



PEMA sequences retriever: fact sheet

Aim	This service downloads the DNA sequences for the specific markers that the user has chosen in the previous service by using the European Nucleotide Archive (ENA) accession numbers.
Input	This service uses the selected ARMS samples and gene markers chosen within the previous services and listed in the <i>MasterARMS_filtered_path.csv</i> file.
Requirements	This service requires ENA accession numbers to query specific DNA sequences.
Analytical tools	This service queries the ENA and uses the python script <i>enaDataGet</i> from <i>enaBrowserTools</i> to download the DNA sequences requested by the user.
Output	The DNA sequences will be downloaded as <i>fastq</i> . Two <i>fastq</i> files for each DNA sequence will be downloaded representing, respectively, the forward and reverse reads of the genetic sequence. Both <i>fastq</i> files will be used to run analysis using P.E.M.A. in the next service (see “PEMA runner” fact sheet for details).
Citations	
Metadata	https://metadatalogue.lifewatch.eu/srv/eng/catalog.search#/metadata/e6289cf6-dde7-4584-89e6-bd7e907a4b5f
Further readings	European Nucleotide Archive - https://www.ebi.ac.uk/ena enaBrowserTools - https://github.com/enasequence/enaBrowserTools