and can distinguish between nearby sampling locations or mark your Malaise trap location more precisely in cases where the trap must be disassembled and reassembled each month. Please include the three backslashes as part of the entry, e.g., ///protected.cheetahs.slippery.
  7. **TIME\_OF\_COLLECTION:** Time of day (local time) at which the collection **ended** in 24-hour clock format, with hours and minutes separated by a colon e.g. 13:35, 04:53, etc. We do not accept 24:00 for midnight, use 00:00 (first minute of the day) if your collection ends precisely at midnight. This column can be left blank.
  8. **DURATION\_OF\_COLLECTION:** This field captures the duration of the catch (how long the trap was set up and operational) using ISO 8601 standards. The format is complicated and described below in detail – briefly, if you have set a trap for a 24 hour period, enter PT24H. Round up to the nearest hour - we do not require minutes or seconds to be recorded in this field. If you have set a trap for 20 hours and 30 minutes, enter PT21H, etc. This column can be left blank if it isn’t relevant (e.g., for a hand caught specimen).

Duration format in detail in case of activities that require more specific time records: The format is P[n]Y[n]M[n]DT[n]H[n]M[n]S. In this representation, the [n] is replaced by the value for each of the date and time elements that follow the [n]. The capital letters *P*, *Y*, *M*, *W*, *D*, *T*, *H*, *M*, and *S* are designators for each of the date and time elements and are not replaced.

*P* is the duration designator (for *period*) and is always placed at the start of the duration representation.

* + *Y* is the year designator that follows the value for the number of years.
  + *M* is the month designator that follows the value for the number of months.
  + *W* is the week designator that follows the value for the number of weeks.
  + *D* is the day designator that follows the value for the number of days.

*T* is the time designator that precedes the time components of the representation.

* + *H* is the hour designator that follows the value for the number of hours.
  + *M* is the minute designator that follows the value for the number of minutes.
  + *S* is the second designator that follows the value for the number of seconds.
  1. **COLLECTION\_METHOD:** A description of the collection method used. This field has a controlled vocabulary; pick the best fitting term from the drop down menu. Any details about the collection method can be recorded in the column DESCRIPTION\_OF\_COLLECTION\_METHOD. If none of the available terms describe your collection method, select \*\*OTHER\*\* and describe the method in the column DESCRIPTION\_OF\_COLLECTION\_METHOD or request an additional term to be added. This column can be left blank.
  2. **DATE\_OF\_PLATING:** Enter the date when the Malaise trap samples (or other *en masse* traps), were plated. This can be the same day as DATE\_OF\_COLLECTION. This column can be left blank.
  3. **PREDICTED\_ORDER\_OR\_GROUP:** This column can be left blank. The taxonomic Order or higher classification into which the Family and Genus belongs. This should correspond to the taxonomy as represented in the NCBI Taxonomy Database and entered first letter capitalised, rest lower case.
  4. **PREDICTED\_FAMILY:** The taxonomic Family (or Superfamily, Subfamily, Tribe or Subtribe) into which the Genus is placed. This should correspond to the taxonomy as represented in the NCBI Taxonomy Database and entered first letter capitalised, rest lowercase. This column can be left blank.
  5. **PREDICTED\_GENUS:** The taxonomic Genus (or Subgenus) to which the Species belongs. This should correspond to the taxonomy as represented in the NCBI Taxonomy Database, and with the generic component of the scientific name given below. Enter as first letter capitalised, rest lowercase. This column can be left blank.
  6. **PREDICTED\_SCIENTIFIC\_NAME:** The latin binomial / combined genus and species name with a space in between. If the specimen has not been identified to species level, leave the field empty. All samples will then be registered as “*unidentified*” in the validation process. If the well does not contain a sample (e.g. H12), again this field can be left empty as long as ORGANISM\_PART has been registered as “NOT\_APPLICABLE”. For the first word in the binomial name enter its first letter capitalised, rest lowercase and all lower case for the second part of the name. This column can be left blank.
  7. **SPECIMEN\_IDENTITY\_RISK:** Only use this field if you have identified your specimen to species level in PREDICTED\_SCIENTIFIC\_NAME and there is **no (or very low)** risk that you are wrong. In such cases, please enter “N” here to indicate there is “NO” risk of incorrect identity. If you are only able to confidently identify to Genus or higher level, leave this field blank. If there is any risk that the specimen is part of a species complex or group where it can be difficult to be certain of species identity and / or species boundaries, leave this field blank.
  8. **LIFESTAGE:** The lifestage of the specimen from which the sample was derived at the time it was preserved (if this is different from the lifestage when collected e.g. if larvae were collected in the field and reared to adults in the lab, the entry here should be adult). This field has a controlled vocabulary, please use the drop-down menu. If you would like to provide more detailed lifestage information than is available in the drop-down menu, add this to OTHER\_INFORMATION (e.g., L3 stage larva). If the lifestage of the organism is not known, leave this field empty.
  9. **SEX**: The sex of the specimen from which the sample was derived. This field has a controlled vocabulary: use the drop-down menu. If the sex of the organism is not known, leave this field empty.
  10. **SORTING\_SOLUTION\_USED:** Only select Y from the drop down menu if you used the phosphate buffered saline (PBS) solution to morphosort your specimens before plating. Otherwise leave empty.
  11. **CATCH\_BOTTLE\_TEMPERATURE\_STORAGE:** Indicate the temperature at which the Catch Bottle was stored for the majority of the time before specimens were plated. This field has a controlled vocabulary, please use the drop-down menu. If for some reason you do not have this information, you may leave this field empty.
  12. **PLATE\_TEMPERATURE\_STORAGE:** Indicate the temperature at which the specimen plates were stored for the majority of the time before plates were shipped to Sanger. This field has a controlled vocabulary, please use the drop-down menu. If for some reason you do not have this information, you may leave this field empty.
  13. **AMOUNT\_OF\_CATCH\_PLATED**: Indicate whether the whole catch was plated “ALL\_SPECIMENS\_PLATED”, or the catch contained a swarm of specimens that look largely identical “ALL\_SPECIMENS\_PLATED\_APART\_FROM\_SWARM”. For swarms, please plate up to two full plates of the swarm species and place the rest of the swarm specimens back into the catch lot tube. Partially plating your catch is strongly discouraged but if for some reason is required, the term to enter is “SOME\_SPECIMENS\_PLATED”. It is important to record accurate metadata here for abundance analyses. If your catch was not a mass trap event, then please enter “NOT\_APPLICABLE”. This field has a controlled vocabulary, please use the drop-down menu.
  14. **MORPHOSPECIES\_DESCRIPTION:** This is a free text field for you to use to write in descriptive words for morphospecies that you come across often in your catches but you are unable to identify, e.g. “brown fly with yellow stripe on abdomen”. This information can be useful for you to match up species data when you receive your biodiversity report and useful to us when reviewing the sequence data output.
  15. **DESCRIPTION\_OF\_COLLECTION\_METHOD:** This is a free text field for you to use to write as detailed as possible description of the sample collection methods, e.g. “*caught with fibre net within densely wooded area, and immediately placed into the collection container”* or “*manually collected whilst feeding on a cow inside a shed and immediately placed into the collection container”*. If the specimen was collected as larva and reared to adult, mention this here.
  16. **HABITAT**: Free text field to include any comments about the location, habitat or substrate, *e.g. damp mossy ground in moderate shade* or *indoors in air conditioned office space.*  You can use ENVO terms, NVC, or EUNIS.
  17. **PRESERVATION\_APPROACH:** This is free text but should summarise any extra information regarding the temperature and storage time from the point of collection to the point of sample being placed in the well, for example, Catch bottle kept in fridge for 2 weeks, then moved to room temperature (you may abbreviate to RT) for 2 days before specimens were plated out and then plates remained at RT until shipping.
  18. **COLLECTOR\_SAMPLE\_ID:** This is the unique name assigned to the sample by the COLLECTOR.
  19. **VOUCHER\_ID:** Where the entire specimen is not submitted, the remaining specimen can be pinned or stored in preservative. This remaining specimen should have an associated and unique VOUCHER\_ID that should be determined by the Partner such that sequencing data can be linked back to the Voucher Specimen at a later date. When the whole insect is submitted for sequencing, this field should be left empty.
  20. **ELEVATION:** Altitude above sea level, supplied in metres. Do not supply the unit, e.g. use 200 for 200 m above sea level, 100-200 for 100-200 m range above sea level, etc. Please supply elevation of water surface for inland water bodies. Leave this field empty if the elevation was not recorded
  21. **OTHER\_INFORMATION:** This is a free text field for further relevant information not captured by the other fields. Scientific names of other species expected to be present in this specific sample, taking consideration of the ORGANISM\_PART. Occasionally, the relationships between submitted samples may be known and important. This can be reflected in the COLLECTOR\_SAMPLE\_ID and described here (e.g. AB43\_F1 and AB43\_Mother). If there is nothing else to add here, this field should be left empty. You can enter additional data for **COLLECTION\_LOCATION** and **LIFESTAGE** if relevant.
  22. **MISC\_METADATA:** Please discuss this by emailing [bioscan.info@sanger.ac.uk](mailto:bioscan.info@sanger.ac.uk) before filling in the manifest if additional data for your samples exists but is not captured by any existing fields. In such a case, we will make every effort to collect and standardise additional metadata. This column can be copy / pasted to create as many additional columns as required to capture any additional metadata of interest, for example, this might include temperature, humidity, windspeed, baited traps. Please change the field from MISC\_METADATA to the proposed name of the new field, and standardise your entries using ALL CAPs and no spaces, e.g. a new field might be “BAITED\_TRAP” and terms might be “CARRION”, “OVERRIPE\_FRUIT”.
  23. **IDENTIFIED\_BY:** Only enter data here if you entered data in **PREDICTED\_SCIENTIFIC\_NAME** and if **SPECIMEN\_IDENTITY\_RISK is “N”.** Enter the name of the person or people who identified the specimen, only if identified down to species level. Use ALL CAPs, and separate names with | (vertical pipe symbol), e.g., “CAROLUS LINNAEUS | JEAN-BAPTISTE LAMARCK”. If a contributor has identified a specimen to species name, the columns that capture their contact information should be completed in TAB 1. We will only use this information to contact the identifier if there has been a discrepancy with the scientific name (e.g. spelling). We note that storage of names with affiliations in a database brings the system under the aegis of the GPDR regulations, and we must ask partners to agree to their data being stored and to those data being propagated to secondary databases (including ENA and the final collections of record).

# Document History

| ***Version*** | ***Date*** | ***Changes*** | ***Contributors*** |
| --- | --- | --- | --- |
| **1.0** | May 2021 | First version of the BIOSCAN manifest | Lyndall Pereira, Vickie Brookes, Mara Lawniczak, Marilou Boddé, Petra Korlevic, Katie Woodcock |
| **2.0** | June 2022 | based on Darwin Tree of Life manifest but extensively revised to support BIOSCAN collections. Requirements for missing data terms removed.  Allow partial plates for final catch before shipment.  Epicollect not to be used, Google folder - each partner code with own link.  Allow plate level entry into the same manifest - called PLATE\_ONLY under TUBE\_OR\_WELL\_ID column.  Added CONFIRMATION to Contributors tab.  WHOLE\_ORGANISM\_DAMAGED and BLANK\_SAMPLE removed from ORGANISM\_PART, BLANK\_SAMPLE to be replaced with NOT\_APPLICABLE to show empty wells.  Post modification fields added at the end. | Lyndall Pereira, Mara Lawniczak, Petra Korlevic, Alex Makunin nd members of the Darwin Tree of Life Sample Working Group |
| **3.0** | July 2023 | Addition of two new columns CATCH\_SOLUTION and AMOUNT\_OF\_CATCH\_PLATED. Update edits around plates sealed with foil. Updates around G12 as an empty well. Clarification over the content of column W. SPECIMEN\_IDENTITY\_RISK moved to blank is equivalent to Y. Catch Lot guidance refined. Wing removed as organism\_part (change to other\_somatic\_tissue). Sorting solution changed to only record if used - Y in dropdown or leave blank. Removed identifier affiliation from TAB2. Minor edits throughout for clarity. Post validation process text removed. Name change from ‘Recording Sample Metadata SOP’ to ‘Manifest SOP’. Strict naming of manifests in the format [PARTNER CODE]\_[YYMM]\_BIOSCAN\_Manifest\_V3.xslx | Lyndall Pereira, Mara Lawniczak, Alex Makunin, Jemma Salmon |