





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.

FISH-FIT			Max Rubner-Institut
		North Andrews	FISH-FIT Seafood authentication tool for traceability and labelling
DOCUMENTATION	News and updates		
How to use FISH-FIT	New updated user documentation available!		
	What is FISH-FIT ?	Who can use FISH-FIT ?	Login to start !
	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	FISH-FIT was established for European control laboratories to facilitate their work in seafood identification. Please note that currently only public European	Username *
	authenticity testing.	control institutions can register and access to FISH-FIT. Further opening to other institutions and	By logging in you accept the data policy and terms

You can reach the start page of FISH-FIT via the URL 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 <u>INTERREG Atlantic Area</u>, the general partners <u>Seatraces</u> and <u>Seatracenet</u> via the corresponding links, and presents further explanations about FISH-FIT via <u>About FISH-FIT</u> on an additional page *Info: About*. Additionally, a current version of the documentation can always be found in the <u>Documentation</u> section, under <u>How to</u> <u>use FISH-FIT</u>.

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 <u>Contact</u>, <u>Imprint</u>, <u>Data policy</u> and <u>Terms of use</u>.

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: <u>Muséum National d'Histoire Naturelle (MNHN) (Concar-neau Marine Biology Station</u>), <u>Le Mans Université</u>, <u>AZTI | Ciencia y tecnología marina y alimentaria</u>, <u>Instituto de Investigacións Mariñas</u>, <u>Liverpool John Moores University</u> and <u>Instituto Português do Mar e da Atmosfera</u>, <u>I.P. (Portugues Institute of the Sea and the Atmosphere</u>).





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 <u>Registration</u> 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.

FISH-FIT		Max Rubner-Institut
SEATRACES	Access: Registration	
INFO About FISH-FIT	Please enter data (mandatory)	
SeaTraceNet ACCESS	Your name *	
Registration Login	Your email address (an email will be sent to confirm your registration request) *	
How to use FISH-FIT	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 *	
FISH-FIT		MRI 🗱 Max Rubner-Institut
Vinterreg		
SEATRACES	Your phone	
	Your phone	
INFO About FISH-FIT	Your phone Name of organisation *	
INFO About FISH-FIT SeaTraceNet ACCESS	Your phone Name of organisation * Is the organisation private or public? * Please select	
INFO About FISH-FIT SeaTraceNet ACCESS Registration Login	Your phone Name of organisation * Is the organisation private or public? * Please select Street and number *	· · · · · · · · · · · · · · · · · · ·
INFO About FISH-FIT SeaTraceNet ACCESS Registration Login DOCUMENTATION How to use FISH-FIT	Your phone Name of organisation * Is the organisation private or public? * Please select Street and number *	· · · · · · · · · · · · · · · · · · ·
INFO About FISH-FIT SeaTraceNet ACCESS Registration Login DOCUMENTATION How to use FISH-FIT	Your phone Name of organisation * Is the organisation private or public? * Please select Street and number *	· · · · · · · · · · · · · · · · · · ·
INFO About FISH-FIT SeaTraceNet ACCESS Registration Login DOCUMENTATION How to use FISH-FIT	Your phone Name of organisation * Is the organisation private or public? * Please select Street and number * C City * City * Country *	
INFO About FISH-FIT SeaTraceNet ACCESS Registration Login DOCUMENTATION How to use FISH-FIT	Your phone	

FISH-FIT		MRI 🐲 Max Rubner-Institut
SEATRACES	Comments	
INFO		
SeaTraceNet	Do you accept data policy and terms of use below? * Please select	~
• Registration	Request registration	
• Login		
DOCUMENTATION	Data policy	
 How to use FISH-FIT 	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. 	
	2. 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	

3. Login/Logout

Upon receipt of the login data, the username and password can be used via the separate link <u>Login</u>. In addition, a redundant login mask is available via the start page in the <u>Login to start !</u> block. A warning message appears in the event of incorrect entries.

FISH-FIT	MRI 🚝 Max Rubner-Institut
	Access: Login
INFO About FISH-FIT	Please enter username and password
SeaTraceNet ACCESS	Username
Registration Login	Password
• How to use FISH-FIT	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

FISH-FIT			MRI A Max Rubner-Ins
SEATRACES		JOANY	Seafood authentication tool for traceability and labelling
INFO			
 About FISH-FIT 	What is FISH-FIT ?	Who can use FISH-FIT ?	Login to start !
 SeaTraceNet 	FISH-FIT was created within the framework of	FISH-FIT was established for European control	Username *
ACCESS	SEATRACES, an European Interreg Atlantic Area	laboratories to facilitate their work in seafood	
 Registration 	project: Smart Traceability and Labeling ToolBox for a Sustainable Seafood Production" to support	identification.	Password *
- Login	EU control laboratories and institutions in seafood authenticity testing.	Please note that currently only public European control institutions can register and access to	
DOCUMENTATION	Teasachility and taballing of fishery and usta and	FISH-FIT. Further opening to other institutions and	By logging in you accept the data policy and terms
 How to use FISH-FIT 	important prerequisites to combat illegal fishing,	phase of establishment.	of use.
	consumer deception and food fraud, which		Login
	represent a serious risk to the economic	To gain access to FISH-FIT, users need to fill in a	
	development of the marine sector in the North	registration form and wait for access permission. After successful registration, the content will be	
	seafood fraud, mainly DNA-methods are used by control institutions for reliable species	visible and authentic material can be requested.	
	Identification.		Lost your password? Then request a password
		Request registration	change with your email address.
	Read more about		

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	Max Rubner-Institut
	Access: Registration (Password change: Step 1)
INFO About FISH-FIT	Please enter data (* mandatory)
 SeaTraceNet ACCESS Registration Login DOCUMENTATION How to use FISH-FIT 	Your email address (an email will be sent to confirm your password change request) * Retype your email address * Control Request password change
	2023 © FISH-FIT / Max Rubner-Institut 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 Investigacións 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.

FISH-FIT	MRI 🚈 Max Rubner-Institut
SEATRACES	Access: Logout
INFO About FISH-FIT	Press button to logout from FISH-FIT
SeaTraceNet ACCESS	
Registration	2023 © FISH-FIT / Max Rubner-Institut Contact Imprint Data policy Terms of use
Logout	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 ► AZTTI Ciencia y tecnología marina y alimentaria ► Instituto de Investigacións Mariñas ► Liverpool John Moores University ► IPMA Portuguese Institute for Sea and Atmosphere ► Max Rubner-Institut
TAXONOMY • Families	
 Genera Species 	
SAMPLES	
 Samples 	
SEQUENCES	
DNA sequences	

4. Families

FISH-FIT		Max Rubner-Institut
	Taxonomy: Families	
INFO About FISH-FIT	FISH-FIT families list:	Filter
SeaTraceNet ACCESS	Family ^ Anguillidae	
 Registration Logout 	Buccinidae Cancridae	
TAXONOMY	Carangidae Cardiidae	
Families Genera	Citharidae Clupeidae	
Species SAMPLES Samples	Engraulidae Gadidae	
Samples SEQUENCES DNA conjunctor	Littorinidae	
Samples SEQUENCES DNA sequences	Littorinidae Loliginidae	

When logged in, you can reach the top level of the FISH-FIT taxonomy via the <u>Families</u> 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.

	MRI 🌾
FISH-FII	Max Rubner-Institut
	Taxonomy: Families
INFO	FISH-FIT families list:
 About FISH-FIT 	10 × Filter
SeaTraceNet	Family \land
ACCESS	Anguillidae
 Registration 	Buccinidae
- Logout	Cancridae
	Carannidae
TAXONOMY	Cardiidae
Families	
• Genera	
 Species 	
SAMPLES	Engraulidae
 Samples 	Gadidae
SEQUENCES	Littorinidae
 DNA sequences 	Showing 1 to 10 of 32 families < 1 2 3 4 >
FISH-FIT	Max Rubner-Institut
	Taxonomy: Families
INFO	FISH-FIT families list:
About FISH-FIT	10 V Filter an
 SeaTraceNet 	Family
ACCESS	Serrarida
 Registration 	
- Logout	
	Cancridae
TAXONOMY	Anguillidae
Families	Showing 1 to 4 of 4 families (filtered from 32 total families)
Genera	
Species	
SAMPLES	2023 © FISH-FIT / Max Rubner-Institut Contact Imprint Data policy Terms of use
 Samples 	The authentic material and DNA sequences are provided jointly by SEATRACES partners from France, Spain, UK, Portugal and Germany: MNHN Marine Station Concarneau > Le
SEQUENCES	Mans Université 🕨 AZTI Ciencia y tecnología marina y alimentaria 🕨 Instituto de Investigacións Mariñas 🕨 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* \vee) or *ascending (arrow up* n) for the respective column.

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

FISH-FIT		MRI 🍣 Max Rubner-Insti
	Taxonomy: Details for family Veneridae	
INFO About FISH-FIT SeaTraceNet Access Registration	BOLD information (boldsystems.org): BOLD FishBase information (fishbase.de): Not available	Synonymized names: Arteminae, Callistinae, Callocardiinae, Circinae, Clementiinae, Dosiniinae, Gafrariidae, Gemminae, Gouldiinae, Lioconchinae, Oncophoridae, Pitarinae, Samarangiinae, Venerinae
- Logout	Containing FISH-FIT genera:	Filter
TAXONOMY	Genus ^	Family
Families	Dosinia	Veneridae
- Genera	Polititapes	Veneridae
Species	Ruditapes	Veneridae
samples	Venus	Veneridae
SEQUENCES	Showing 1 to 4 of 4 gapora	
SEQUENCES	Showing 1 to 4 of 4 genera	
DNA sequences		
DNA sequences	FishBase Information (fishbase.de):	
• DNA sequences	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera:	Samarangunae, renemae Filter
ONA sequences ONA sequences ONA ONA	FishBase information (fishbase.de): Not available Containing FISH-FIT genera:	Summary renormed Filter
DNA sequences DNA sequences DIA Sequences SEATRACES About FISH-FIT SeaTraceNet ACCESS Registration	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ~ Dosinia	Santaranginae, renemae Filter Family Veneridae
DNA sequences DNA sequences DNA sequences SEATRACES About FISH-FIT SeaTraceNet ACCESS Registration Logout	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Poliitapes	Summaringinae, venemiae Filter Family Veneridae Veneridae
 DNA sequences DNA sequences FISH-FIT SEATRACES About FISH-FIT SeaTraceNet ACCESS Registration Logout 	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Ruditapes	Santaranginae, renemae Filter Family Veneridae Veneridae Veneridae
DNA sequences DNA sequences DNA sequences DNA Sequences Seatraces NFO About FISH-FIT SeaTraceNet Access Registration Logout TAXONOMY	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Venus	Filter Veneridae Veneridae Veneridae Veneridae Veneridae
DNA sequences DNA sequences DNA sequences DIA	FishBase information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ~ Dosinia Polititapes Ruditapes Venus Showing 1 to 4 of 4 genera	Filter Veneridae Veneridae Veneridae Veneridae
DNA sequences DNA sequ	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Ruditapes Venus Showing 1 to 4 of 4 genera	Filter Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae
 DNA sequences DNA sequences FISH-FIT SEATRACES SeaTraceNet ACCESS Registration Logout TAXONOMY Families Genera Species 	FishBase information (fishbase.de): Not available	Filter Family Veneridae Veneridae Veneridae Veneridae Veneridae Veneridae
 DNA sequences DNA sequences FISH-FIT SEATRACES REGISTRACES Registration Logout TAXONOMY Families Genera Species SAMPLES 	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Venus Showing 1 to 4 of 4 genera FISH-FIT families list: All ~	Filter
 DNA sequences DNA sequences FISH-FIT SEATRACES About FISH-FIT SeaTraceNet Access Registration Logout TAXONOMY Families Genera Species SAMPLES Samples 	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Ruditapes Venus Showing 1 to 4 of 4 genera FISH-FIT familles list: All ~ Family ^	Filter Veneridae Veneridae Veneridae Veneridae Veneridae
DNA sequences DNA sequ	FishBase Information (fishbase.de): Not available Containing FISH-FIT genera: All ~ Genus ^ Dosinia Polititapes Ruditapes Venus Showing 1 to 4 of 4 genera FISH-FIT families list: All ~ Family ^ Anguillidae	Filter Family Veneridae

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

There are links to <u>BOLD</u> and <u>FishBase</u> 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				MRI 🐲 Max Rubner-Institut
SEATRACES	FishBase information (fishbase.de): Not available	Samaranginae, venemae		
INFO - About FISH-FIT - SeaTraceNet	Containing FISH-FIT genera:		Filter dos	
ACCESS	Genus ^	Family		
Registration	Dosinia	Veneridae		_
- Logout	Showing 1 to 1 of 1 genera (filtered from 4 total genera)		<	
TAXONOMY	FISH-FIT families list:			
Families	All ~		Filter ang	×
Genera	Family \land			
SAMPLES	Anguillidae			
Samples	Carangidae Showing 1 to 2 of 2 families (filtered from 32 total families)		<	
DNA sequences				_

5. Genera

FISH-FIT			Max Rubner-Institut
SEATRACES	Taxonomy: Genera		
INFO About FISH-FIT	FISH-FIT genera list:		Filter
SeaTraceNet ACCESS	Genus A	Family Pectinidae	
 Registration Logout 	Allothunnus	Scombridae	
	Anguilla Boops	Anguillidae Sparidae	
Families	Brosme Buccinum	Lotidae Buccinidae	
Genera Species	Cancer	Cancridae	
SAMPLES Samples 	Cerastoderma	Cardiidae Citharidae	
SEQUENCES	Dosinia	Veneridae	
 DNA sequences 		chgraditude	

The second level of the FISH-FIT taxonomy is accessed via the <u>Genera</u> 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 <u>SeaLifeBase</u> 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.

FISH-FIT			Max Rubner-Institut
SEATRACES	Taxonomy: Details for genus Gadus		
INFO About FISH-FIT SeaTraceNet ACCESS Registration Logout	BOLD information (boldsystems.org): BOLD FishBase information (fishbase.de): FishBase SeaLifeBase information (sealifebase.org): SeaLifeBase	Synonymized names: Gadum, Morhua, Morrhua	
TAXONOMY • Families • Genera • Species	Containing FISH-FIT species:	Family	Filter Genus
SAMPLES	Gadus chalcogrammus Gadus mothua	Gadidae	Gadus
Samples SEQUENCES DNA sequences	Showing 1 to 2 of 2 species	Guinas	< 1 >

6. Species

FISH-FIT			Max Rubner-Institut
TAXONOMY	Taxonomy: Species		
Families	Comment of the		
Genera Species	All V		Filter
SAMPLES	Species <	Genus	Family
 Samples 	Aequipecten opercularis	Aequipecten	Pectinidae
SEQUENCES	Allothunnus fallai	Allothunnus	Scombridae
 DNA sequences 	Anguilla anguilla	Anguilla	Anguillidae
UTILITIES	Boops boops	Boops	Sparidae
 Alignment search 	Brosme brosme	Brosme	Lotidae
BIOBANK	Buccinum undatum	Buccinum	Buccinidae
Authentic materials	Cancer pagurus	Cancer	Cancridae
Material request	Cerastoderma edule	Cerastoderma	Cardiidae
Method collection	Citharus linguatula	Citharus	Citharidae
DOCUMENTATION	Dosinia exoleta	Dosinia	Veneridae
 How to use FISH-FIT 	Engraulis encrasicolus	Engraulis	Engraulidae

The lowest level of the taxonomy are the species, which are accessed via the link <u>Species</u>. 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.

FISH-FIT						MRI 👹 Max Rubner-Institu
• Families	Taxonomy: Details	s for species Epiner	ohelus marginatus			
Genera Species SAMPLES Samples SEQUENCES DNA sequences	BOLD information (bol BOLD FishBase information FishBase SeaLifeBase informati Not available	dsystems.org): (fishbase.de): on (sealifebase.org):		Synonymized names: Cerna gigas, Cernua gigas, Epin Epinephelus guaza, Holocentrus Serranus aspersus, Serranus cer Serranus marginatus	ephelus brachysoma, Ep gigas, Mycteroperca m mioides, Serranus fimbr	ninephelus gigas, arginata, Perca gigas, iatus, Serranus gigas,
Alignment search BIOBANK	Containing FISH-FIT s	amples:			Filte	er
Authentic materials Material request	Sample ~	DNA sequences	Authentic material	Species	Family	Genus
ETHODS	AZTI_GPD003	COI Avai	lable AZTI_GPD003	Epinephelus marginatus	Serranidae	Epinephelus
Method collection	AZTI_GPD004	COI	AZTI_GPD004	Epinephelus marginatus	Serranidae	Epinephelus
CUMENTATION	Showing 1 to 2 of 2 sa	mples				
How to use FISH-FIT						

7. Samples

The listing of the species samples contained in FISH-FIT can be accessed via the link <u>Samples</u>.

FISH-FIT						MRI 👹 Max Rubner-Institu
TAXONOMY	Samples					
· Families						
Genera	FISH-FIT samples list:					
- Species	All ~					Filter mri
SAMPLES	Sample 🔿	Species	Family	Genus	DNA sequences	Authentic material
Samples	MRI_A275	Limanda limanda	Pleuronectidae	Limanda	COI cyt b	MRI_A275
SEQUENCES	MRI_A277	Merlangius merlangus	Gadidae	Merlangius	cyt b COI	MRI_A277
 DNA sequences 	MRI_A279	Gadus morhua	Gadidae	Gadus	cyt b COI	MRI_A279
ITILITIES	MRI_A280	Mullus surmuletus	Mullidae	Mullus	cyt b COI	MRI_A280
 Alignment search 	MRI_A286	Hippoglossoides platessoides	Pleuronectidae	Hippoglossoides	cyt b COI	MRI_A286
BIOBANK	MRI_A294	Platichthys flesus	Pleuronectidae	Platichthys	cyt b COI	MRI_A294
Material request	MRI_A296	Scophthalmus maximus	Scophthalmidae	Scophthalmus	cyt b	MRI_A296
METHODS	MRI_A297	Sander lucioperca	Percidae	Sander	cyt b COI	MRI_A297
 Method collection 	MRI_A329	Scophthalmus maximus	Scophthalmidae	Scophthalmus	cyt b 16S	MRI_A329
OCUMENTATION	MRI_A340	Pleuronectes platessa	Pleuronectidae	Pleuronectes	cyt b COI	MRI_A340
 How to use FISH-FIT 	MRI_A363	Microstomus kitt	Pleuronectidae	Microstomus	cyt b COI	MRI_A363

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).

ISH-FIT		Max Rubner-Instit
XONOMY	Details for sample MRI_A329	
Families		
Genera	PDF version	
Species		
/IPLES	Unique complemente	Institute
Samples	MRI_A329	Max Rubner-Institut
UENCES	Species:	Palmaille 9 22767 Hamburg
DNA sequences	Scophthalmus maximus	Germany
ITIES	Morphological identification:	Show on Google Maps
Alignment search	Yes	Project:
BANK	_	TI_Solea-771
Authentic materials		
Material request	Production method:	Sample location:
THODS	Wild	North Sea; (German Bay; Germany)
Method collection	Fishing method:	GPS not available
	Bottom trawl	Date (DD-MM-YYYY):
OMENTATION		11-12-2019
		MRI
SH-FIT		MRRI Max Rubner-In
	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b	Max Rubner-In
	Containing DNA sequence 1: MRL_A329_CYTB Marker: Cytochrome b Length: 414 bp	MRI Max Rubner-Ir
SH-FIT	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol:	MRRI Max Rubner-Ir
SH-FIT ONOMY Families Genera Species	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5°; denaturation: 94*C/0.40 min; annealing: 50°C/1.20 min; a	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT ONOMY Families Genera Species	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95"/5"; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format:	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
ONOMY Families Genera Species IPLES	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5*; denaturation: 94*C/0.40 min; annealing: 50*C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAGATCGCAAAT	Implification: 72°C / 1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT ONOMY Families Genera Species HPLES Samples	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5'; denaturation: 94*C/0.40 min; annealing: 50*C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAGATCGCAAAA TCTTGGCCTCTGCTTAGCCACTCAATCACTCATTACCGGAACTCTTTTAGCTATGCCACTCA	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT ONOMY Families Genera Species HPLES Samples UENCES	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95°/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTTCTGTTATGACCAGCCATCATTACCGGACTCTTTTTGCCTTATGATTT GGATTAATCCGAAAACCTACACGCCGACCTCTTCTTCTTCTTAGTATTT GGATTAATCCGGAAACCTACACGCCGAACTGCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT ONOMY Families Genera Species HPLES Samples UENCES DNA sequences	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95'/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCAGCCAACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT GTTGATTAATCCGAAAACCTACACGCCAACGGCGCATCCTTCTTCTTGTGTATTG GGAGTTAATCCGGAAACCTACACGCCAACGGCGCATCCTTCTTCTTCTTATGTATTT GGAGTTAATCCGGAAACCTACACGCCAACGGCGCATCCTTCTTCTTCTTCTTCTCCCGTTAGCACTA	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
ONOMY Families Genera Species IPLES Samples UENCES DNA sequences JTIES	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5*; denaturation: 94*C/0.40 min; annealing: 50*C/1.20 min; at Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCAACCCTATCCTAAGATCGCAAAAT TCTTGGCCTCGCTTAGCCAGCCACCCAACTCATTACGGGACTCTTTTAGCTATGGCACTA GTGATTAATCCGAAACCTACACGCCAACGGCGCATCCTTCTTCTTATGTATT GGAGTTAATCCGAAACCTACAGCCCAACTGACTCGTCGGCCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
ONOMY Families Genera Species HPLES Samples UENCES DNA sequences LTTES Alignment search	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5'; denaturation: 94*C/0.40 min; annealing: 50*C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGAAAATCCCACCCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGAAAATCCCACCCCTATCTTAAGATCGCAACAT GTTGATTAATCCGAAACCTACACGCCCACGGCGCATCCTTCTTGCTATTGTATTT GGAGTTAATCCGAAACCTACACGCCAACGGCGCATCCTTCTTCTCTTATGTATTT GGAGTTATCCTTCTTCTCGTTATAGCAACTGCCTTCGTCGGCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: 114735-M13-24F	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT SH-FIT SNOMY Families Genera Species APLES Samples UENCES DNA sequences LITIES Alignment search BANK	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95°/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGAAAATCCCACCCTATCTTAGCTATGCACTA GTGATTAATCCGAAACCTACAGCCCAACGGCGCATCCTTCTTAGCTATTGCACTA GGAGTTATCCTTCTTCTCTCTTCTGTTATGCAACTGCCTTCGTCGGCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTTCCCAGTCAGCAAAAACCACCGCTTGTTATTCAACTA-3'	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT SH-FIT ONOMY Families Genera Species APLES Samples UENCES DNA sequences LITIES Alignment search BANK Authentic materials	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95'/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT GTTGATTAATCCGAAACCTACAGCCAACGGCGCATCCTTCTTGGCTATGGCATFA GTTGATTAATCCGAAACCTACAGCCCAACGGCGCATCCTTCTTGGCTATGGCATFA GGAGTTATCCTTCTTCTTCTGGTTATAGCAACTGCCTTCGTCGGGCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTTCCCAGTCACGCAAAACCACCGCTTGTTATTCAACTA-3' Reverse primer 1: H15149ad-M13-24R: 5' - CCGAGTACAATTTGCCACAGGGCTCCTCARAATGAYATTTGTCCTCA-3'	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
INTERES SAMPLES Samples DNA sequences LITTES Alignment search BANK Authentic materials Material request	Containing DNA sequence 1: MRI_A329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95'/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a: Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCACCAGCCTACGAAAATCCCACCCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCTGCTTAGCCACTCACTCACTACGGGCGCATCCTTTTAGCTATGCACTA GTTGATTATCCGAAACCTACACGCCAACGGCGCATCCTTCTTCTTATGTATTH GAGTTATCCTTCTTCTCGTTATAGCAAACCGCGCGCATCCTTCTCTTCTTATGTATTH GAGTTATCCTTCTTCTCGTTATAGCAAACCGCGCGCATCCTTCTCTTCTTATGTATTH GAGTTATCCTTCTTCCCGTTATAGCAAACCACCGCTGCTTCTTCTGCGGCTATGTCTCCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTCCCAGTCACGACGACAACCACCGTTGTTATTCAACTA-3' Reverse primer 1: H15149ad-M13-24R: 5' - CGGATAACAATTTCACACAGGGCCCTCCACAAATGAYATTTGTCCTCA-3'	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
INTERES SAMPLES Samples NUENCES DNA sequences LITIES Alignment search BANK Authentic materials Material request THODS	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95'75'; denaturation: 94'C/0.40 min; annealing: 50°C/1.20 min; at Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCCTATCCTAAGATCGCAAAAT CGTGGCTCTGGCTTAGCCACCGCCTACGAAAATCCCACCCCTATCCTAAGATCGCAAGAT GTTGATTAATGCCGAAACCTACCAGCCTACGAAAATCCCACCCCTATTGCTATGGCACTA GTTGATTAATCCGCAAACCTACACGCCAACGGGCGCATCCTTCTTGTGTATGTA	Implification: 72°C / 1.20 min; 35 cycles; final elongation: 72°C/5 min.
INTERESTICTION OF THE SECTION OF THE	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95*/5'; denaturation: 94*C/0.40 min; annealing: 50*C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAAT TCTTGGCCTCIGCTTAGCCAGTCACTCATTACCGGACTCTTTTAGCTATGCACTA GTTGATTAATCCGAAACCTACAGCCCACTGATAACGGCACTCCTTCTTCTTATGTATTT GGAGTTATCCTTCTTCTCTCTGTTATAGCAACTGCCTTCGTGGGCTATGTTCTCCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTCCCAGTCACGAGAAAACCACCGTTGTTATTCAACTA-3' Reverse primer 1: H15149ad-M13-24R: 5' - CGGATAACAATTTCACACAGGGCICCTCARAATGAYATTTGTCCTCA-3'	Implification: 72°C / 1.20 min; 35 cycles; final elongation: 72°C/5 min.
INTERESTICTION	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95°/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTCTGCTTAGCCACTCAATTACCGGACTCTTTTAGCTATGCACTA GTTGATTAATCCGAAACCTACCAGCCCACTGATAACGGCACTCTTTTAGCTATGCACTA GTTGATTAATCCGAAACCTACCAGCCCACTGGCCATCCTTCTTCATGTATTT GGAGTTATCCTTCTTCTCTCTGTTATAGCAACTGCCTTCGTCGGGCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTTCCCAGTCAGCAGAAAACCCACCGTTGTTATTCAACTA-3' Reverse primer 1: H15149ad-M13-24R: 5' - CGGATAACAATTTCACACAGGGCICCTCARAATGAYATTTGTCCTCA-3' Containing DNA sequence 2: MRLA329_16S.M13-24F Marker: 16S Length: 833 bp	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 min.
SH-FIT SH-FIT CONOMY Families Genera Species APLES Samples UVENCES DNA sequences LITIES Alignment search BANK Authentic materials Material request THODS Method collection CUMENTATION How to use FISH-FIT	Containing DNA sequence 1: MRLA329_CYTB Marker: Cytochrome b Length: 414 bp PCR protocol: Initial denaturation: 95'/5'; denaturation: 94°C/0.40 min; annealing: 50°C/1.20 min; a Sequence in FASTA format: >MRI_A329_CYTB CAGGGAACCTTAATGACCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTTGGTTAGCCAGCCTACGAAAATCCCACCCTATCCTAAAGATCGCAAAT TCTTGGCCTCTGCTTAGCCAGCCTACGCCAACGGCGCATCCTTCTTGGCTATGCATAT GGAGTTATCCTTCTTCTTCTGTTATAGCAACGCCCACCGCTCGTTCTTGGCTATGGCTAT GGAGTTATCCTTCTTCTTCTGGTTATAGCAACTGCCTTCGTCGGGCTATGTTCTTCCC Primers: Reference: Following: K. Kappel & Schröder (2016) Food Control 59, 478-486 or DIN Forward primer 1: L14735-M13-24F: 5' - CCAGGGTTTTCCCAGTCACGAAAAACCACCGTTGTTATTCAACTA-3' Reverse primer 1: H15149ad-M13-24R: 5' - CGGGATAACAATTTCACACAGGGCCCTCCARAATGAYATTTGTCCTCA-3' Containing DNA sequence 2: MRLA329_16S.M13-24F Marker: 16S Length: 583 bp PCB protocol:	Implification: 72°C /1.20 min; 35 cycles; final elongation: 72°C/5 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		Max Rubner-Institut
TAXONOMY • Families	Containing authentic material 1: MRL_A329 Available	
- Genera	Quantity: 2000 mg	
Species SAMPLES Samples	Quality: Public 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 PCB sequence analysis with only one reliable gene marker (for example: cyt h or COI)	
SEQUENCES DNA sequences	Storing conditions: -80 ° C, Ethanol & -20 ° C	
Alignment search	Permission required under the Nagoya Protocol?	
BIOBANK • Authentic materials	Add MRI_A329 to material request	
Material request		
METHODS · Method collection DOCUMENTATION · How to use FISH-FIT	Images	
FISH-FIT		MRI E



PDF version (of details for sample MRI_329):

	■ / 8 - 83% + E �	• • •
	Vincerreg SEATRACES MIRI ASI2 (Begehändense masimus) / Date: 19-10-2023 Sample overview: MRL ASI2 (Begehändense masimus) / Date: 19-10-2023 Sample overview: MRL ASI2 (Begehändense masimus) / Date: 19-10-2023	Å
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	Page 2 of 8	
≡ samples	3 / 8 − 83% + ⊡ ◊	± 6 :
	<page-header> picture 100,000,000,000,000,000,000,000,000,000</page-header>	
	Page 3 of 8 Page 4 of 8	

FISH-FIT: User documentation / Date: 09-10-2023





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 <u>DNA sequences</u>. 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).

FISH-FIT								MRI Max Rubne	r-Institu
TAXONOMY	DNA sequences								
 Families 									
 Genera 	FISH-FIT DNA sequences I	st:							
 Species 	All ~						Filter	azti ele	×
SAMPLES	Sequence ~	Sample	Marker	Length	Primers	Species	Family	Genus	
 Samples 	AZTI_ELE023_COI	AZTI_ELE023	COI	652 bp	F1 VF2 -T1-	Anguilla anguilla	Anguillidae	Anguilla	
SEQUENCES					M13F (-21)				
DNA sequences					M13R (-27)				
UTILITIES				Forward primer 2	F2 FishF2-t1- M13F (-21)				
 Alignment search 					R2 FR1d-t1-				
BIOBANK					M13R (-27)				
. Authentic materials	AZTI_ELE023_cytb	AZTI_ELE023	cyt b	413 bp	F1 L14735- M13-24F	Anguilla anguilla	Anguillidae	Anguilla	
- Autoentic fildteridis					R1 H15149				
 Material request 					M13-24R				
METHODS	Showing 1 to 2 of 2 seque	nces (filtered from 142 total	sesquences)					< 1 →	
 Method collection 								_	
DOCUMENTATION									
 How to use FISH-FIT 									
	2023 © FISH-FIT / Max Rul	oner-Institut				Contact	Imprint Data po	olicy Terms of	use

9. Alignment search

The <u>Alignment search</u> 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.

TAXONOMY Utilities: Alignment search • Families Enter a single DNA sequence in FASTA format: • Species > Samples • Samples > Samples • Sompies > TAXGCCAGCCCCCCCCTCAAAGATCGCCAATGACGACTAATTATGGAAACTTCGCCGCGACGACAATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAAACATTATGGAACCCCCTGAAGAATGCCCCTGAAGAATGCCCCTGAAGAATGCCCTTACATACA	FISH-FIT	MRI 🔅 Max Rubner-Institut
Families Genera Genera Genera Species SAMPLES Samples Samples Somples Som	TAXONOMY	Utilities: Alignment search
• Genera Enter a single DNA sequence in FASTA format: • Species > TEST_Mer Luccius_bilinearis • Samples > TEST_Mer Luccius_bilinearis • Samples > TEST_Mer Luccius_bilinearis • Samples > TEST_Mer Luccius_bilinearis • Sopecies > TEST_Mer Luccius_bilinearis • Samples > TEST_Mer Luccius_bilinearis • Samples > CatattocGeaccatacattocTacacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocGeaccatacattocCeaccattocCatattotAtacacGeaccatacattocGeaccatacattocCeattotCatattotAtacacGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCeattotAtacacGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCataGeaccattotTtacCataCatattotCataGeaGeaccatacattotCataGeaGeaccatacattotCata	 Families 	
 Species SAMPLES Samples	• Genera	Enter a single DNA sequence in FASTA format:
SAMPLES ATAGCCAGCCTCCGAACCCACCCCCTCTAAGAATCGCTAATGAAGACCTGCCTG	 Species 	>TEST Merluccius bilinearis
 Samples Samples TGTCTAGCGGCCCAAAGCGCTCAACGGGCACTATTTTAGCAATACACTACCACCGCGAAAGCGTCGAAATAGCCTTCTCGTCGTCGTACACACTGCGGCGCCTAATTTAGGAAACCTTGAAACCTTAGGAGCACCTACCT	SAMPLES	ATAGCCAGCCTCCGAACCCCCCCCCTCCTAAAGATCGCTAATGACGCATTAGTAGACCTGCCTG
SEQUENCES GGGGTCGTACTCTTTCTCCTAGTATAATGACCGCCTTCGTAGGCTACGTCCTCCCCTGAGGACAAATGTCCTTTTGAGGGGCCACTGTCATCAAAACTTAATGTCTGCTGTGATAGCTGGCC · DNA sequences CCTACGTGGGCAACACCCTCGTTCAATGAATCTGAGGGGGGCTTTTCAGTTGACAACGCCACTGAAAAATGCCCTTTCGCATTTCACTTCACTTCTTATTCCCCACACAAGACCCGCTGTTAACTCAGATGCAGATAAAATCCCCTTTCGCCAACCAA	 Samples 	TGTCTAGCGGCCCAAATCCTAACAGGACTATTTTTAGCAATACACTACACCGCCAAACGTCGAAATAGCCTTCTCATCCGTCGTACACATCTGCCGCGGACGTAAATTATGGAAGA CTAATTCGCAACATACACGCCAACGGCGCCTCCTTCTTCTTTATCTGCCTCTACATACA
DNA sequences DNA sequences CLCLTACETIGEGGAALACCCLCGTTCAATGAACTGGGCGAAACGGCCACTCTAACCCGATTCTTCGCATTTCACTTCTTTTTGTAGCTGCCC TTTACAATACTTCACCTCCTCCTGAAAACTGGGCGCAAACAACGCCCAGGACTAAACTCAGGACGAACAACCTCCCCCATACTTTACCCACAAGACACCTC CTAGGTTTTGCCCATCCTCCTGGAAACTGGCCCACCCCATGCTAGGAGGACCCAGACAACTTCACCCCCTGCTACGCCCACCCCGATGGCTGAAAATACGGCCGGAATGGCCAGAAACTGCCCGGATGGCTGAACATCCTCGCCGCTCTTTTCCTCTCGCCAACGCGCGGAATGGCCGAAAACTAGGGCCTGACATTTCGTCCTCGCCGTCGTCCTAGGCAGACAACTTCGTCCGACCCCGCGCTTTTTCTCATTCTAGTCCTGAATGGCGGAATGGCCAGAA Highment search BIOBANK Authentic materials Material request Method collection Bearch alignments A trelevant results found. Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications. <i>PloS one</i> , <i>8</i> (12), e82138.	SEQUENCES	GGGGTCGTACTCTTTCCCAGGTTATAATGACCGCCCTTCGTAGGCTACGTCCTCCCCTGAGGACAAATGTCCTTTTGAGGCGCCACTGTCATCACAAACTTAATGTCTGCTGTA
UTILITIES CTAGGTTTTGCCATCCTCCTCAGCACTAACAGCCCTGCCCCTCTTTTCCCCCAACCTGCAGGAGCAACTTCACCCCGCTGCTACACCACCTGCTATACTCGACGACGACCTGCCTTTACACCACCCCATACTAGTTGTACCCC A Alignment search AttTAAACCTGAGTGATATTTCCTCTTTGCCATGCCTATGCTCACCCACC	 DNA sequences 	CCCTACGTGGGCAACACCCTCGTTCAATGAATCTGAGGGGGCTTTTCAGTTGACAACGCCACTCTAACCCGATTCTTCGCATTTCACTTCTTATTCCCCTTTGTTGTAGCTGCC TTTACAATACTTCACCTCCTTTTCCTCCATGAAACTGGCTCAAACAACCCCCATAGGACTTAACTCAGATGCAGATAAAATCCCCCTTCCACCCATACTTTACCTACAAAGACCTG
Alignment search Authentic materials Material request Method collection A relevant results found. Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013), Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications. <i>PloS one</i> , <i>8</i> (12), e82138.	UTILITIES	
BIOBANK • Authentic materials • Material request • Method collection • Method collection • Documentation • Documentation • Documentation • Documentation • Method collection • Documentation • Docu	Alignment search	TTCCTGCACACCTCAAAGCAGCGAGGACTGACATTCGTCCCATCACCAACCTACTCTCTGAATACTTGTAGCAGAGAGTATATTGATCCTAACGTGAATGCGCGGAATGCCAGTA
· Authentic materials Search alignments · Material request Search alignments · Method collection 4 relevant results found. · DOCUMENTATION Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman · How to use FISH-FIT How to use FISH-FIT	BIOBANK	GAACACCCCTTCATTATTATCGGACAAGTGGCATCAGTCCTGTACTTCTCCCTGTTCCTAGTCATATTTCCCGCCGTAGGCATGGCTGAAAATAAGGCTCTCGAATGAAACT •
Material request METHODS A relevant results found. Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications. <i>PloS one, 8</i> (12), e82138.	 Authentic materials 	Saarah alianmante
METHODS Method collection Meth	 Material request 	
Method collection A relevant results found. Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications. <i>PloS one, 8</i> (12), e82138.	METHODS	
DOCUMENTATION Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman C/C++ library for use in genomic applications. <i>PloS one, 8</i> (12), e82138.	 Method collection 	4 relevant results found.
How to use FISH-FIT	DOCUMENTATION	Based on the SSW (SIMD Smith-Waterman) C/C++ library (Zhao et al., 2013). Zhao, M., Lee, W. P., Garrison, E. P., & Marth, G. T. (2013). SSW library: an SIMD Smith-Waterman
	 How to use FISH-FIT 	0,000 million use in genuine applications. Plus one, a(12), eo2130.

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 <u>SIMD Smith-Waterman C/C++ library by Zhao et al., 2013</u>, 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)

FISH-FIT					MRI 🐲 Max Rubner-Institut
	C/C++ library for us	use in g	enomic applications. <i>PloS one, 8</i> (12), e82138.		
TAXONOMY					
Families	Target sample: II	IIM_MB	IL2		
• Genera	Target sequence	e marke	ar: Cytochrome h		
 Species 	Target species: A	Morluo			
SAMPLES	Target species. A	Menuc			
 Samples 	larget length: 41	13 bp 7	Query length: 1138 bp / Query cover: 35,33%		
SEQUENCES	Alignment quality	ity: 98,7	vith bad query cover of 35,33%		
 DNA sequences 	Gaps: 3 of 1 coher	erent / I	Vismatches: 2 of 2 coherent		
UTILITIES	Target:	12	ATGGCCAGCCTCCGAAAAACCCACCCCCTCCTAAAGATCGCTAATGACGCATTAGTAGAC	71	
Alignment search	Query:	1	ATAGCCAGCCTCCGAACCCACCCCCTCCTAAAGATCGCTAATGACGCATTAGTAGAC	57	
BIOBANK	Toursto	70	CTCCCTCCCCCCCCA, A CATCTCCA, CATCA, A A CTTTCCCTCTCTTA, CCCCTCTCT	101	
Authentic materials	larget:	12		151	
 Material request 	Query:	58	CTGCCTGCCCCCTCCAACATCTCGACATGATGAAACTTTGGGTCTCTTTTAGGCCTCTGT	117	
METHODS	Target: 1	132	CTAGCGGCCCAAATCCTAACAGGACTATTTTTAGCAATACACTACACCGCAAACGTCGAA	191	
 Method collection 	Query: 1	118	CTAGCGGCCCAAATCCTAACAGGACTATTTTTAGCAATACACTACACCGCAAACGTCGAA	177	
DOCUMENTATION	-			254	
How to use FISH-FIT	Target: 1	192		251	
	Ouerv: 1	178	ΑΤΔGCCTTCTCATCCGTCGTΔCΔCΔTCTGCCGCGΔCGTΔΔΔTTΔTGGΔΔGΔCTΔΔTTCGC	237	Ŧ
					*
					MRI 🛎
FISH-FIT					MRI 🐲 Max Rubner-Institut
FISH-FIT	iarget: 5	5/3	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 415		MRI E
FISH-FIT TAXONOMY	iarget: 5 Query: 3	373 358	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 415		MRI E
TAXONOMY • Families	larget: 3 Query: 3	373 358	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413		Max Rubner-Institut
TAXONOMY • Families • Genera	Target : 5	373 358 AZTI H	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 		Max Rubner-Institut
TAXONOMY • Families • Genera • Species	Query: 3	373 358 AZTI_H	CTITIAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Max Rubner-Institut
TAXONOMY • Families • Genera • Species	Target sample: A Target sequence	373 358 AZTI_H e marke	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398		Max Rubner-Institut
TAXONOMY • Families • Genera • Species SAMPLES • Samples	Target sample: A Target sequence Target species: A	373 358 AZTI_H e marke <i>Merluc</i>	KE003 Mr. Cytochrome b		Max Rubner-Institut
ESCHAFET TAXONOMY • Families • Genera • Species SAMPLES • Samples	Target : 5 Query : 3 Target sample: A Target sequence Target species: A Target length: 41	358 AZTI_H e marke <i>Merluc</i> 14 bp /	KE003 Ar: Cytochrome b cius merluccius Query length: 1138 bp / Query cover: 35,24%		Max Rubner-Institut
EXENTER TAXONOMY A Families A Genera B Species SAMPLES A Samples SEQUENCES D NA Sequences	Target : 3 Query : 3 Target sample: A Target sequence Target sequence Target sequence Target sequence Target length: 41 Alignment quality	373 358 AZTI_H e marke Merluce 14 bp / 14 bp /	KE003 Ar: Cytochrome b Cius merluccius Query length: 1138 bp / Query cover: 35,24% With bad query cover of 35,24%		Max Rubner-Institut
EXENTER OF CONTRACTOR OF CONTR	Larget : 5 Query : 3 Target sample: A Target sequence Target species: Target species: A Target length: 41 Alignment quality Gaps: 3 of 1 coher 3	AZTI_H e marke Merluc 14 bp / 14 ty: 88,0	CTITIAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 398 br: Cytochrome b 398 cius merluccius 398 Query length: 1138 bp / Query cover: 35,24% 398 With bad query cover of 35,24* 398 Wismatches: 45 of 42 coherent		Max Rubner-Institut
EXEMPTION FAMILIES CAMPLES SEQUENCES DNA sequences UTILITIES C Alignment search	I arget: 3 Query: 3 Target sample: A Target sequence Target species: Target length: 41 Alignment quality Gaps: Target : 3 of 1 cohort	5/3 358 AZTI_H e marke <i>Meriuc</i> 14 bp / 14 v; ee,e	CTITIAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	72	Max Rubner-Institut
EXEMPTED TAXONOMY A Families A Genera B Species SAMPLES SAMPLES B Samples SEQUENCES D NA sequences UTILITES A Lignment search BIOBANK	Target: 3 Query: 3 Target sample: A Target sequence Target sequence Target sequence 1 Target length: 41 Alignment quality Gaps: Target : 3 Ouery: 3	5/3 358 AZTI_H e marke Merluc 14 bp / 14 bp / 13 1	CTITIAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 R: Cytochrome b cius merluccius Query length: 1138 bp / Query cover: 35,24% with bad query cover of 35,24% Wismatches: 45 of 42 coherent ATGGCCAGCCTCCGAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGAC ATGGCCAGCCTCCGAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGAAC ATGGCCAGCCTCCGAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGAAC	72	Max Rubner-Institut
TAXONOMY • Families • Genera • Species SAMPLES • Samples SEQUENCES • DNA sequences UTILITIES • Alignment search BIOBANK • Authentic materials	Target : 5 Query : 3 Target sample: A Target sequence Target species: Target species: A Target length: 41 Alignment quality Gaps: Target : 5 Query : 5	5/5 358 AZTI_H e marke <i>Merluc</i> 14 bp / 14 bp / 13 1	CTITIAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 er: Cytochrome b cius merluccius Query length: 1138 bp / Query cover: 35,24% Wismatches: 49 of 42 coherent ATGGCCAGCCTCCGAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGAGAC ATGGCCAGCCTCCGAAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGACATTAGTAGAAC ATAGCCAGCCTCCGAACCCACCCCCTCCTAAAGATCGCTAATGACGCATTAGTAGAAC	72 57	Max Rubner-Institut
TIXCONOMY • Families • Genera • Species SAMPLES • Samples SEQUENCES • DNA sequences UTILITIES • Alignment search BIOBANK • Authentic materials • Material request	Target : 3 Query : 3 Target sample: A Target sequence Target sequence Target species: A Target length: 41 Alignment quality Gaps: Target : 3 Query : Target : Target : 5	AZTI_H e marke <i>Merluc</i> 14 bp / 13 1 73	CTICITAGIAATAAIGACCGCCTTCGIAGGCIACGICCTCCC 413 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	72 57 132	Max Rubner-Institut
EXEMPLES A Samples SEQUENCES CINITIES A Idjament search EDEANK A Unitient materials A Material request EXEMPLES	I arget: 3 Query: 3 Target sample: A Target sequence Target species: Target species: A Target length: 41 Alignment quality Gaps: Target : 3 Query: Target: Query: Target: Query: Target:	AZTI_H e marke Meriuc 14 bp / 14 ty: aa, 1 13 1 73 58	KE003 with bud query cover: 35,24% with bud query cover: 35,24% with bud query cover: 35,24%	72 57 132 117	Max Rubner-Institut
EXEMPTED TXXONOMY A Families A Genera B Species SAMPLES A Samples SEQUENCES A NA sequences UTILITES A Lignment search EIOBANK A Authentic materialS A Material request METHODS A Method collection	I arget: 3 Query: 3 Target sample: A Target sequence Target sequence Target species: A Target length: 41 Alignment quality Gaps: Gaps: 3of 1 coher Target: 2 Query: 1 Query: 1 Target: 1	3/3 358 AZTI_H e market <i>Merluc</i> 14 bp / 14 bp / 13 1 73 58 133	CTICTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 KC003	72 57 132 117	Max Rubner-Institut
CINCUMENTITION	Target: 5 Query: 3 Target sample: A Target sequence Target species: Target species: A Target length: 41 Alignment quality Gaps: Gaps: 3of 1 coher Target: 1 Query: 1 Target: 1 Query: 1 Target: 1 Query: 1	AZTI_H e marke Merluc: 14 bp / tty: 86,0 rent / / 13 1 73 58 133	CTTTTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 er: Cytochrome b cius merluccius Query length: 1138 bp / Query cover: 35,24% With bud query cover of 35,345 Wismatches: 43 of 42 coherent ATGGCCAGCCTCCGAAAAACTCATCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGAAC CTCCTGCCCCCCCAAAAACTCATCCCCCTTCTAAAGATTGCTAATGATGCATTAGTAGAAC CTTCCTGCCCCCCTCTAACCATCTCAACATTATGAAACTTCGGGTCCTCTCCTAGGCCTCTGC CTTCCTGCCCCCCTCTAACAGTCGAAAACTTCGAGACTTTGGGTCCTCTTTAGGCCTCTGC TTAGCCGCCAAATCTTAACAGGGCTATTTCTAGCGATACATTATACCGCAAACGTCAGG CTTCCGGCCCAAATCTTAACAGGGCTATTTCTAGCGATACATTATACCGCAAACGTCAGG	72 57 132 117 192	Max Rubner-Institut
EXEMPTED TXXONOMY A Families A Genera B Species SAMPLES A Samples SEQUENCES A NA sequences UTILITIES A Idjament search EVOLANK A Uthentic materials A Material request METHODS A Method collection DCUMENTATION A How to use FISH-FIT	Iarget: 3 Query: 3 Target sample: A Target sequence Target sequence Target species: A Target length: 41 Alignment quality Gaps: Gaps: 3 of 1 cohort Target: 1 Query: 1 Target: 1 Query: 1	5/3 358 AZTI_H e marke <i>Merluc</i> 14 bp / 14 bp / 13 1 1 3 58 133 118	CTICTAGTAATAATGACCGCCTTCGTAGGCTACGTCCTCCC 413 CTCCTAGTTATAATGACCGCCTTCGTAGGCTACGTCCTCCC 398 KE003 KC003	72 57 132 117 192	Max Rubner-Institut

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 <u>Authentic materials</u>. 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**.

									MRI 👹
	Disk sulu Author								
	Biobank: Authen	itic materials							
	FISH-FIT authentic r	naterials list:							
	All ~							Filter	
	Material 🔿	Sample	Available	Quality	Storage	Nagoya	Species	Family	Genus
			quantity		conditions	2			
•	AZTI_ALBOO1	AZTI_ALB001	210 mg	*AM	RNAlater & -20 ° C	No	Thunnus alalunga	Scombridae	Thunnus
	AZTI_ALB002	AZTI_ALB002	230 mg	*AM No	o permission required	No	Thunnus alalunga	Scombridae	Thunnus
				_	U C	_			
	AZTI_ALB003	AZTI_ALB003	450 mg	*AM	RNAlater & -20 ° C	No	Thunnus alalunga	Scombridae	Thunnus
	AZTI_ALB048	AZTI_ALB048	500 mg	*AM	RNAlater & -20 °	No	Thunnus alalunga	Scombridae	Thunnus
				_	0	_		a 1.11	-
	AZTI_ALB050	AZTI_ALB050	300 mg	**AM	RNAlater & -20 ° C	No	Thunnus alalunga	Scombridae	Thunnus
	AZTI_ALK003	AZTI_ALK003	450 mg	*AM	RNAlater & -20 °	No	Gadus chalcogrammus	Gadidae	Gadus
				_	C	_			
	AZTI_ANE2001	AZTI_ANE2001	400 mg	*AM	RNAlater & -20 ° C	No	Engraulis encrasicolus	Engraulidae	Engraulis
									Max Rubner-I
	LJMU_OM_1	LJMU_OM_1	300 mg	*AM	Ethanol & -20 ° C	No	Oblada melanura	Sparidae	Oblada
	LJMU_OM_2	LJMU_OM_2	250 mg	*AM	Ethanol & -20 ° C	No	Oblada melanura	Sparidae	
	LJMU_PE_1	LJMU_PE_1	100 mg	*AM	Ethanol & -20 ° C	No	Pagellus erythrinus		Oblada
	LJMU_PE_2	LJMU_PE_2	100 mg				r agonao orjannao	Sparidae	Oblada Pagellus
	LJMU_SP_1			*AM	Ethanol & -20 ° C	No	Pagellus erythrinus	Sparidae Sparidae	Oblada Pagellus Pagellus
		LJMU_SP_1	250 mg	*AM	Ethanol & -20 ° C Ethanol & -20 ° C	No	Pagellus erythrinus Sardina pilchardus	Sparidae Sparidae Clupeidae	Oblada Pagellus Pagellus Sardina
	LJMU_SP_2	LJMU_SP_1	250 mg 250 mg	*AM *AM	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C	No No No	Pagellus erythrinus Sardina pilchardus Sardina pilchardus	Sparidae Sparidae Clupeidae Clupeidae	Oblada Pagellus Pagellus Sardina Sardina
	LJMU_SP_2	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1	250 mg 250 mg 20 mg	TAM TAM TAM	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C	No No No	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii	Sparidae Sparidae Clupeidae Clupeidae Gadidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus
	LJMU_SP_2 LJMU_TE_1 LJMU_TE_3	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3	250 mg 250 mg 20 mg 30 mg	*AM *AM *AM The laboratory is / is not accredited. The origin of	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C	No No No No No	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii	Sparidae Sparidae Clupeidae Gadidae Gadidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus Trisopterus
	LIMU_SP_2 LIMU_TE_1 LIMU_TE_3 MNHN_Spau_CC11	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_Spau_CC11	250 mg 250 mg 20 mg 30 mg 500 mg	AM AM AM The laboratory is / is not accredited. The origin of the seafood sample is not traceable (for	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C	No No No No No Required	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Sparus aurata	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus Trisopterus Sparus
	LIMU_SP_2 LIMU_TE_1 LIMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC16	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC16	250 mg 250 mg 20 mg 30 mg 500 mg 760 mg	AM AM AM AM The laboratory is / is not accredited. The origin of the seafood sample is not traceable (for example caught by research vessel with all	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C D ° C	No No No No Required Required	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii Sparus aurata	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae Sparidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus Trisopterus Sparus Sparus
	LIMU_SP.2 LIMU_TE_1 LIMU_TE_3 MNHRLSpou_CC11 MNHRLSpou_CC16 MNHRLSpou_CC30	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC30	250 mg 250 mg 20 mg 30 mg 500 mg 760 mg	AM AM AM AM The laboratory is / is not accredited. The origin of the seafood sample is not traceable (for example caught by cath data). The identity of the seafood sample is specified by PCR	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C 0 ° C 0 ° C	No No No No Required Required	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Sparus aurata Sparus aurata Sparus aurata	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae Sparidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus Trisopterus Sparus Sparus Sparus
	LIMU_SP_2 LIMU_TE_1 LIMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC16 MNHN_Spau_CC30 MNHN_Spau_CC30	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC30 MNHN_ST037	250 mg 250 mg 20 mg 30 mg 500 mg 270 mg 650 mg	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 res specified by PCR sequence analysis with only one reliable gene	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C 0 ° C 0 ° C 0 ° C 0 ° C	NO NO NO NO NO Required Required Required	Pagellus erythrinus Sardina pilchardus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii Sparus aurata Sparus aurata Sparus aurata Magallana gigas	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae Sparidae Sparidae Sparidae	Oblada Pagellus Pagellus Sardina Sardina Trisopterus Trisopterus Sparus Sparus Sparus Magallana
	LIMU_SP_2 LIMU_TE_1 LIMU_TE_3 MNNN_Spau_CC11 MNNN_Spau_CC13 MNNN_Spau_CC30 MNNN_ST037 MNNN_ST037	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 JMU_TE_3 MNHN_Spau_CC10 MNHN_Spau_CC30 MNHN_ST037 MNHN_ST042	250 mg 250 mg 20 mg 30 mg 500 mg 270 mg 650 mg 300 mg	AM AM AM AM AM The laboratory is / is not accredited. The origin of the seafood sample is not traceated. The origin of the seafood sample is example caught by research vessel with all catch delab. The identity of the seafood sample is specified by PCR sequence analysis with only one reliable gene marker (for example: cyt b or COI).	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C hanol & -20 ° C 0 ° C 0 ° C 0 ° C 0 ° C 0 ° C	No No No No Required Required Required Required	Pagellus erythrinus Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii Sparus aurata Sparus aurata Magallana gigas Magallana gigas	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae Sparidae Sparidae Ostreidae	Oblada Pagellus Pagellus Sardina Sardina Sardina Trisopterus Trisopterus Sparus Sparus Sparus Sparus Magallana Magallana
	LIMU_SP_2 LIMU_TE_1 LIMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC16 MNHN_Stat MNHN_Stat MNHN_Stat2 MNHN_Stat2	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC30 MNHN_ST042 MNHN_ST042 MNHN_ST063	250 mg 250 mg 20 mg 500 mg 270 mg 650 mg 300 mg 1100 mg	AM AM AM AM CAM The laboratory is / Is not accredited. The origin of the seafood sample is not traceable (for example caught by 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 CO). AM	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C 0 ° C 0 ° C 0 ° C 0 ° C 80 ° C	No No No No Required Required Required Required Required Required	Pagellus erythrinus Pagellus erythrinus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Sparus aurata Sparus aurata Sparus aurata Magallana gigas Ostrea edulis	Sparidae Sparidae Clupeidae Clupeidae Gadidae Gadidae Sparidae Sparidae Sparidae Ostreidae Ostreidae	ObladaPagellusPagellusSardinaSardinaTrisopterusSparusSparusSparusMagallanaMagallanaOstrea
	LIMU_SP.2 LIMU_TE_1 LIMU_TE_3 MNHN_Spau_CC11 MNHN_Spau_CC10 IMNHN_ST037 MNHN_ST042 MNHN_ST043 MNHN_ST043 MNHN_ST043	LJMU_SP_1 JJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_SPAU_CC11 MNHN_SPAU_CC30 MNHN_ST037 MNHN_ST042 MNHN_ST063 MNHN_ST063	250 mg 250 mg 20 mg 500 mg 270 mg 650 mg 300 mg 1100 mg	AM AM	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C annol & -20 ° C 0 ° C 0 ° C 0 ° C 0 ° C 80 ° C	NO NO NO NO NO NO Required Required Required Required Required Required Required	Pagellus erythrinus Pagellus erythrinus Sardina pilchardus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii Sparus aurata Sparus aurata Magallana gigas Ostrea edulis Magallana angulata	Sparidae Sparidae Clupeidae Clupeidae Cadidae Gadidae Sparidae Sparidae Sparidae Ostreidae Ostreidae Ostreidae	ObladaPagellusPagellusSardinaSardinaTrisopterusTrisopterusSparusSparusSparusMagallanaOstreaMagallana
	LIMU_SP.2 LIMU_TE_1 LIMU_TE_3 MNNN_Spau_CC11 MNNN_Spau_CC13 MNNN_Spau_CC30 MNNN_ST037 MNNN_ST037 MNNN_ST032 MNNN_ST032 MNNN_ST032 MNNN_ST032	LJMU_SP_1 LJMU_SP_3 LJMU_TE_1 LJMU_TE_3 MNHN_SPAU_CC10 MNHN_SPAU_CC30 MNHN_ST037 MNHN_ST042 MNHN_ST063 MNHN_ST070 MNHN_ST133	250 mg 250 mg 30 mg 500 mg 270 mg 650 mg 300 mg 1100 mg 1200 mg	AM	Ethanol & -20 ° C Ethanol & -20 ° C Ethanol & -20 ° C D	No No No No Required	Pagellus erythrinus Pagellus erythrinus Sardina pilchardus Sardina pilchardus Sardina pilchardus Trisopterus esmarkii Trisopterus esmarkii Sparus aurata Sparus aurata Sparus aurata Magallana gigas Ostrea edulis Magallana angulata Paceten maximus	Sparidae Sparidae Clupeidae Clupeidae Cadidae Gadidae Sparidae Sparidae Sparidae Ostreidae Ostreidae Ostreidae Costreidae	ObladaPagellusPagellusSardinaSardinaSardinaTrisopterusSparusSparusSparusMagallanaMagallanaOstreaMagallanaPecten

FISH-FIT									MRI 🐲
	Authentic material: MF	RI_A329							
TAXONOMY	Available								
Families	Quantity: 2000 mg								
- Genera	Quality:								
 Species 	*AM								
SAMPLES	1. The laboratory is /	is not accredited.	ot traccable /f	or oxomplo	aught hu racaarch vas	and with all act	coh data)		
Samples	3. The identity of the	seafood sample is in	specified by P	CR sequenc	e analysis with only or	ne reliable gene	e marker (for example: cyt b c	r COI).	
SEQUENCES	Storing conditions:								
 DNA sequences 	-80 ° C, Ethanol & -20 °	С							
	Permission required u	nder the Nagoya Pr	otocol?						
UTILITIES	No								
 Alignment search 	Add MRI A329 to ma	aterial request							
BIOBANK									
Authentic materials									
 Material request 	FISH-FIT authentic ma	terials list:							
METHODS	10 ~							Filter	
Mathed a llastics									
 wiethod collection 	Material <	Sample	Quantity	Quality	Storage conditions	Nagoya	Species	Family	Genus
DOCUMENTATION				_		_			
 How to use FISH-FIT 	AZTI_ALBOO1	AZTI_ALB001	210 mg	*AM	RNAlater & -20 ° C	No	Thunnus alalunga	Scombridae	Thunnus
	A771 AL 0002		220 mg	****	RNAlater & -20 ° C		Thunnue alalunga	Scombridge	Thuppus

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 <u>Material request</u>). It should be noted here that currently a maximum of three materials may be contained in one login session; this is indicated accordingly.

FISH-FIT									Маз	RI 🔅
TAXONOMY	Biobank: Mater	ial request								
Families										
- Genera	Please enter dat	a (* mandatory)								
 Species 	Limit of 3 materi	als already reached !								
SAMPLES										
 Samples 										
SEQUENCES	Save status of m	naterial request								
DNA sequences	You reached the ur	oper limit for the transfe	r request with 3 aut	hentic materia	ils I					
UTILITIES										
 Alignment search 	Mater	Available ial quantity	Intended quantity	Sample	Quality	Storage conditions	Nagoya ?	Species	Family	Genus
BIOBANK	Remove MRI_	275 5000 mg	10 mg *	MRI_A275	*AM	-80 ° C	No	Limanda limanda	Pleuronectidae	Limanda
Authentic materials						Ethanol & -20 ° C				
Material request	Remove	5000 mg	15 mg *	MRI_A277	**AM	-80 ° C Ethanol & -20 ° C	No	Merlangius merlangus	Gadidae	Merlangius
METHODS	Remove MRL	279 500(Up to 30 m	10 🛟 mg *	MRI_A279	*AM	-80 ° C	No	Gadus morhua	Gadidae	Gadus
 Method collection 		_				Ethanol & -20 ° C	_			
DOCUMENTATION										
 How to use FISH-FIT 	Your name *									

FISH-FIT		MRI Max Rubner-Institut					
	Reflicive Maximum Source No Methaligues Gaudale 15 mg * MRL_AL// MAX -80 C No Methaligues Gaudale Ethanol & -20 ° C merlangues	wenangius					
TAXONOMY	Remove MRLA279 5000 mg 10 mg * MRLA279 MM -80 ° C No Gadus morhua Gadidae	Gadus					
 Families 	Ethanol & -20 ° C						
- Genera							
 Species 	Your name *						
SAMPLES	John Doe						
 Samples 	Your email address						
SEQUENCES	(an email will be sent to confirm your material request) *						
DNA sequences	jonni@uoe-msatate.au Retyne vour email address *						
UTILITIES	john@doe-institute.tld						
 Alignment search 	Your phone						
BIOBANK	+00 000 000 000 000						
Authentic materials							
Material request	Name of organisation *						
METHODS	Doe Institute						
 Method collection 	Is the organisation private or public? *						
DOCUMENTATION	Public	~					
 How to use FISH-FIT 	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.

FISH-FIT									MRI 萘 Max Rubner-Institut
TAXONOMY • Families	Comments Example.								
- Genera									
Species									
SAMPLES	Do you accept the "D	ata policy" and "Terms of	use" below? *						
Samples	Yes, I accept the	data policy and terms o	f use.						~
SEQUENCES	Data policy								~
DNA sequences	Tormo of upo								
UTILITIES	remis of use								~
Alignment search	Request materi	al							
BIOBANK									
Authentic materials									
Material request	FISH-FIT authentic	materials list:							
METHODS	10 ~							Filter	
Method collection	Material ~	Sample	Ouantity	Ouality	Storage	Nagoya	Species	Family	Genus
DOCUMENTATION					conditions	2		,	
 Samples SEQUENCES DNA sequences UTILITIES Alignment search BIOBANK Authentic materials Material request METHODS Method collection DOCUMENTATION 	Ves, I accept the of Data policy Terms of use Request material 10 ~ Material ~	al materials list:	f use.	Quality	Storage conditions	Nagoya ?	Species Thunnus sistungs	Filter	Genus

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

(III) III) MRI 拳 FISH-FIT Rubner-Institut TAXONOMY Method collection Families Genera Standard operation procedures (SOPs): All 🗸 Filter Species SAMPLES Method Format Samples Simple seafood sample analysis decision tree PDF SEQUENCES Standard Operating Procedure for the detection/authentication of Octopus vulgaris in foodstuffs by Recombinase Polymerase Amplification (RPA) and Latera PDF DNA sequences Flow assay (LFA) UTILITIES Standard Operating Procedure for the genetic identification of crustacean species using cytochrome c oxidase I and 16S rRNA gene segments PDF Alignment search Standard Operating Procedure for the genetic identification of fish species using DNA barcoding (mitochondrial cytochrome-c-oxidase I sequencing) PDF BIOBANK Standard Operation Procedure FISH-FIT PDF Authentic materials Standard Operation Procedure for the Identification of Mytilus species by Melting Curve Analysis Material request METHODS Standard Operation Procedure for the identification of scallops species PDF Method collection Standard Operation Procedure for the Identification of the geographic origin of Mytilus galloprovincialis PDF DOCUMENTATION Showing 1 to 8 of 8 methods < 1 How to use FISH-FIT

An overview of the methods stored in FISH-FIT can be reached via the Method collection link.

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.

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Samples			Filter
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DNA sequences	BaTAnS Table	$https://www.bvl.bund.de/DE/Arbeitsbereiche/09_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungen/01_Amtliche_Sammlung_Untersuchungen/01_Amtliche_Sammlung_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungen/01_Aufgaben/04_Amtliche_Sammlung_Untersuchungen/01_Amtliche_Sammlung_Untersuchungen/01_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Sammlung_Untersuchungaben/04_Amtliche_Amtli$	Intersuchungsverfahren/untersuchungen_9
ITIES	CEN /TS 17303 -	https://www.en-standard.eu/din-cen-ts-17303-foodstuffs-dna-barcoding-of-fish-and-fish-products-using-defined to the standard st	ined-mitochondrial-cytochrome-b-and-cyto
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Authentic materials	864 LEGB	https://www.methodepsammlung.hvl.de/de	
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How to use FISH-FIT	Links to projects:		

FISH-FIT		Max Rubner-Institut
	Publications of interest:	
TAXONOMY	All ~	Filter
 Families 	Publication ~	Content
Genera		
 Species 	Ali et al., 2022	Yellowfin tuna LAMP
SAMPLES	Carreiro et al., 2023	Tuna DNA sequencing
 Samples 	del Socorro Toxqui Rodríguez et al., 2023	Seafood metabarcoding nanopore
SEQUENCES	Frigerio et al., 2022	RPA-LFA mackerel
 DNA sequences 	Giusti et al., 2023	Seafood mislabelling in Italy
UTILITIES	Kappel and Schröder, 2020	Snapper barcoding
 Alignment search 	Prasetyo et al., 2022	Closed-tube barcoding ray and sharks
BIOBANK	Varunjikar et al., 2022	Seafood proteomics and DNAseq
 Authentic materials 	Vinas and Tudela, 2009	Tuna DNA sequencing
 Material request 	Yao et al., 2022	Patagonian toothfish real-time PCR
METHODS	Showing 1 to 11 of 11 publications	
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