

VEE KVALITEET. VEEST KESKKONNA DNA PROOVIDE
VÕTMINE, KOGUMINE JA SÄILITAMINE

Water quality - Sampling, capture and preservation of
environmental DNA from water

EESTI STANDARDI EESSÕNA

NATIONAL FOREWORD

<p>See Eesti standard EVS-EN 17805:2023 sisaldab Euroopa standardi EN 17805:2023 ingliskeelset teksti.</p> <p>Standard on jõustunud sellekohase teate avaldamisega EVS Teatajas.</p> <p>Euroopa standardimisorganisatsioonid on teinud Euroopa standardi rahvuslikele liikmetele kättesaadavaks 15.03.2023.</p> <p>Standard on kättesaadav Eesti Standardimis- ja Akrediteerimiskeskusest.</p>	<p>This Estonian standard EVS-EN 17805:2023 consists of the English text of the European standard EN 17805:2023.</p> <p>This standard has been endorsed with a notification published in the official bulletin of the Estonian Centre for Standardisation and Accreditation.</p> <p>Date of Availability of the European standard is 15.03.2023.</p> <p>The standard is available from the Estonian Centre for Standardisation and Accreditation.</p>
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ICS 13.060.70

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EUROPEAN STANDARD

EN 17805

NORME EUROPÉENNE

EUROPÄISCHE NORM

March 2023

ICS 13.060.70

English Version

Water quality - Sampling, capture and preservation of environmental DNA from water

Qualité de l'eau - Échantillonnage, collecte et conservation de l'ADN environnemental prélevé dans l'eau

Wasserbeschaffenheit - Probenahme, Erfassung und Konservierung von Umwelt-DNA in Wasser

This European Standard was approved by CEN on 30 January 2023.

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EUROPEAN COMMITTEE FOR STANDARDIZATION
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European foreword

This document (EN 17805:2023) has been prepared by Technical Committee CEN/TC 230 "Water analysis", the secretariat of which is held by DIN.

This European Standard shall be given the status of a national standard, either by publication of an identical text or by endorsement, at the latest by September 2023, and conflicting national standards shall be withdrawn at the latest by September 2023.

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Introduction

WARNING — Persons using this document should be familiar with water sampling protocols to assess biological diversity. This document does not purport to address all of the safety problems, if any, associated with its use. It is the responsibility of the user to establish appropriate health and safety practices.

Moreover, the need of notification, obtaining certificates or permits prior to sampling, depending on national or international laws and regulations such as the Nagoya Protocol on Access to Genetic Resources (<https://www.cbd.int/abs/>), needs to be considered.

The monitoring of organisms is key to the assessment of the status of aquatic ecosystems and is required by national and international legislation such as the European Union Water Framework Directive (2000/60/EC). A range of methods have been described how to monitor organisms in aquatic environments, leading to a wide range of European standards (e.g. EN 14011:2003, EN 14757:2015, EN 15460:2007). These approaches, however, necessitate the capture and/or collection of the organisms of interest, which can be a laborious and time-consuming process.

The possibility to detect the presence of organisms and/or quantify relative abundance (e.g. [6]) in aquatic environments via the analysis of environmental DNA (eDNA) provides a novel means to monitor biodiversity across a wide range of taxonomic groups, including microorganisms, plants and animals ([7][8][9]). This approach allows to examine organismic diversity without the need to directly isolate and capture organisms and it is expected to play a key role for future biomonitoring aiming at temporally and spatially highly resolved species inventories [10]. Albeit the power of the eDNA approach has been repeatedly reported [11], there is a great need for standardizing the application of eDNA-based assessment of aquatic biodiversity ([12], [13]). Note, however, that eDNA-based biomonitoring currently does not allow to obtain certain population parameters (e.g. individual size, sex) which can be obtained by traditional sampling techniques.

This document provides guidance how to sample and preserve eDNA from water samples, addressing the first and crucial step for any further downstream eDNA-based analyses of biodiversity. A specific technical report for the routine sampling of benthic diatoms from rivers and lakes adapted for metabarcoding analyses is CEN/TR 17245:2018.

1 Scope

This document specifies procedures for sampling, capture and preservation of environmental DNA (eDNA) in aquatic environments, stemming from organisms that are or have recently been present in a waterbody, have visited it or whose DNA has been introduced to the waterbody through some mechanism. This document also covers procedures for avoiding sample contamination and ensuring DNA quality, key properties of the filtering procedure and equipment and reporting standards.

This document does not include the collection of eDNA from biofilms, sediments or similar sample types and does not cover sampling designs.

2 Normative references

There are no normative references in this document.

3 Terms and definitions

For the purposes of this document, the following terms and definitions apply.

ISO and IEC maintain terminology databases for use in standardization at the following addresses:

- IEC Electropedia: available at <https://www.electropedia.org/>
- ISO Online browsing platform: available at <https://www.iso.org/obp>

3.1

cross-contamination

unintended transfer of any source of and/or DNA from one sample to another sample

3.2

decontamination

procedure to remove any source and/or trace of DNA from material that might come into contact with the sample

3.3

enclosed filter

filtering device where the filter membrane is encapsulated and where the inflow and outflow can be closed for transport and storage

Note 1 to entry: The eDNA contained on the filter is typically extracted without removing the membrane from the filter capsule greatly reducing the risk of contamination of samples. See Figure A.1 C. in Annex A.

3.4

environmental DNA

eDNA

material stemming e.g. from dead or from living organisms and include single-stranded (ss) and double-stranded (ds) DNA fragments from nuclear and mitochondrial/plastid DNA of eukaryotes as well as plasmid DNA of prokaryotes

Note 1 to entry: Subsuming DNA from various sources such as unicellular or small multicellular organisms or tissue particles (e.g. shed cells, faeces) and gametes of multicellular organisms.