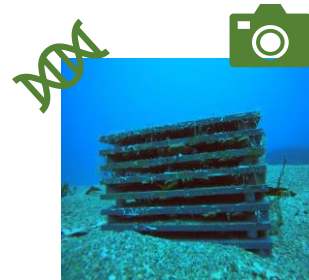


ARMS OTU unifier: fact sheet



Aim	This service copies and renames the PEMA output file (OTU table) produced by the “PEMA runner” service. This service allows the user to keep a copy of the original OTU table whereas the output of this service will be further analysed and transformed using the next services included in the analytical workflow.
Input	A <i>final_table.tsv</i> which is the OTU table produced by the “PEMA runner” service.
Requirements	This service requires that the “PEMA runner” service has run correctly and produced the expected outputs including the <i>final_table.tsv</i> file.
Analytical tools	None.
Output	A <i>unified_species.csv</i> file which is a copy of the OTU table (<i>final_table.tsv</i>) produced by the “PEMA runner” service. The columns correspond to the sequence/samples processed, whereas the first column is an ID column and the final one contains the species taxonomic information. The specific columns for each sequence/sample contain integers values with the number of reads assigned to each sample and taxon and the title of these columns is the ENA accession number.
Citations	Haris Zafeiropoulos, Ha Quoc Viet, Katerina Vasileiadou, Antonis Potirakis, Christos Arvanitidis, Pantelis Topalis, Christina Pavloudi, Evangelos Pafilis, PEMA: a flexible Pipeline for Environmental DNA Metabarcoding Analysis of the 16S/18S ribosomal RNA, ITS, and COI marker genes, GigaScience, Volume 9, Issue 3, March 2020, giaa022, https://doi.org/10.1093/gigascience/giaa022
Metadata	https://metadatalogue.lifewatch.eu/srv/eng/catalog.search#/metadata/e6289cf6-dde7-4584-89e6-bd7e907a4b5f
Further readings	PEMA article - https://doi.org/10.1093/gigascience/giaa022 PEMA GitHub - https://github.com/hariszaf/pema