



# FISH-FIT

## User documentation



Date: 09-10-2023

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## 1. FISH-FIT

**FISH-FIT** can be operated via desktop, tablet and smartphone. This user documentation uses the output on a desktop browser as a reference. The operating steps are analogously comprehensible for the other output devices tablet and smartphone.

You can reach the start page of FISH-FIT via the URL [www.fish-fit.org](http://www.fish-fit.org).

On the left side there is always the main menu, which in the unregistered state (see below: *Registration* as well as *Login/Logout*) allows the direct access to the start page via the FISH-FIT logo and provides information about the European funding program [INTERREG Atlantic Area](#), the general partners [Seatraces](#) and [Seatracenet](#) via the corresponding links, and presents further explanations about FISH-FIT via [About FISH-FIT](#) on an additional page *Info: About*. Additionally, a current version of the documentation can always be found in the [Documentation](#) section, under [How to use FISH-FIT](#).

Separated from the main menu, the logo of the [Max Rubner Institute](#), which runs FISH-FIT, on the right side leads to its website.

With eventual [News and updates](#) notes at the top of the page, scrolling to the bottom always leads to the corresponding links to [Contact](#), [Imprint](#), [Data policy](#) and [Terms of use](#).

This is concluded with a listing and corresponding linking of FISH-FIT partner institutions for authentic materials and DNA sequences in text and logo format (currently including: [Muséum National d'Histoire Naturelle \(MNHN\) \(Concarneau Marine Biology Station\)](#), [Le Mans Université](#), [AZTI | Ciencia y tecnología marina y alimentaria](#), [Instituto de Investigaciones Mariñas](#), [Liverpool John Moores University](#) and [Instituto Português do Mar e da Atmosfera, I.P. \(Portugal Lisboa\) \(Portuguese Institute of the Sea and the Atmosphere\)](#)).

## 2. Registration

Login data for the activation of the current provided FISH-FIT function blocks Families, Genera, Species, Samples, DNA sequences, Alignment search, Authentic materials, Material request and Method collection can be requested via the link [Registration](#) in the main menu. After correct completion of the mandatory fields (incorrect entries will be intercepted and noted accordingly), the registration will be summarized and an e-mail with a code to be confirmed will be

sent to the inquirer. On the part of FISH-FIT the data will be checked again manually, then the corresponding login data will be sent. **These data are to be kept well.** Depending on the assigned rights, certain function blocks and/or data sets are then enabled after a login.

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**SEATRACES**

INFO

- About FISH-FIT
- SeaTraceNet

ACCESS

- Registration**
- Login

DOCUMENTATION

- How to use FISH-FIT

**Access: Registration**

Please enter data ( mandatory)

Your name \*

Your email address  
(an email will be sent to confirm your registration request) \*

Retype your email address \*

Your password  
(min. of 8 characters, at least one uppercase, one lowercase, one digit and one special character) \*

Retype your password \*

Your phone

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Your phone

Name of organisation \*

Is the organisation private or public? \*

Street and number \*

Postal or ZIP code \*

City \*

Country \*

Comments

**FISH-FIT**

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Comments

Do you accept data policy and terms of use below? \*

Please select ...

**Request registration**

**Data policy**

Information about data protection in accordance with Article 13 and 14 General Data Protection Regulation (GDPR): use of the "FISH-FIT" online database

- Name of the processing activity**  
Personal data is processed for the purpose of activation as well as the use of the controller's "FISH-FIT" online database.
- Controller's name and contact details**  
**Prof. Dr. Pablo Steinberg**  
 Max Rubner-Institut  
 Federal Research Institute for Nutrition and Food  
 Haid-und-Neu-Str. 9  
 76131 Karlsruhe, Germany  
 Phone: +49 721 6625-0  
 Fax: +49 721 6625-111  
 Email: kontakt/poststelle@mri.bund.de
- Contact details of the data protection officer**

### 3. Login/Logout

Upon receipt of the login data, the username and password can be used via the separate link [Login](#). In addition, a redundant login mask is available via the start page in the **Login to start !** block. A warning message appears in the event of incorrect entries.

**FISH-FIT**

interreg Atlantic Area

**SEATRACES**

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Access: **Login**

Please enter username and password

Username

Password

**Login to FISH-FIT**

By logging in you accept the data policy and terms of use below.  
Lost your password? [Then request a password change with your email address.](#)

**Data policy**

Information about data protection in accordance with Article 13 and 14 General Data Protection Regulation (GDPR): use of the "FISH-FIT" online database

- Name of the processing activity**  
Personal data is processed for the purpose of activation as well as the use of the controller's "FISH-FIT" online database.
- Controller's name and contact details**  
**Prof. Dr. Pablo Steinberg**  
 Max Rubner-Institut

**FISH-FIT**

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**Seafood authentication tool for traceability and labelling**

**What is FISH-FIT ?**

FISH-FIT was created within the framework of *SEATRACES, an European Interreg Atlantic Area project: "Smart Traceability and Labeling ToolBox for a Sustainable Seafood Production"* to support EU control laboratories and institutions in seafood authenticity testing.

Traceability and labelling of fishery products are important prerequisites to combat illegal fishing, consumer deception and food fraud, which represent a serious risk to the economic development of the marine sector in the North Atlantic region. To uncover mislabelling and seafood fraud, mainly DNA-methods are used by control institutions for reliable species identification.

[► Read more about](#)

**Who can use FISH-FIT ?**

FISH-FIT was established for European control laboratories to facilitate their work in seafood identification.

Please note that currently **only public European control institutions** can register and access to FISH-FIT. Further opening to other institutions and laboratories may be considered after an initial phase of establishment.

To gain access to FISH-FIT, users need to fill in a registration form and wait for access permission. After successful registration, the content will be visible and authentic material can be requested.

[► Request registration](#)

**Login to start !**

Username \*

Password \*

By logging in you accept the [data policy](#) and [terms of use](#).

[Login](#)

Lost your password? [Then request a password change with your email address.](#)

If the password is lost on the user side, a password change can be initiated autonomously by the user specifying his or her email address after clicking the links ["Then request a password change with your email address."](#)

**FISH-FIT**

interreg Atlantic Area

**SEATRACES**

INFO

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ACCESS

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**Access: Registration (Password change: Step 1)**

Please enter data ( mandatory)

Your email address  
(an email will be sent to confirm your password change request) \*

Retype your email address \*

[Request password change](#)

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[Contact](#) [Imprint](#) [Data policy](#) [Terms of use](#)

The authentic material and DNA sequences are provided jointly by SEATRACES partners from France, Spain, UK, Portugal and Germany: [MNHN Marine Station Concarneau](#) ► [Le Mans Université](#) ► [AZTI](#) | Ciencia y tecnología marina y alimentaria ► [Instituto de Investigaciones Mariñas](#) ► [Liverpool John Moores University](#) ► [IPMA Portuguese Institute for Sea and Atmosphere](#) ► [Max Rubner-Institut](#)

After filling out, an email will be sent to the provided address with a code to confirm the password change request.

A successful login is confirmed with a corresponding page. Here and via the link changing from [Login](#) to [Logout](#) you can logout of the FISH-FIT session.

The screenshot shows the 'Logout' page of the FISH-FIT application. The page layout includes a sidebar on the left with navigation links under categories: INFO (About FISH-FIT, SeaTraceNet), ACCESS (Registration, Logout), TAXONOMY (Families, Genera, Species), SAMPLES (Samples), and SEQUENCES (DNA sequences). The main content area is titled 'Access: Logout' and features a large blue button labeled 'Press button to logout from FISH-FIT'. Below the button, there is a copyright notice: '2023 © FISH-FIT / Max Rubner-Institut'. To the right of the notice are links for 'Contact', 'Imprint', 'Data policy', and 'Terms of use'. A paragraph of text describes the joint provision of authentic material and DNA sequences by SEATRACES partners from France, Spain, UK, Portugal, and Germany, listing institutions like MNHN Marine Station Concarneau, Le Mans Université, AZTI, CIENCIA y tecnología marina y alimentaria, Instituto de Investigacions Mariñas, Liverpool John Moores University, and IPMA. At the bottom, logos for AZTI, CSIC, and IPMA are displayed.

## 4. Families

The screenshot displays the 'Taxonomy: Families' page. The main heading is 'Taxonomy: Families'. Below it, the text 'FISH-FIT families list:' is followed by a dropdown menu set to 'All' and a 'Filter' input field. A list of fish families is shown, each on a separate line with a small upward arrow to its left, indicating it can be expanded. The families listed are: Anguillidae, Buccinidae, Cancridae, Carangidae, Cardiidae, Citharidae, Clupeidae, Engraulidae, Gadidae, Littorinidae, and Loliginidae.

When logged in, you can reach the top level of the FISH-FIT taxonomy via the [Families](#) link. Here the families contained in FISH-FIT are listed page by page, whereby you can specify the entries displayed per page via a number filter under



FISH-FIT families list (with page switches at the end of the list). A filter on the right side can be used to search for specific entries.

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TAXONOMY

- Families**
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

**Taxonomy: Families**

FISH-FIT families list:

10

Family
<a href="#">Anguillidae</a>
<a href="#">Buccinidae</a>
<a href="#">Cancridae</a>
<a href="#">Carangidae</a>
<a href="#">Cardiidae</a>
<a href="#">Citharidae</a>
<a href="#">Clupeidae</a>
<a href="#">Engraulidae</a>
<a href="#">Gadidae</a>
<a href="#">Littorinidae</a>

Showing 1 to 10 of 32 families

< 1 2 3 4 >

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SEATRACES

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TAXONOMY

- Families**
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

**Taxonomy: Families**

FISH-FIT families list:

10

Family
<a href="#">Serranidae</a>
<a href="#">Carangidae</a>
<a href="#">Cancridae</a>
<a href="#">Anguillidae</a>

Showing 1 to 4 of 4 families (filtered from 32 total families)

< 1 >

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[Contact](#) [Imprint](#) [Data policy](#) [Terms of use](#)

The authentic material and DNA sequences are provided jointly by SEATRACES partners from France, Spain, UK, Portugal and Germany: MNHN Marine Station Concarneau ▶ Le Mans Université ▶ AZTI | Ciencia y tecnología marina y alimentaria ▶ Instituto de Investigaciones Marías ▶ Liverpool John Moores University ▶ IPMA Portuguese Institute for Sea and Atmosphere ▶ Max Rubner-Institut

By clicking on the column headers of the list (here: **Families**) the sorting can be determined *descending* (arrow down ▼) or *ascending* (arrow up ▲) for the respective column.

**This operating principle (if available) applies to all lists in FISH-FIT.**

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**SEATRACES**

**INFO**

- About FISH-FIT
- SeaTraceNet

**ACCESS**

- Registration
- Logout

**TAXONOMY**

- Families**
- Genera
- Species

**SAMPLES**

- Samples

**SEQUENCES**

- DNA sequences

**Taxonomy: Details for family Veneridae**

**BOLD information (boldsystems.org):**  
[BOLD](#)

**FishBase information (fishbase.de):**  
Not available

**Synonymized names:**  
 Arteminae, Callistinae, Callocardiinae, Circinae, Clementiinae, Dosiniinae, Gafraziidae, Gemminae, Gouldiinae, Lioconchinae, Oncophoridae, Pitarinae, Samarangiinae, Venerinae

**Containing FISH-FIT genera:**

All

Genus ^	Family
<a href="#">Dosinia</a>	Veneridae
<a href="#">Polittitapes</a>	Veneridae
<a href="#">Ruditapes</a>	Veneridae
<a href="#">Venus</a>	Veneridae

Showing 1 to 4 of 4 genera < 1 >

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**SEATRACES**

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**ACCESS**

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**TAXONOMY**

- Families**
- Genera
- Species

**SAMPLES**

- Samples

**SEQUENCES**

- DNA sequences

**FishBase information (fishbase.de):**  
Not available

**Containing FISH-FIT genera:**

All

Genus ^	Family
<a href="#">Dosinia</a>	Veneridae
<a href="#">Polittitapes</a>	Veneridae
<a href="#">Ruditapes</a>	Veneridae
<a href="#">Venus</a>	Veneridae

Showing 1 to 4 of 4 genera < 1 >

**FISH-FIT families list:**

All

Family ^
<a href="#">Anguillidae</a>
<a href="#">Buccinidae</a>

By clicking on a name in the list, further details for the family are displayed.

There are links to [BOLD](#) and [FishBase](#) available, synonymized names and the genera contained in FISH-FIT for the respective family in the already known list format with a redundant list of the FISH-FIT families.

**These redundant lists are appended for all function block detail pages, where appropriate.** Clicking on one of the included genera will take you directly to the relevant detail page.

In particular, the filter options can be used for each list individually.

FISH-FIT

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FishBase information (fishbase.de): **Not available**

Containing FISH-FIT genera:

Genus	Family
Dosinia	Veneridae

Showing 1 to 1 of 1 genera (filtered from 4 total genera)

FISH-FIT families list:

Family
Anguillidae
Carangidae

Showing 1 to 2 of 2 families (filtered from 32 total families)

## 5. Genera

FISH-FIT

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Taxonomy: **Genera**

FISH-FIT genera list:

Genus	Family
Aequipecten	Pectinidae
Allothunnus	Scombridae
Anguilla	Anguillidae
Boops	Sparidae
Brosme	Lotidae
Buccinum	Buccinidae
Cancer	Cancriidae
Cerastoderma	Cardiidae
Citharus	Citharidae
Dosinia	Veneridae
Engraulis	Engraulidae

The second level of the FISH-FIT taxonomy is accessed via the [Genera](#) link. Analogous to the presentation of the families, the genera contained in FISH-FIT are listed here. By clicking on a genus name you get to the corresponding detail page, which contains in addition to the information of the families corresponding [SeaLifeBase](#) information (if

available). Accordingly, the species contained for the selected genus (Containing FISH-FIT species) are listed. Clicking on one of the species (or the superordinate family) leads to the corresponding detail page.

**Taxonomy: Details for genus Gadus**

BOLD information (boldsystems.org): [BOLD](#)

FishBase information (fishbase.de): [FishBase](#)

SeaLifeBase information (sealifebase.org): [SeaLifeBase](#)

Synonymized names:  
Gadum, Morhua, Morrhua

Containing FISH-FIT species:

Species	Family	Genus
<a href="#">Gadus chalcogrammus</a>	Gadidae	Gadus
<a href="#">Gadus morhua</a>	Gadidae	Gadus

Showing 1 to 2 of 2 species

## 6. Species

**Taxonomy: Species**

FISH-FIT species list:

Species	Genus	Family
<a href="#">Aequipecten opercularis</a>	Aequipecten	Pectinidae
<a href="#">Allothunnus fallai</a>	Allothunnus	Scombridae
<a href="#">Anguilla anguilla</a>	Anguilla	Anguillidae
<a href="#">Boops boops</a>	Boops	Sparidae
<a href="#">Brosme brosme</a>	Brosme	Lotidae
<a href="#">Buccinum undatum</a>	Buccinum	Buccinidae
<a href="#">Cancer pagurus</a>	Cancer	Cancriidae
<a href="#">Cerastoderma edule</a>	Cerastoderma	Cardiidae
<a href="#">Citharus linguatula</a>	Citharus	Citharidae
<a href="#">Dosinia exoleta</a>	Dosinia	Veneridae
<a href="#">Engraulis encrasicolus</a>	Engraulis	Engraulidae

The lowest level of the taxonomy are the species, which are accessed via the link [Species](#). In the relevant species details, among other data already discussed, containing samples can be reached directly, sequences (FASTA format)

including information on the gene markers are provided, and in addition, authentic materials are linked and their availability can be obtained.

The screenshot displays the 'Taxonomy: Details for species *Epinephelus marginatus*' page. On the left is a navigation menu with categories: TAXONOMY (Families, Genera, Species), SAMPLES (Samples), SEQUENCES (DNA sequences), UTILITIES (Alignment search), BIOBANK (Authentic materials, Material request), METHODS (Method collection), and DOCUMENTATION (How to use FISH-FIT). The main content area includes:

- BOLD information (boldsystems.org):** A blue 'BOLD' button.
- FishBase information (fishbase.de):** A blue 'FishBase' button.
- SeaLifeBase information (sealifebase.org):** A red 'Not available' button.
- Synonymized names:** A list of related species names including *Cerna gigas*, *Cernua gigas*, *Epinephelus brachysoma*, *Epinephelus gigas*, *Epinephelus guaza*, *Holocentrus gigas*, *Mycteroperca marginata*, *Perca gigas*, *Serranus aspersus*, *Serranus cernioides*, *Serranus fimbriatus*, *Serranus gigas*, and *Serranus marginatus*.
- Containing FISH-FIT samples:** A table with a filter dropdown set to 'All'. The table lists two samples:

Sample	DNA sequences	Authentic material	Species	Family	Genus
AZTL_GPD003	COI	Available <a href="#">AZTL_GPD003</a>	<i>Epinephelus marginatus</i>	Serranidae	Epinephelus
AZTL_GPD004	COI	<a href="#">AZTL_GPD004</a>	<i>Epinephelus marginatus</i>	Serranidae	Epinephelus

Showing 1 to 2 of 2 samples

## 7. Samples

The listing of the species samples contained in FISH-FIT can be accessed via the link [Samples](#).

The screenshot displays the 'Samples' page. The navigation menu is identical to the previous screenshot. The main content area shows:

- FISH-FIT samples list:** A filter dropdown set to 'All' and a search filter set to 'mri'.
- Table of samples:**

Sample	Species	Family	Genus	DNA sequences	Authentic material
MRI_A275	<i>Limanda limanda</i>	Pleuronectidae	Limanda	COI cyt b	<a href="#">MRI_A275</a>
MRI_A277	<i>Merlangius merlangus</i>	Gadidae	Merlangius	cyt b COI	<a href="#">MRI_A277</a>
MRI_A279	<i>Gadus morhua</i>	Gadidae	Gadus	cyt b COI	<a href="#">MRI_A279</a>
MRI_A280	<i>Mullus surmuletus</i>	Mullidae	Mullus	cyt b COI	<a href="#">MRI_A280</a>
MRI_A286	<i>Hippoglossoides platessoides</i>	Pleuronectidae	Hippoglossoides	cyt b COI	<a href="#">MRI_A286</a>
MRI_A294	<i>Platichthys flesus</i>	Pleuronectidae	Platichthys	cyt b COI	<a href="#">MRI_A294</a>
MRI_A296	<i>Scophthalmus maximus</i>	Scophthalmidae	Scophthalmus	cyt b	<a href="#">MRI_A296</a>
MRI_A297	<i>Sander lucioperca</i>	Percidae	Sander	cyt b COI	<a href="#">MRI_A297</a>
MRI_A329	<i>Scophthalmus maximus</i>	Scophthalmidae	Scophthalmus	cyt b 16S	<a href="#">MRI_A329</a>
MRI_A340	<i>Pleuronectes platessa</i>	Pleuronectidae	Pleuronectes	cyt b COI	<a href="#">MRI_A340</a>
MRI_A363	<i>Microstomus kitt</i>	Pleuronectidae	Microstomus	cyt b COI	<a href="#">MRI_A363</a>

The sample name (Sample) leads to the detail page, which provides detailed information on morphological identification, assigned institute, production method and fishing method, included FASTA sequences with marker, length, PCR protocol and primers, authentic materials with availability status, quality and storage conditions as well as the information whether the sample is subject to special requirements concerning the Nagoya Protocol.

The **PDF version** button can be used to print or save the above information in PDF format (see the illustrations at the end of this section).

**Containing DNA sequence 1:** MRI\_A329\_CYT B  
 Marker: Cytochrome b  
 Length: 414 bp

**PCR protocol:**  
 Initial denaturation: 95°/5'; denaturation: 94°/0.40 min; annealing: 50°/1.20 min; amplification: 72°/1.20 min; 35 cycles; final elongation: 72°/5 min.

**Sequence in FASTA format:**  
 >MRI\_A329\_CYT B  
 CAGGGAACCTTAATGACCAGCCTACGAAAATCCACCCTATCCTAAAGATCGAAATGATGCTTTAGTAGATCCCTGCCCCCTCTAATATCTCAGTTTGATGAAACTTTGCTCTCT  
 TCTTGCCCTCTGCTTAGCCACTCAACTCATTACCGGACTCTTTTAGCTATGCACTATACCGGGATATCGCAACAGCCTTTACCTCGTCGCCCATATCACCCGAGACGTTAATACG  
 GTTGATTAATCGGAAACCTACACGCCAACGGGGCATCCTTCTTCTTATGTATTTATGCACATATCGGCCGAGGTCTGTACTACGGCTCTTACCTTTATAAAGAAACCTGAAACGTG  
 GGAGTTATCCTTCTTCTCGTTATAGCAACTGCCTTCGTCCGCTATGTTCTTCC

**Primers:**  
 Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN CEN/ TS 17303


**Forward primer 1:** L14735-M13-24F:  
 5' - CCAGGTTTTCCAGTCACGAAAACCCAGCTTGTATTCAACTA - 3'

**Reverse primer 1:** H15149ad-M13-24R:  
 5' - CGGATAACAATTTACACAGGGCICCTCARAATGAYATTTGCTCCTA - 3'


**Containing DNA sequence 2:** MRI\_A329\_16S.M13-24F  
 Marker: 16S  
 Length: 583 bp

**PCR protocol:**  
 Initial denaturation: 95°/5 min; denaturation: 94°/1 min; annealing: 55°/1 min; amplification: 72°/1 min; 35 cycles; final elongation: 72°/10 min

This is completed by an image gallery with thumbnails and full images as well as the possibility to add authentic sample material to a material request (**Add ... to material request**) for external institutes (see below: *Authentic materials*).



**FISH-FIT**



- TAXONOMY
  - Families
  - Genera
  - Species
- SAMPLES
  - **Samples**
- SEQUENCES
  - DNA sequences
- UTILITIES
  - Alignment search
- BIOBANK
  - Authentic materials
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- METHODS
  - Method collection
- DOCUMENTATION
  - How to use FISH-FIT

**Containing authentic material 1: MRI\_A329**

Available

Quantity: 2000 mg

Quality:

\*AM




1. The laboratory is / is not accredited.
2. The origin of the seafood sample is not traceable (for example caught by research vessel with all catch data).
3. The identity of the seafood sample is specified by PCR sequence analysis with only one reliable gene marker (for example: cyt b or COI).


Storing conditions:  
-80 ° C, Ethanol & -20 ° C

Permission required under the Nagoya Protocol?  
No


Add MRI\_A329 to material request

**Images**



**FISH-FIT**



- TAXONOMY
  - Families
  - Genera
  - Species
- SAMPLES
  - **Samples**
- SEQUENCES
  - DNA sequences
- UTILITIES
  - Alignment search
- BIOBANK
  - Authentic materials
  - Material request
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  - Method collection
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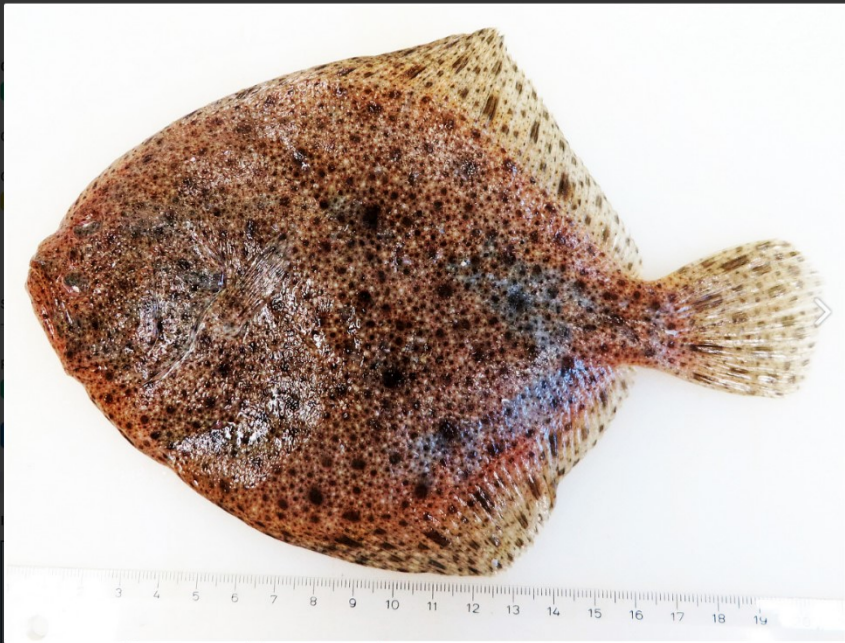
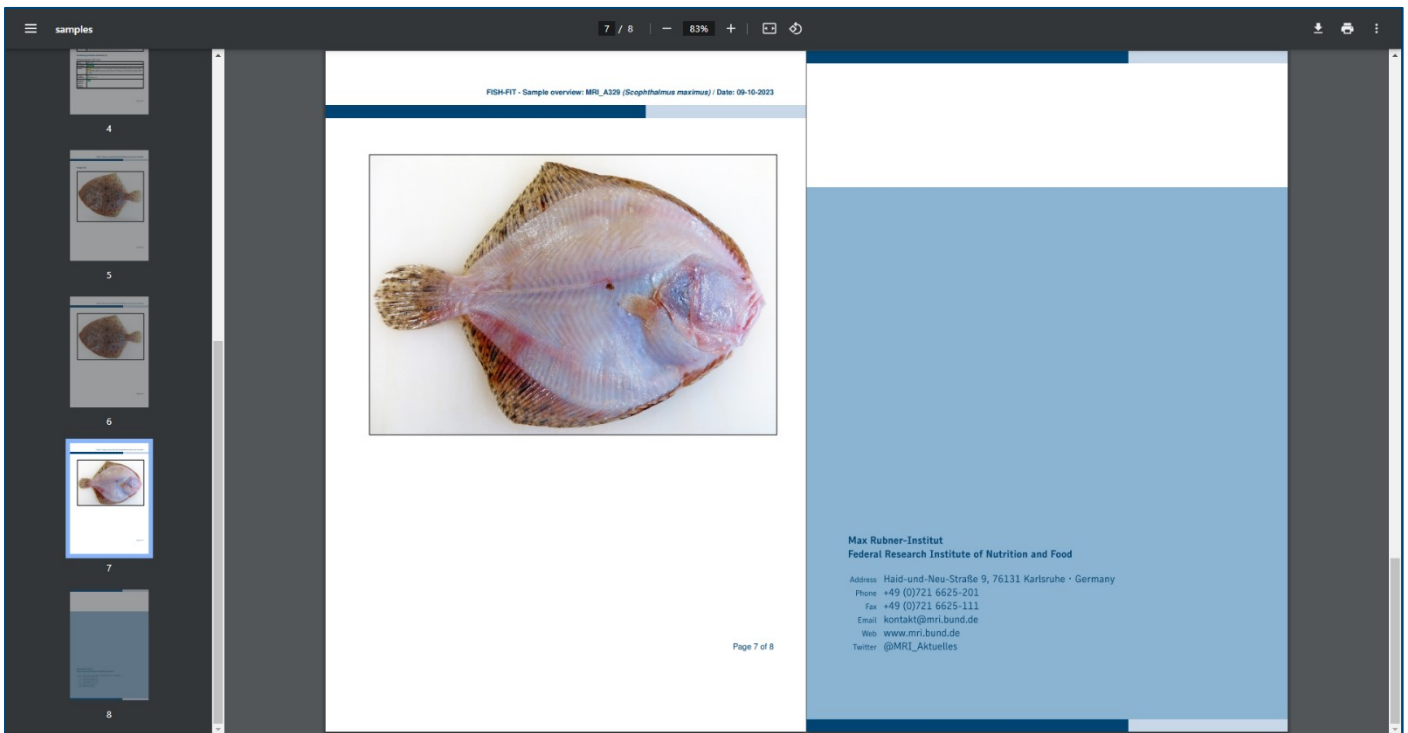
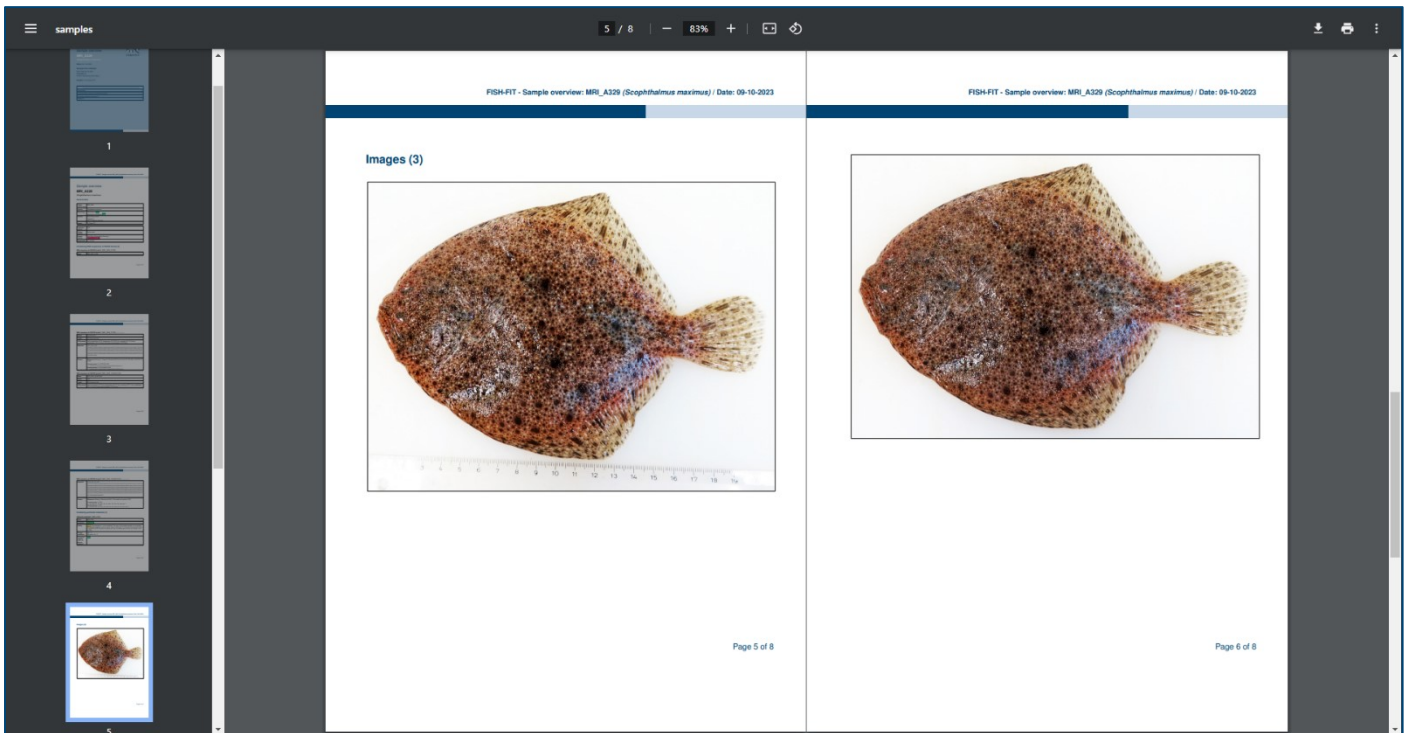


Image 1 of 3

PDF version (of details for sample MRI\_329):





## 8. DNA sequences

A dedicated overview of the DNA sequences (in FASTA format) contained in FISH-FIT can be obtained by clicking on the link [DNA sequences](#). This offers a condensed listing of the sample sequences with somewhat thinned out information compared to the sample detail pages, which can be accessed by clicking on the relevant sequence name (Sequence).

## 9. Alignment search

The [Alignment search](#) link calls up the module for sequence alignment.

A single sequence in FASTA format can be entered in the input field, which is variable in height; any incorrect entries are intercepted and noted accordingly.

By calling **Search alignments**, the relevant alignments are listed in descending order up to a quality of currently 85% with the corresponding DNA sequences contained in FISH-FIT. (The [SIMD Smith-Waterman C/C++ library by Zhao et al., 2013](#), serves as the basis for this). Besides the Alignment quality the results include the Target sample, the Target sequence marker, the Target species, the Target length and Query length as well the Query cover.

**Gaps** and **Mismatches** are highlighted accordingly and counted both individually and in coherent groups (... of ... coherent)

C/C++ library for use in genomic applications. *PloS one*, 8(12), e82138.

Target sample: **IIM\_MBIL2**

Target sequence marker: Cytochrome b

Target species: *Merluccius bilinearis*

Target length: 413 bp / Query length: 1138 bp / Query cover: 35,33%

Alignment quality: **98,75%** with bad query cover of **35,33%**

Gaps: **3 of 1 coherent** / Mismatches: **2 of 2 coherent**

Target:	12	ATGGCCAGCCTCGAAAAACCCACCCCTCCTAAAGATCGTAATGACGCATTAGTAGAC	71
Query:	1	ATAGCCAGCCTCCG--AAACCCACCCCTCCTAAAGATCGTAATGACGCATTAGTAGAC	57
Target:	72	CTGCCTGCCCCCTCCAACATCTCGACATGATGAACTTTGGGTCTCTTTAGGCCTCTGT	131
Query:	58	CTGCCTGCCCCCTCCAACATCTCGACATGATGAACTTTGGGTCTCTTTAGGCCTCTGT	117
Target:	132	CTAGCGGCCAAATCCTAACAGGACTATTTTAGCAATACACTACACCGCAAACGTCGAA	191
Query:	118	CTAGCGGCCAAATCCTAACAGGACTATTTTAGCAATACACTACACCGCAAACGTCGAA	177
Target:	192	ATAGCCTTCTCATCCGTCGTACACATCTGCCGCGACGTAATAATGGATGACTAATTCGC	251
Query:	178	ATAGCCTTCTCATCCGTCGTACACATCTGCCGCGACGTAATAATGGATGACTAATTCGC	237

Target sample: **AZTL\_HKE003**

Target sequence marker: Cytochrome b

Target species: *Merluccius merluccius*

Target length: 414 bp / Query length: 1138 bp / Query cover: 35,24%

Alignment quality: **88,00%** with bad query cover of **35,24%**

Gaps: **3 of 1 coherent** / Mismatches: **45 of 42 coherent**

Target:	373	CTTTTAGTAAATGACCGCTTCGTAGGTACGTCCTCCC	413
Query:	358	CTCCTAGTTATAATGACCGCTTCGTAGGTACGTCCTCCC	398
Target:	13	ATGGCCAGCCTCGAAAAACTCATCCCTCCTAAAGATTGTAATGATGACATTAGTAGAC	72
Query:	1	ATAGCCAGCCTCCG--AAACCCACCCCTCCTAAAGATCGTAATGACGCATTAGTAGAC	57
Target:	73	CTTCTGCCCCCTCAACCTCTCAACATTATGAACTTCGGGTCTCTCTAGGCCTCTGC	132
Query:	58	CTGCCTGCCCCCTCCAACATCTCGACATGATGAACTTTGGGTCTCTTTAGGCCTCTGT	117
Target:	133	TTAGCGGCCAAATCCTAACAGGCTATTTTAGCGATACATTATACCGCAAACGTCGAG	192
Query:	118	CTAGCGGCCAAATCCTAACAGGACTATTTTAGCAATACACTACACCGCAAACGTCGAA	177
Target:	193	ATAGCTTCTCATCCGTCGTACACATCTGCCGCGACGTAATAATGGATGACTAATTCGC	252

## 10. Authentic materials

If the focus is on the authentic materials of FISH-FIT, you can access the corresponding and dedicated overview for this context via the link [Authentic materials](#). Here, too, all relevant data sets (with availability status) are listed in a condensed view and a thinned out detail pages are provided. On those pages, sample material can also be added to a material request for external institutions via the link **Add ... to material request**.

**Biobank: Authentic materials**

FISH-FIT authentic materials list:

All Filter

Material	Sample	Available quantity	Quality	Storage conditions	Nagoya	Species	Family	Genus
AZTI_ALB001	AZTI_ALB001	210 mg	*AM	RNAlater & -20 ° C	No	<i>Thunnus alalunga</i>	Scombridae	Thunnus
AZTI_ALB002	AZTI_ALB002	230 mg	*AM	No permission required	No	<i>Thunnus alalunga</i>	Scombridae	Thunnus
AZTI_ALB003	AZTI_ALB003	450 mg	*AM	RNAlater & -20 ° C	No	<i>Thunnus alalunga</i>	Scombridae	Thunnus
AZTI_ALB048	AZTI_ALB048	500 mg	*AM	RNAlater & -20 ° C	No	<i>Thunnus alalunga</i>	Scombridae	Thunnus
AZTI_ALB050	AZTI_ALB050	300 mg	**AM	RNAlater & -20 ° C	No	<i>Thunnus alalunga</i>	Scombridae	Thunnus
AZTI_ALK003	AZTI_ALK003	450 mg	*AM	RNAlater & -20 ° C	No	<i>Gadus chalcogrammus</i>	Gadidae	Gadus
AZTI_ANE2001	AZTI_ANE2001	400 mg	*AM	RNAlater & -20 ° C	No	<i>Engraulis encrasicolus</i>	Engraulidae	Engraulis

LJMU_OM_1	LJMU_OM_1	300 mg	*AM	Ethanol & -20 ° C	No	<i>Oblada melanura</i>	Sparidae	Oblada
LJMU_OM_2	LJMU_OM_2	250 mg	*AM	Ethanol & -20 ° C	No	<i>Oblada melanura</i>	Sparidae	Oblada
LJMU_PE_1	LJMU_PE_1	100 mg	*AM	Ethanol & -20 ° C	No	<i>Pagellus erythrinus</i>	Sparidae	Pagellus
LJMU_PE_2	LJMU_PE_2	100 mg	*AM	Ethanol & -20 ° C	No	<i>Pagellus erythrinus</i>	Sparidae	Pagellus
LJMU_SP_1	LJMU_SP_1	250 mg	*AM	Ethanol & -20 ° C	No	<i>Sardina pilchardus</i>	Clupeidae	Sardina
LJMU_SP_2	LJMU_SP_3	250 mg	*AM	Ethanol & -20 ° C	No	<i>Sardina pilchardus</i>	Clupeidae	Sardina
LJMU_TE_1	LJMU_TE_1	20 mg	*AM	Ethanol & -20 ° C	No	<i>Trisopterus esmarkii</i>	Gadidae	Trisopterus
LJMU_TE_3	LJMU_TE_3	30 mg	*AM	Ethanol & -20 ° C	No	<i>Trisopterus esmarkii</i>	Gadidae	Trisopterus
MNHN_Spau_CC11	MNHN_Spau_CC11	500 mg	*AM	Ethanol & -20 ° C	Required	<i>Sparus aurata</i>	Sparidae	Sparus
MNHN_Spau_CC16	MNHN_Spau_CC16	760 mg	*AM	Ethanol & -20 ° C	Required	<i>Sparus aurata</i>	Sparidae	Sparus
MNHN_Spau_CC30	MNHN_Spau_CC30	270 mg	*AM	Ethanol & -20 ° C	Required	<i>Sparus aurata</i>	Sparidae	Sparus
MNHN_ST037	MNHN_ST037	650 mg	*AM	Ethanol & -20 ° C	Required	<i>Magallana gigas</i>	Ostreidae	Magallana
MNHN_ST042	MNHN_ST042	300 mg	*AM	Ethanol & -20 ° C	Required	<i>Magallana gigas</i>	Ostreidae	Magallana
MNHN_ST063	MNHN_ST063	1100 mg	*AM	-80 ° C	Required	<i>Ostrea edulis</i>	Ostreidae	Ostrea
MNHN_ST070	MNHN_ST070	1200 mg	*AM	-80 ° C	Required	<i>Magallana angulata</i>	Ostreidae	Magallana
MNHN_ST133	MNHN_ST133	1700 mg	*AM	-80 ° C	Required	<i>Pecten maximus</i>	Pectinidae	Pecten

The laboratory is / is not accredited. The origin of the seafood sample is not traceable (for example caught by research vessel with all catch data). The identity of the seafood sample is specified by PCR sequence analysis with only one reliable gene marker (for example: cyt b or COI).

## 11. Material request

By clicking on the link **Add ... to material request** within a detail page for samples or authentic material, the corresponding material is collected on the designated material request (always accessible by clicking on [Material request](#)). **It should be noted here that currently a maximum of three materials may be contained in one login session; this is indicated accordingly.**

The screenshot shows the FISH-FIT interface with a sidebar on the left containing navigation menus: TAXONOMY (Families, Genera, Species), SAMPLES (Samples), SEQUENCES (DNA sequences), UTILITIES (Alignment search), BIOBANK (Authentic materials, Material request), METHODS (Method collection), and DOCUMENTATION (How to use FISH-FIT). The main content area displays a list of materials with columns for 'Remove', 'Material ID', 'Quantity', 'Quality', 'Storage conditions', 'Nagoya', 'Species', 'Family', and 'Genus'. Two materials are visible: MRL\_A277 (5000 mg, 15 mg quality, -80 °C Ethanol & -20 °C, No, merlangius merlangus, Gadidae, merlangius) and MRL\_A279 (5000 mg, 10 mg quality, -80 °C Ethanol & -20 °C, No, Gadus morhua, Gadidae, Gadus). Below the list is a registration form with fields for: Your name (John Doe), Your email address (john@doe-institute.tld), Retype your email address (john@doe-institute.tld), Your phone (+00 000 000 000 000), Name of organisation (Doe Institute), Is the organisation private or public? (Public), and Street and number (Doe Street 0).

With **Remove** a material can be removed from the list, and the **Intended quantity** can be limited upwards by definition in FISH-FIT. Also here the values are intercepted accordingly.

With **Save status of material request** the material request can be saved during the login session, so that among other things like name, email address etc. (which are pre-filled from the stored registration and still changeable subsequently), the values for the desired quantities do not have to be entered again when adding another material.

Analogous to the registration process (see above: *Registration*), the request for the authentic materials can be initiated via **Request material** after carefully reading the legal requirements and references to the Nagoya Protocol.

The screenshot shows the FISH-FIT interface with the sidebar on the left. The main content area displays the 'Request material' form. It includes a 'Comments' field with the text 'Example.', a dropdown menu for 'Do you accept the "Data policy" and "Terms of use" below?' with the selected option 'Yes, I accept the data policy and terms of use.', and two links for 'Data policy' and 'Terms of use'. A blue 'Request material' button is located below the form. Below the button is a section titled 'FISH-FIT authentic materials list:' with a dropdown menu set to '10' and a 'Filter' button. A table of materials is displayed below, with columns: Material, Sample, Quantity, Quality, Storage conditions, Nagoya, Species, Family, and Genus. The first row shows a material with Sample 'AZTL-ALB001', Quantity '210 mg', Quality '\*\*\*', Storage conditions 'DNA later & -20 °C', Nagoya status '?', Species 'Thynnus alalunga', Family 'Scombridae', and Genus 'Thynnus'.

## The materials may only be used for taxonomic verification.

After correct completion of the mandatory fields (incorrect entries will also be intercepted and noted here) and acceptance of the legal requirements, the material request is summarized and an email with a code to be confirmed as well as a PDF attachment (RECOGNITION STATEMENT ON TISSUE MATERIAL TRANSFER) to be filled, signed and returned is sent to the requesting person or institution. After further verification by FISH-FIT, the request is responded to accordingly and further communication will be started.

## 12. Method collection

An overview of the methods stored in FISH-FIT can be reached via the [Method collection](#) link.

The screenshot displays the 'Method collection' interface. On the left is a sidebar with a navigation menu. The main content area is titled 'Method collection' and shows a list of 8 methods under the heading 'Standard operation procedures (SOPs)'. Each method entry includes a title, a 'Format' column with a 'PDF' button, and a 'Filter' input field. The methods listed are:

- Simple seafood sample analysis decision tree
- Standard Operating Procedure for the detection/authentication of *Octopus vulgaris* in foodstuffs by Recombinase Polymerase Amplification (RPA) and Lateral Flow assay (LFA)
- Standard Operating Procedure for the genetic identification of crustacean species using cytochrome c oxidase I and 16S rRNA gene segments
- Standard Operating Procedure for the genetic identification of fish species using DNA barcoding (mitochondrial cytochrome-c-oxidase I sequencing)
- Standard Operation Procedure FISH-FIT
- Standard Operation Procedure for the Identification of *Mytilus* species by Melting Curve Analysis
- Standard Operation Procedure for the identification of scallops species
- Standard Operation Procedure for the Identification of the geographic origin of *Mytilus galloprovincialis*



The page also features a sidebar with navigation options like 'Taxonomy', 'Samples', 'Sequences', 'Utilities', 'Biobank', 'Methods', and 'Documentation'.

There the methods are listed in currently six groups:

1. Standard operation procedures (SOPs)
2. Official methods (ISO, CEN, DIN, §64 LFGB Methodensammlung (German only), BaTAns, publications)
3. Links to projects
4. Seatraces publications
5. Labelfish publications
6. Publications of interest

Clicking on the accompanying method, project or publication name links, you can access the respective detail page, which shows further information such as a short description, corresponding copyright, additional literature references and/or DOIs, depending on the method group concerned.

If available, a thumbnail (preview) on the detail page can be used to open resp. download the corresponding PDF file of the method. The same effect can be achieved in the overview by clicking on the PDF link **PDF** under **Format**.

TAXONOMY

- Families
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

UTILITIES

- Alignment search

BIOBANK

- Authentic materials
- Material request

METHODS

- Method collection

DOCUMENTATION

- How to use FISH-FIT

Standard Operation Procedure for the identification of scallops species PDF

Standard Operation Procedure for the Identification of the geographic origin of *Mytilus galloprovincialis* PDF

Showing 1 to 8 of 8 methods < 1 >

Official methods (ISO, CEN, DIN, §64 LFGB Methodensammlung (German only), BaTAns, publications):



All ▾
Filter

Method ▾	URL
BaTAns Table	<a href="https://www.bvl.bund.de/DE/Arbeitsbereiche/09_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungsverfahren/untersuchungen...">https://www.bvl.bund.de/DE/Arbeitsbereiche/09_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungsverfahren/untersuchungen...</a>
CEN /TS 17303 - English version	<a href="https://www.en-standard.eu/din-cen-ts-17303-foodstuffs-dna-barcoding-of-fish-and-fish-products-using-defined-mitochondrial-cytochrome-b-and-cyto...">https://www.en-standard.eu/din-cen-ts-17303-foodstuffs-dna-barcoding-of-fish-and-fish-products-using-defined-mitochondrial-cytochrome-b-and-cyto...</a>
DIN CEN /TS 17303 - Deutsche Version	<a href="https://www.beuth.de/de/technische-regel/din-cen-ts-17303/290395887">https://www.beuth.de/de/technische-regel/din-cen-ts-17303/290395887</a>
§64 LFGB Methodensammlung BVL	<a href="https://www.methodensammlung-bvl.de/de">https://www.methodensammlung-bvl.de/de</a>

Showing 1 to 4 of 4 methods < 1 >

Links to projects:

All ▾
Filter

TAXONOMY

- Families
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

UTILITIES

- Alignment search

BIOBANK

- Authentic materials
- Material request

METHODS

- Method collection

DOCUMENTATION

- How to use FISH-FIT



Publications of interest:

All ▾
Filter

Publication ▾	Content
Ali et al., 2022	Yellowfin tuna LAMP
Carreiro et al., 2023	Tuna DNA sequencing
del Socorro Toxqui Rodríguez et al., 2023	Seafood metabarcoding nanopore
Frigerio et al., 2022	RPA-LFA mackerel
Giusti et al., 2023	Seafood mislabelling in Italy
Kappel and Schröder, 2020	Snapper barcoding
Prasetyo et al., 2022	Closed-tube barcoding ray and sharks
Varunjikar et al., 2022	Seafood proteomics and DNaseq
Vinas and Tudela, 2009	Tuna DNA sequencing
Yao et al., 2022	Patagonian toothfish real-time PCR

Showing 1 to 11 of 11 publications < 1 >



TAXONOMY

- Families
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

UTILITIES

- Alignment search

BIOBANK

- Authentic materials
- Material request

METHODS

- Method collection


DOCUMENTATION

- How to use FISH-FIT

### Details for method

**Name:**  
Simple seafood sample analysis decision tree

**Copyright:**  
SEATRACES Consortium 2021



Click on image to show the method PDF



**Description:**

A simple decision tree has been developed as an instructional tool and provides an overview of how to analyse seafood samples at a given stage of processing.

The processing degree of the seafood sample is important for the choice of analysis: If it is fresh, frozen, smoked or cooked, then universal gene markers and universally applied PCR protocols for seafood without any restrictions on the fragment length can be used. However, if the seafood product is canned, then specific primers and protocols amplifying shorter fragments need to be used as the high temperatures during the sterilization process lead to a high DNA degradation into short fragments of app. ≤ 200 bp.

As a strategic approach, it is recommended to first check the taxonomy of the species – if it is labelled - in specific databases in order to decide on the most promising gene marker with the largest number of available sequences in databases.

Additional literature:

TAXONOMY

- Families
- Genera
- Species

SAMPLES

- Samples

SEQUENCES

- DNA sequences

UTILITIES

- Alignment search

BIOBANK


- Authentic materials
- Material request

METHODS

- Method collection

DOCUMENTATION

- How to use FISH-FIT



Click on image to show the method PDF

As a strategic approach, it is recommended to first check the taxonomy of the species – if it is labelled - in specific databases in order to decide on the most promising gene marker with the largest number of available sequences in databases.

Additional literature:

All ▾
Filter

Name ^	Info	URL
<a href="#">A universal DNA mini-barcode for biodiversity analysis</a>	Meusnier, I., Singer, G.A., Landry, J.F. et al. A universal DNA mini-barcode for biodiversity analysis. <i>BMC Genomics</i> . 9, 214 (2008).	<a href="https://doi.org/10.1186/1471-2164-9-214">https://doi.org/10.1186/1471-2164-9-214</a>
<a href="#">Advances in DNA metabarcoding for food and wildlife forensic species identification</a>	Staats, M., Arulandhu, A.J., Gravendeel, B. et al. Advances in DNA metabarcoding for food and wildlife forensic species identification. <i>Anal Bioanal Chem</i> 408, 4615–4630 (2016).	<a href="https://doi.org/10.1007/s00216-016-9595-8">https://doi.org/10.1007/s00216-016-9595-8</a>
<a href="#">DNA primers for amplification of mitochondrial cytochrome c oxidase subunit from diverse metazoan invertebrates</a>	Folmer, O., Black, M., Hoeh, W., Lutz, R. and Vrijenhoek, R.: DNA primers for amplification of mitochondrial cytochrome c oxidase subunit from diverse metazoan invertebrates. <i>Molecular marine Biology and Biotechnology</i> (1994), 3 (5), 294-299.	<a href="https://pubmed.ncbi.nlm.nih.gov/7881515">https://pubmed.ncbi.nlm.nih.gov/7881515</a>
<a href="#">Enhanced primers for amplification</a>	Lobo, J., Costa, P.M., Teixeira, M.A. et al. Enhanced	<a href="https://doi.org/10.1186/1472-6785-13-34">https://doi.org/10.1186/1472-6785-13-34</a>

**Max Rubner-Institut (MRI)**  
**Federal Research Institute of Nutrition and Food**

Email [fish-fit@mri.bund.de](mailto:fish-fit@mri.bund.de)

Web [www.fish-fit.org](http://www.fish-fit.org)