

QUICK-START GUIDE FOR PUBLISHING eDNA DATA TO OBIS

- 1. Gather all your data:** ASV/OTU table, taxonomic assignment table, sequence files, all available metadata (study metadata, sample collection, laboratory procedures, bioinformatic steps, reference library, ...)
- 2. Format them into Darwin Core Archive with the following structure:**
 - **Occurrence core table:** Each row represents a single occurrence, a sequence detected at a specific time and location, along with its taxonomic annotation (if applicable).
 - **DNA Derived Data extension table:** This table captures information about the sampled DNA itself.
- 3.** Make sure all columns are named with standard **Darwin Core vocabulary terms**.
- 4.** Make sure you include these **mandatory and recommended fields**:

OBIS mandatory fields

occurrenceID
eventDate
decimalLongitude
decimalLatitude
scientificName WoRMS
eventID event core
occurrenceStatus
basisOfRecord

OBIS strongly recommended fields

scientificNameID AphiaID
organismQuantity
organismQuantityType
associatedSequences
sampleSizeValue
sampleSizeUnit
samplingProtocol
identificationRemarks
identificationReferences
verbatimIdentification
taxonConceptID
materialSampleID

DNA strongly recommended fields

DNA_sequence	tax_class
sop	ampliconSize
target_gene	env_broad_scale
target_subfragment	env_local_scale
pcr_cond	env_medium
annealingTemp	lib_layout
annealingTempUnit	seq_meth
pcr_primer_forward	otu_db
pcr_primer_reverse	otu_class_appr
pcr_primer_name_forward	otu_seq_comp_appr
pcr_primer_name_reverse	

- 5.** The full OBIS checklist of Darwin Core Terms is available in the OBIS manual in section 13, 'Formatting data tables'. The FAIR eDNA project also provides a checklist of recommended eDNA metadata.
- 6.** Contact the appropriate **OBIS node** to publish your data to the **IPT**. The node can assist with the final steps to share your data through OBIS. You can find endorsed OBIS nodes at obis.org/about/nodes/.

LEARN MORE
FROM THE
OBIS MANUAL

Visit manual.obis.org/dna_data