DATA MANAGEMENT PLAN

PROJECT	
Project number:	**101079234**
Project acronym:	**BIOLAWEB**
Project name:	**Boosting Institute of Chemistry, Technology and Metallurgy in Water Biomonitoring**

DATA MANAGEMENT PLAN	
Date:	**25.07.2025**
Version:	**V3.0**

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1. Data Summary

The overarching aim of the BIOLAWEB project is to raise EU scientific excellence and innovation capacity in eDNA based biomonitoring by strengthening the research and administration capacity of the coordinating institution from the Widening country through twinning with internationally leading counterparts in Europe. The succesful completion of BIOLAWEB research and networking activities widely relies on generation and use/re-use of different types of data described in the next sub-sections.

1.1. Re-use of existing data

The BIOLAWEB project will strongly rely on DNA sequences available in international OA databases such as the reference barcoding library Diat.barcode, BOLD and GenBank within the National Center for Biotechnology Information (NCBI). These data are neccessary to compare the results generated in the BIOLAWEB project.

Available nucleotide data and metadata on the species of algae, cyanobacteria and macrophytes will be used for research linked with Work Package 4 (Task 4.1, 4.2 and 4.3). Raw nucleotide data are often stored in text-based fortmat such as FASTA or FASTQ. The expected size of genomic data that are re-used by BIOLAWEB is up to several GB, and largely depends on target species and degree of processing of the dataset.

1.2. Generation of new data

The BIOLAWEB generated data on water chemistry, macrophyte, benthic diatoms and phytoplankton assemblages from study lakes. When it comes to new DNA sequences of diatom, phytoplankton and macrophyte species, so far 42 new sequences of diatoms were added in Diat.barcode reference library. BIOLAWEB also collected data from internal surveys (questionnaires and interviews).

1.3. Data types, purpose, formats, size, origin, and utility outside the project

When it comes to the content, BIOLAWEB has produced textual, numerical and grafical data, and as to their nature, the generated data have been qualitative or quantitative, raw or processed. Specifically, BIOLAWEB datasets include: (i) quantitative and qualitative physical, chemical, and species data (species names and abundances of algae and macrophytes, including mapping data), (ii) DNA sequences from metabarcoding of the samples collected, and (iii) relevant third-party data from stakeholders. Table 1 summarizes data sets linked with project tasks/objectives, their purpose and format in which data will be stored during the BIOLAWEB project. Finally, for data sharing purposes such as reports (internal and external), the Adobe Portable Document Format (.pdf) has been used.

2. FAIR data

Data that are output of the research activities within BIOLAWEB project will be made openly available upon publication in peer-reviewed journals. Also, data such as FASTQ files will be archived in the Zenodo before the end of the project, with embargo until publication(s) acceptance, but with possibility that editor/reviewers gain access to these data during the manuscript processing. Each partner involved in research and training activities and thus taking part in data generation is responsible for their processing, organization and compliance with the FAIR principles.

2.1. Making data Findable, including provisions for metadata

Persistent identifier

The BIOLAWEB consortium will store generated and collected data in an open online research data repository. The BIOLAWEB team decided to use a digital repository of the Institute of Chemistry, Technology and Metallurgy, University of Belgrade, CeR - Central Repository ICTM (https://cer.ihtm.bg.ac.rs/handle/123456789/7506) as its data archive, based on the compliance of the repository structure and facilities with the FAIR data principles. This CeR repository allows

researchers to deposit both publications and data, providing tools to link them to these through **persistent identifiers (Handle, DOI)** and data citations.

Quality-assured sequence data for diatoms are submitted to Diat.barcode database V13 (https://doi.org/10.15454/TOMBYZ). Sequences of macrophytes will be submitted to GenBank, an annotated collection of all publicly available DNA sequences.

In addition to the CeR repository, the consortium has agreed that certain data (publications, abstracts and sequences) generated from the BIOLAWEB project will be deposited on the Zenodo platform (https://zenodo.org/communities/biolaweb/).

Metadata types and standards

The CeR repository provides the possibility to add extensive metadata about researchers' publications, posters, and presentations (e.g., around 29 metadata for each publication including file name, size, format, date accessioned, date available, rights, license, for mapping results – lake name, organism group, method used for mapping/counting/measuring, coordinates, sampling date, etc.).

The Zenodo repository provides the possibility to add extensive metadata pertaining to researchers' publications, presentations, etc. This includes more than 30 metadata points for each publication, encompassing details such as file name, size, format, accession date, availability date, rights, and licensing information.

Quality-assured macrophyte barcoding sequence data will be submitted to GenBank and accesion numbers will be released after acceptance of papers in Open Access journals. All data submitted to GenBank contain the necessary metadata required by GenBank, including species name, sampling location, collection date, publication reference and a persistent identifier for each entry. GenBank is an annotated collection of all publicly available DNA sequences, so that the quality-assured data of macrophytes generated in BIOLAWEB can be easily found and accessed. Regarding the other raw sequences obtained by metabarcoding, they will be added as supplement material to the papers, and uploaded on Zenodo after acceptance of journal publications.

Sequence data related to diatoms are also integrated into the reference barcoding library Diat.barcode. For each sequence, all necessary metadata are given and follow the CEN TR 17244 (CEN, 2018. Water quality - CEN/TR 17244 - Technical report for the management of diatom barcodes 1–11.). Diat.barcode V13 is an open-access library available at https://doi.org/10.15454/TOMBYZ.

Table 1. BIOLAWEB project data summary

Data type	Task	Description	Data utility
Dataset 1	Task 1.2: Internal communication	Purpose: To collect information for preparing consortium and internal meetings, presentations and minutes from the meetings Data origin: List of participants, presentations, pictures, promo video materials Format: .docx, .pdf,.xlsx, .ppt, .png, .jpg, .mp4 Expected size: biannual consortium meetings (non-video files: **~200 MB**; 2 video files (.mp4): **~1.2 GB**, weekly UB-ICTM internal meetings: **~300 MB**	All files from internal UB-ICTM meetings are restricted to the BIOLAWEB consortium. Pictures and promo videos from kick-off/consortium meetings are publicly available.

Dataset 2	Task 2.1 Expert visit	<u>Purpose</u>: To collect data on the internal structure of UB-ICTM (Objective 1 – Scientific strategy for UB-ICTM) <u>Data origin</u>: Attendance list, pictures, presentations, expert visit report <u>Format</u>: .pdf, .ppt, .png, .jpg <u>Expected size</u>: .pdf and .ppt files **~30 MB,** .jpg meeting pictures **~25 MB**	Restricted to BIOLAWEB consortium.
Dataset 3	Task 2.2 Systematic survey of current research excellence indicators of UB-ICTM	<u>Purpose</u>: To collect information on UB-ICTM research performance in the field of aquatic ecology (Objective 1 – Scientific strategy for UB-ICTM) <u>Data origin</u>: Questionnaire <u>Format</u>: .pdf, .docx <u>Expected size</u>: pdf and .docx files **~2 MB**	Restricted to BIOLAWEB consortium.
Dataset 4	Task 2.3 Identification of short and long-term research needs of UB-ICTM	<u>Purpose</u>: To collect data on UB-ICTM existing knowledge gaps and needs in the field of biomonitoring (Objective 1 – Scientific strategy for UB-ICTM) <u>Data origin</u>: Attendance list related to the interview with researchers, pictures <u>Format</u>: .pdf,.docx, .jpg <u>Expected size</u>: .pdf and .docx **~1 MB**, .jpg pictures **~1.5 MB**	Restricted to BIOLAWEB consortium.
Dataset 5	Task 2.4 Formulating Strategy and Action plan	<u>Purpose</u>: To collect information for creating Science and Innovation Strategy of UB-ICTM (Objective 1 – Scientific strategy for UB-ICTM) <u>Data origin</u>: Science and Innovation Strategy of UB-ICTM in the field of biomonitoring <u>Format</u>: .pdf, .docx <u>Expected size</u>: pdf and .docx files **~1.5 MB**	Restricted to BIOLAWEB consortium.
Dataset 6	Task 3.1: Methods for developing ecological status indices	<u>Purpose</u>: teaching material; no new data will be generated within this task <u>Data origin</u>: n.a. <u>Format</u>: .ppt, .pdf <u>Expected size</u>: **~120 MB**	Primarily restricted to BIOLAWEB consortium. A somewhat reduced version (to respect copyrights) are publicly available (D3.3).
Dataset 7	Task 3.2: Metabarcoding of diatoms and phytoplankton	<u>Purpose</u>: teaching material, HTS sequencing data <u>Data origin</u>: n.a. <u>Format</u>: .pdf + fastq <u>Expected size</u>: **~1.2 GB**	Teaching material : Accessible to any participants of the courses. Sequencing data: Open-access published via journal papers and Diat.barcode.
Dataset 8	Task 3.3: eDNA of macrophytes	<u>Purpose</u>: teaching material; no new data will be generated within this task	Teaching material: Accessible to any participants of the courses.

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		Data origin: n.a. Format: .ppt, .doc, .xls Expected size: **~15 MB**	
Dataset 9	Task 4.1: eDNA for ecological status assessment (ESA) using diatoms	Purpose: To collect information on diatom composition in the sampled lakes using morphological and genetic approaches. Data origin: sampling reports, list of species Format: .xls Expected size: **~3 MB**	New diatom sequences are available in updated version of the Diat.barcode database, V13 https://doi.org/10.15454/TOMBYZ
Dataset 10	Task 4.2: eDNA for ecological status assessment using phytoplankton	Purpose: To collect information on phytoplankton composition in the sampled lakes using a morphological and genetic approach Data origin: sampling reports, list of species Format: .xls, .pdf, .docx, .jpg Expected size: **~4.5 GB**	Primarily restricted to the BIOLAWEB consortium. Then, open-access publication.
Dataset 11	Task 4.3: eDNA for ecological status assessment using macrophytes	Purpose: to develop a novel method to detect the occurrence of macrophytes from a water sample Data origin: macrophyte DNA sequences from 4 lakes in Serbia, and macrophyte mapping data from the same lakes Format: .xls, raw sequence reads (fastq, fasta) Expected size: **~10 GB**	The data from "traditional" and genetic macrophyte mapping will be published in scientific publications and in the digital repository of UB-ICTM and the Zenodo platform.
Dataset 12	Task 4.3: Maps for purpose of publishing articles, abstracts, ppt, poster, etc.	Purpose: to visualize areas of research. Data origin: different maps for 4 lakes in Serbia. Maps include different types of layers beside the lakes themselves. Different thematic maps are created depending on the purpose and research goals. Format: .jpg, .pdf, .png, .tiff Expected size: **~10 MB**	These data are useful for the scientific community (within freshwater ecology). The data from mapping will be published in scientific publications and in the digital repository of UB-ICTM.
Dataset 13	Task 5.1 Expert visit for need analysis in project management	Purpose: Bilateral discussion to estimate needs in project management. Data origin: Attendance list, pictures, presentations, expert visit report Format: .docx, .pdf, .ppt, .jpg Expected size: .docx, .pdf and .ppt files **~10 MB**; .jpg meeting pictures **~75 MB**	Restricted to UB-ICTM staff and BIOLAWEB consortium.
Dataset 14	Task 5.2 Setting up a new Research Management Office	Purpose: To collect information on potential candidates for the new office Data origin: application material, evaluation material	Strictly and confidentially used by UB-ICTM (Human Resources Department).

		Format: .pdf, .docx Expected size: pdf and .docx files **~4 MB**	
Dataset 15	Task 5.4 Organization of workshops, on-site and virtual trainings in project management	Purpose: To collect data for workshops and trainings Data origin: Attendance list, presentations, pictures Format: .docx, .xlsx, .pdf, .ppt, .jpg Expected size: .docx, .xlsx, .pdf, .ppt **~13 MB,** .jpg event pictures **~15 MB**	Materials (except the attendance list) will be made openly available (D5.2).
Dataset 16	Task 5.5 Support of ICPO** at UB-ICTM to researchers in project submission and implementation	Purpose: To collect data for info days and trainings Data origin: Presentations, training material, pictures Format: .docx, .xlsx, .pdf, .ppt, .jpg Expected size: .docx, .xlsx, .pdf, .ppt **~25 MB,** .jpg event pictures **~15 MB**	Most of materials (except the attendance list) will be made openly available through deliverable D5.2. Only presentations of external experts (upon their request) will be restricted to UB-ICTM staff.
Dataset 17	Task 6.2: Communication resources and tools	Purpose: To collect quantitative data on visitors of BIOLAWEB website, social media, Festival of Science and Researchers' night Data origin: Web site, Google Analytics Format: .jpg (Google Analytics screenshot) Expected size: **~10 MB**	Restricted to UB-ICTM staff and BIOLAWEB consortium.
Dataset 18	Task 6.3: Generation of roundtables with relevant stakeholders	Purpose: To collect information on roundtable participants and stakeholders Data origin: Attendance list, pictures, presentations, roundtable minutes Format: .docx, .pdf, .ppt, .jpg Expected size: .docx, .pdf and .ppt files **~50 MB,** .jpg event pictures **~30 MB**	Most of materials (except the attendance list) will be made openly available and shared with stakeholders.
Dataset 19	Task 6.4: Field work with stakeholders	Purpose: Field work with stakeholders Data origin: Attendance list, pictures, reports Format: .pdf, .jpg Expected size: .pdf files **~2 MB**, .jpg pictures **~15 MB**	Restricted to BIOLAWEB consortium.
Dataset 20	Task 6.5: Scientific dissemination	Purpose: To disseminate project results Data origin: peer-reviewed scientific articles and conference papers Format: .pdf, .docx, .jpg Expected size: **~800 MB**	The journal articles and conference abstracts will be made publicly available (Open Access and digital repositories CER and the Zenodo platform).

**International Cooperation and Project Office (ICPO) is a new and officially accepted name (with acronym) for the established office. IRMO was an initial acronym used in the project proposal.

2.2. Making data Accessible

Repository

The BIOLAWEB consortium identified CeR as a trusted repository suitable for storing datasets generated during the project. It is based on the platform DSpace (https://dspace.org/) which is one of the most popular platforms for Open Science. Within CeR, the BIOLAWEB project data are deposited and organized in a specific part of the repository (catalog) intended for international projects to facilitate data reuse (https://cer.ihtm.bg.ac.rs/handle/123456789/7506). The CeR repository ensures that the data is assigned an identifier and resolves the identifier into a digital object.

Zenodo has become an important resource in the academic community as it facilitates the sharing and access of scientific data, contributing to transparency, collaboration, and research advancement. Data published on Zenodo receive permanent digital identifiers (DOIs), making it easier to cite and track them in academic works. Zenodo integrates with other tools and services such as GitHub (for coding), ORCID (for researcher identification), and OpenAIRE (for promoting open access). Zenodo allows for the publication of various data formats, including text documents, images, video recordings, datasets, and other types of digital content.

To avoid potential duplication of entries on the Zenodo platform, a Data Protection Officer (DPO) is responsible for entering data into the database.

GenBank is an annotated collection of all publicly available DNA sequences, a well-established international database so that the quality-assured data generated in BIOLAWEB can be easily accessed.

Embargo and restricted access

Following the HORIZON EUROPE guidelines, scientific data will be made available for re-use (the sequence data, the mapping data, and the water chemistry) as well as workshops materials. Data that are input for scientific publications will be integrated in ZENODO before the end of the project, with a foreseen embargo period lasting until their acceptance by editor(s). Personal data collected during expert interviews/on-line questionnaires have been used for internal processing, anonymized, and restricted to the BIOLAWEB consortium (Table 2). The attendance lists with contacts of participants, as well as photographs from project events, are uploaded to the secure web-based platform with restricted access granted by the Project Coordinator and Data Protection Officer.

Table 2. Description of internal data created during the BIOLAWEB project

Data type	Utility	Description and purpose
Internal strategy datasets	Datasets were used to develop Science and Innovation Strategy and Action Plan (Objective 1)	All generated data from expert interviews and filled questionnaires remained restricted to the BIOLAWEB consortium.
Personal datasets	To make a list of potential workshops, trainings and roundtables attendees and their expectations (Objectives 2, 3 and 5).	Attendance lists and filled questionnaires (workshops, trainings, roundtables, etc.) remained restricted to the BIOLAWEB consortium.

The BIOLAWEB team has been ensured Open Access (OA) to peer-reviewed scientific publications at the latest at the time of publication, and their deposition in a trusted repository (CeR) under the latest available version of the Creative Commons Attribution International Public Licence (CC BY) or a licence with equivalent rights. Moreover, scientific publications (accepted journal articles and conference proceedings), as well as training materials that are base for public project deliverables has been uploaded to the BIOLAWEB website as soon as reasonably possible.

Metadata

In the CeR repository, metadata associated with scientific publications, project presentations and

reports will be openly available and licenced under a public domain (CC0) during the project lifetime and at least five years after the project ends.

GenBank is an annotated collection of all publicly available DNA sequences, and metadata are provided in a standardized way. This ensures that all macrophyte sequence data will be provided with the necessary metadata including species name, sampling location, collection date, publication reference and a persistent identifier for each entry. The BIOLAWEB team will ensure that all data will be made publicly available in GenBank or Zenodo immediately after publication.

2.3. Making data Interoperable

The BIOLAWEB team has not generated project specific ontologies nor vocabularies and has followed well-established standards linked with the open repository CeR which fulfils the criterion of interoperability. This repository uses general standard Dublin Core that makes BIOLAWEB data interoperable with other services that provide or offer metadata about scientific publications.

All data submitted to GenBank follow the community-endorsed standard and therefore are in an interoperable format.

The sequencing data will be analysed using reference barcoding databases developed in former research programs (Diat.barcode and Phytool). These reference libraries are used by a worldwide audience of scientists working on algal metabarcoding.

2.4. Increase data Reuse

BIOLAWEB has made research publications available through the deposition of a copy of the published, or final, peer-reviewed version, in identified suitable institutional repositories. Datasets uploaded in the CeR or Zenodo repository are freely accessible, immediately in case of Gold Open Access (OA), or after an embargo period - Green Open Access. Potential users are expected to adhere with the CeR or Zenodo terms of Use.

BIOLAWEB has published the project results (list of scientific publications, reports and other results) on the project website, taking into account the EC deadline. When it comes to data that are sensitive or not openly available, a secured web-based platform and a period of minimum 5 years after the project end has been selected.

Datasets generated in the BIOLAWEB project and deposited in the CeR or Zenodo repository under an Open Access license can be used without restrictions by third parties at least 5 years after the end of the project. Data deposited in GenBank are freely available "for eternity ".

The provenance of research data generated in the BIOLAWEB project has been tracked and those responsible for its generation has been adequately credited for their work using appropriate Creative Commons copyright licenses. Data submitted to GenBank follow a community-endorsed standard and have therefore been thoroughly documented.

Data quality assurance

The members of the Project Executive Board approve data collection and deposition in the open repository by checking the following critical data quality dimensions: 1. **Integrity** (data stability during the lifecycle); 2. **Validity** (data items can be traced); 3. **Accuracy** (data fits reality); 4. **Consistency** (values in former and latter datasets are consistent); 5. **Timeliness** (the time between expected and actual data availability); 6. **Currency** (data is up-to-date) and 7. **Completeness** (no missing values in table/box fields). After the end of the project, this role will be transferred to the repository administrator at UB-ICTM.

In general, only quality-assured data have been published and submitted to GenBank or Zenodo, thereby ensuring that only valid data will be made publicly available.

3. Other research outputs

Diatom samples collected in the BIOLAWEB project were deposited in the Diatom Collection of Serbia (DCSR) at the University of Belgrade, Institute of Chemistry, Technology and Metallurgy, National Institute of the Republic of Serbia.

Teaching material generated in WP3 are made available on our website and as project deliverables. In some cases, we made a slightly reduced version available, to avoid copyright issues (generally related to illustrations which may be used for teaching purposes only).

In the framework of the BIOLAWEB project, protocols used for diatoms and phytoplankton metabarcoding are protocols already developed in other projects of INRAE. Bioinformatic pipelines and scripts are based on open-source software and packages such as R that is commonly used in DNA datasets analysis. BIOLAWEB members has refered in deliverables to these protocols and scripts which are open-accessible on platforms of INRAE (see list at: https://carrtel-collection.hub.inrae.fr/barcoding-databases/diat.barcode and https://carrtel-collection.hub.inrae.fr/barcoding-databases). Changes that are made to these protocols, BIOLAWEB members have notified and made these modified protocols open-accessible. The protocols for macrophytes generated in the project have been openly available via CeR and as project deliverable.

4. Allocation of resources

No costs for the curation of data related to DCSR are foreseen. Submission of data to GenBank is part of the publication process and is free of charge. No costs are incurred for further archiving.

Data protection and long-term storage

UB-ICTM is responsible for data management of diatom, phytoplankton and macrophyte sequence data. The Data Protection Officer (DPO) will be responsible for overall data management in the BIOLAWEB project.

The Data Protection Officer (DPO) of the BIOLAWEB project is:

Dr Vladimir Petrović,
University of Belgrade
National Institute of the Republic of Serbia
Institute of Chemistry, Technology and Metallurgy
Department of Ecology and TechnoEconomics
Njegoševa 12, 11000 Belgrade, Serbia
Phone: +381 60 5866885
E-mail: petrovic@ihtm.bg.ac.rs

The Data Protection Officer (DPO) of the BIOLAWEB project is responsible for:

- the highest standards of the security measure to prevent unauthorized access to personal data. DPO should follow the data minimization principle, where all data that are not relevant will be immediately deleted from the record;
- the storage of the data, collection, recording, organization, structuring restriction, erasure, availability, and destruction of the data;
- ensuring that essential documents are not destroyed before the end of the required retention of 5 years and that after that they will be destroyed in their entirety making sure that they cannot be recovered. Data retained for auditing processes will be stored securely and further processed for those purposes only;
- provide the data subjects with the information on the purposes and procedures of their data processing, as well as their data protection rights.

The coordinating institution of the BIOLAWEB project (UB-ICTM) has used CeR for long-term storage of research data and metadata produced in BIOLAWEB. Data are machine-readable, citable and published in a registered long-term open access repository. Each dataset has been

accompanied by a full metadata description, explaining their contents, origin, methods, licensing, citation, etc.

Data submitted to GenBank are foreseen to be archived "for eternity," and necessary resources are provided by the international scientific community.

5. Data security

During the implementation of the BIOLAWEB project, datasets, either generated or reused, will be archived on the storage system of the beneficiaries. Each partner has its own policy for data management and follows national and institutional guidelines concerning data security. The secure storage and data sharing is responsibility of each partner. BIOLAWEB internal survey data and documents related to the Science Strategy and Action Plan (D2.2) are datasets that must be kept confidential. Sensitive project data are stored on a dedicated external hard disc with a minimum of 3 months backup time and will not be made openly available. A personal data storage will not take longer than 6 months after the end of the BIOLAWEB project.

GenBank is part of the International Nucleotide Sequence Database Collaboration. It is a long-standing foundational initiative that operates between DDBJ (DNA Databank of Japan), EMBL-EBI (EMBL's European Bioinformatics Institute) and NCBI (National Center for Biotechnology Information, USA). Long-term storage and data security are therefore ensured in the best possible way.

After the end of the project, the responsibility for secure long-term preservation and curation will be transferred to the repositories storing datasets.

6. Ethics

It is planned to collect local resources in the Republic of Serbia that might include samples of endangered flora. The project will comply with Serbian law with respect to sample collection. This activity is related to WP4 (Research and partnership) and WP3 (Training and networking). Samples containing diatoms, phytoplankton, and macrophytes including *Chara* species will be transferred from Serbia to France and from Serbia to Norway. They will be used only for the purpose of the project (material for training, material used for contributing new sequences to the reference barcoding library, material used for scientific publications). Each Partner is responsible for compliance with the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization to the Convention on Biological Diversity.

Questionnaires and other surveys dealing with personal data used in the project has included a disclaimer informing participants on the purpose of data collection and the way the information is going to be further used within the scope of the project (e.g., confidentiality). Moreover, during the project lifespan, personal data in terms of video, sound, and images have been collected for the project reporting, and dissemination and communication purposes only after informing the attendees and obtaining their consent by signing the attendance list with an appropriate disclaimer.

7. Other issues

No other procedures for data management are foreseen.

HISTORY OF CHANGES		
VERSION	PUBLICATION DATE	CHANGE
1.0	23.03.2023	Initial version
2.0	29.03.2024	Updated version
3.0	25.07.2025	Revised version

QUALITY CONTROL		
ACTIVITY	NAME	DATE
V3.0 created	Dr Miloš Ćirić	01.07.2025
V3.0 reviewed	Dr Andreas Ballot, Dr Susanne Schneider, Dr Frédéric Rimet, Dr Danijela Vidaković	08.07.2025
V3.0 revised	Dr Vladimir Petrović, Dr Srđan Miletić, Kristina Petrović, Željka Milovanović	11.07.2025