

# Guideline & Documentation

(API and table column description)  
of the TRACE Molecular Biology Database (WP 3.4)  
Version 0.7, 31.12.2007

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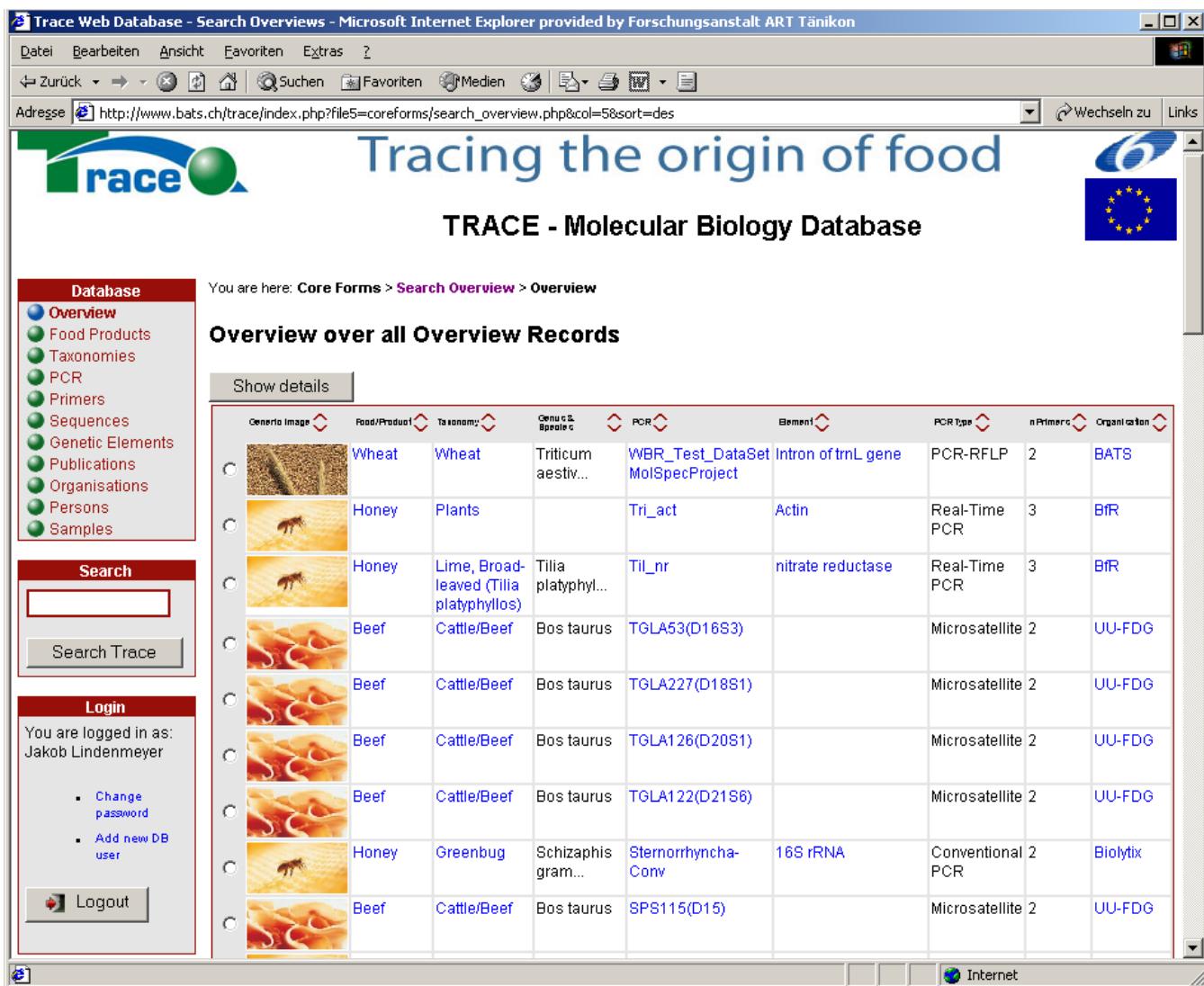
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## 1 Introduction: A short user-guideline

Under the address [www.bats.ch/trace/](http://www.bats.ch/trace/) the TRACE online database offers a webfrontend for the TRACE molecular biology database. The advantages of an online-database are:

- It makes the data accessible to clients with lack of database software.
- It makes the data available to alternative devices like handhelds and mobiles.

On the following pages the most important screen shots of the TRACE molecular biology online database.



Generic Image	Food/Product	Taxonomy	Genus & Species	PCR	Element	PCR Type	nPrimers	Organisation
	Wheat	Wheat	Triticum aestiv...	WBR_Test_DataSet MolSpecProject	Intron of trnL gene	PCR-RFLP	2	BATS
	Honey	Plants		Tri_act	Actin	Real-Time PCR	3	BfR
	Honey	Lime, Broad-leaved (Tilia platyphyllos)	Tilia platyphyl...	Til_nr	nitrate reductase	Real-Time PCR	3	BfR
	Beef	Cattle/Beef	Bos taurus	TGLA53(D16S3)		Microsatellite	2	UU-FDG
	Beef	Cattle/Beef	Bos taurus	TGLA227(D18S1)		Microsatellite	2	UU-FDG
	Beef	Cattle/Beef	Bos taurus	TGLA126(D20S1)		Microsatellite	2	UU-FDG
	Beef	Cattle/Beef	Bos taurus	TGLA122(D21S6)		Microsatellite	2	UU-FDG
	Honey	Greenbug	Schizaphis gram...	Sternorhyncha-Conv	16S rRNA	Conventional PCR	2	Biolytix
	Beef	Cattle/Beef	Bos taurus	SPS115(D15)		Microsatellite	2	UU-FDG

Figure 1: Starting page of the TRACE molecular biology database: The overview over the records.

As a historic comparison: The next page shows the same overview-form and a single record in the old frontend-design.

**Food Trace Ability**  
**Molecular Biology Database**

eMail address: krais@bats.ch Password: \*\*\*\*\* Login 

**Database**

- Overview
- Food Products
- Taxonomies
- PCR
- Primers
- Sequences
- Genetic Elements
- Publications
- Organisations
- Persons
- Samples

You are here: Core Forms > Search Overview > Overview

**Overview over all Overview Records**

Show details

Food/Product Taxonomy & Species	Genus & Species	PCR	Element	PCR Type	nPrimers	Organisation	
Apeninne beef	Cattle	Bos-pde	Phosphodiesterase	Real-Time PCR	4	BfR	
Apeninne beef	Cattle	Bos-pde0	Phosphodiesterase	Real-Time PCR	4	BfR	
Chicken	Chicken	Gallus gallus	Gal-Oalb	Ovalbumin	Real-Time PCR	3	BfR
Chicken	Chicken	Gallus gallus	Gal-Oalb-2	Ovalbumin	Real-Time PCR	3	BfR
Chicken	Chicken	Gallus gallus	Chicken	D-Loop	Real-Time PCR	3	TUGRAZ
Farro della Garfagnana	Wheat	Triticum aestivum L.	WBR	Intron of trnL gene	PCR-RFLP	2	BATS
Honey	Honey		CorsicanHoneyPCR			0	BATS
Mineral water	Water		MineralWaterPCR		Real-Time PCR - Light Cycler	0	BATS

Figure 2: Old version of the overview form

**Food Trace Ability**  
**Molecular Biology Database**

eMail address: krais@bats.ch Password: \*\*\*\*\* Login 

**Database**

- Overview
- Food Products
- Taxonomies
- PCR
- Primers
- Sequences
- Genetic Elements
- Publications
- Organisations
- Persons
- Samples

You are here: Core Forms > Search Overview > Overview

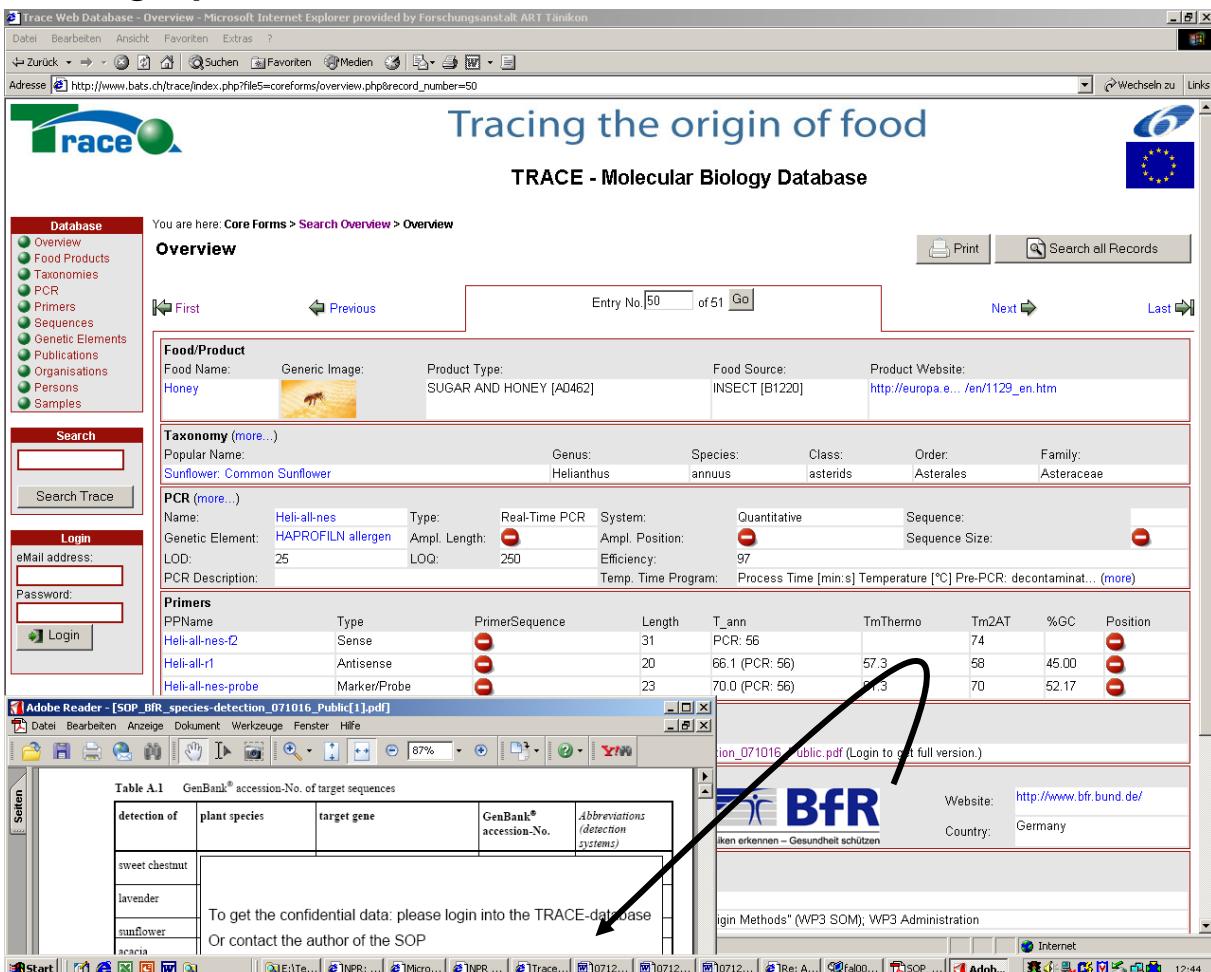
**Overview**

First Previous Entry No 9 of 9 Go  Search all Records

<b>Food/Product</b>					
Food Name: Honey	Generic Image: 	Product Type: SUGAR AND HONEY [A0462]	Food Source: INSECT [B1220]	Taxonomy Name: Honey	Product Website: <a href="http://europa.e.../en/1129_en.htm">http://europa.e.../en/1129_en.htm</a>
<b>Taxonomy</b>	Popular Name: Honey	Genus:	Species:	Class:	Order: Family:
<b>PCR</b>	Name: CorsicanHoneyPCR	Type:	System: Qualitative (Light Cycler; TaqMan; Matsunaga)	Sequence:	
Genetic Element:		Ampl.Length:	GenomSize:	AnnTemp:	
<b>Organisation Data</b>	Acronym: BATS Phone: +41 61 690 93 10				

Figure 3: Old version of the form of a single record

## 1.1 Login procedure



You are here: Core Forms > Search Overview > Overview

**Overview**

First Previous Entry No. 50 of 51 Go Next Last

<b>Food/Product</b>	Food Name: Generic Image: Honey	Product Type: SUGAR AND HONEY [A0462]	Food Source: INSECT [B1220]	Product Website: <a href="http://europa.e.../en/1129_en.htm">http://europa.e.../en/1129_en.htm</a>
<b>Taxonomy (more...)</b>				
Popular Name: Sunflower: Common Sunflower	Genus: Helianthus	Species: annuus	Class: asterids	Order: Asterales Family: Asteraceae
<b>PCR (more...)</b>				
Name: Heli-all-nes	Type: Real-Time PCR	System: Quantitative	Sequence:	Sequence Size:
Genetic Element: HAPROFIL allergen	Ampl. Length: 250	Ampl. Position: 250	Efficiency: 97	Temp. Time Program: Process Time [min:s] Temperature [°C] Pre-PCR: decontaminat... (more)
<b>Primers</b>				
PPName	Type	PrimerSequence	Length	T <sub>m</sub> ann
Heli-all-nes-f2	Sense	(red)	31	PCR: 56
Heli-all-r1	Antisense	(red)	20	66.1 (PCR: 56)
Heli-all-nes-probe	Marker/Probe	(red)	23	57.3 70.0 (PCR: 56)

Adobe Reader - [SOP\_BfR\_species-detection\_071016\_Public[1].pdf]  
 Datei Bearbeiten Anzeige Dokument Werkzeuge Fenster Hilfe

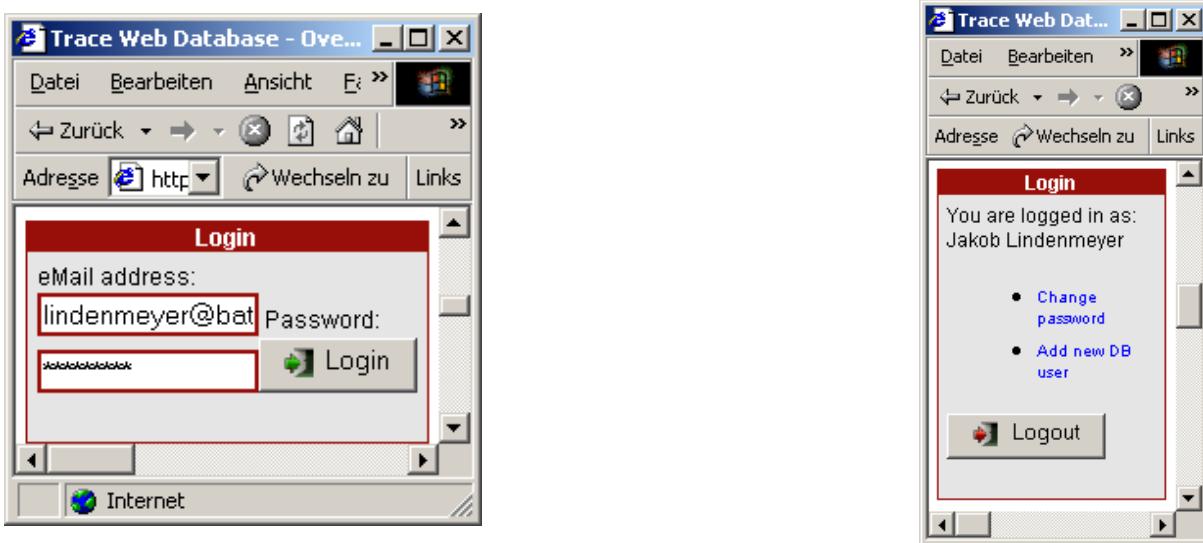
Table A.1 GenBank® accession-No. of target sequences

detection of	plant species	target gene	GenBank® accession-No.	Abbreviations (detection systems)
sweet chestnut				
lavender				
sunflower				
acacia				

To get the confidential data: please login into the TRACE-database  
Or contact the author of the SOP

BfR  
Bundesamt für Risikobewertung  
Risiken erkennen – Gesundheit schützen  
Website: <http://www.bfr.bund.de/>  
Country: Germany

**Figure 4: Public record before the login:** The confidential information is covered by a no-access-sign and the PDF-table does not contain any data.



**Login**

eMail address: lindenmeyer@bats.ch Password:

**Login**

You are logged in as: Jakob Lindenmeyer

- Change password
- Add new DB user

Logout

**Figure 5: Login-window before (left) and after (right) the login-process.**

Trace Web Database - Overview - Microsoft Internet Explorer provided by Forschungsanstalt ART Fähnikon

Datei Bearbeiten Ansicht Favoriten Extras ?  
 Zurück Suchen Favoriten Medien Drucken E-Mail Links  
 Adresse http://www.bats.ch/trace/index.php?file5=coreforms/overview.php&record\_number=50 Wechseln zu

**Tracing the origin of food**

TRACE - Molecular Biology Database

You are here: Core Forms > Search Overview > Overview

**Overview**

First Previous Entry No. 50 of 51 Go Next Last

**Food/Product**

Food Name: Honey	Generic Image: 	Product Type: SUGAR AND HONEY [A0462]	Food Source: INSECT [B1220]	Product Website: <a href="http://europa.e.../en/1129_en.htm">http://europa.e.../en/1129_en.htm</a>
------------------	--	---------------------------------------	-----------------------------	--

**Taxonomy (more...)**

Popular Name: Sunflower: Common Sunflower	Genus: Helianthus	Species: annuus	Class: asterids	Order: Asterales	Family: Asteraceae
---	-------------------	-----------------	-----------------	------------------	--------------------

**PCR (more...)**

Name: Heli-all-nes	Type: Real-Time PCR	System: Quantitative	Sequence:
Genetic Element: HAPROFILN allergen	Ampl. Length: 106	Ampl. Position:	Sequence Size:
LOD: 25	LOQ: 250	Efficiency:	97
PCR Description:	Temp. Time Program: Process Time [min:s] Temperature [°C] Pre-PCR: decontaminat... (more)		

**Primers**

PPName	Type	PrimerSequence	Length	T_anno	TmThermo	Tm2AT	%GC	Position
Heli-all-nes-f2	Sense	CgT CAA TAC TTg TTA ATA TTA TTA AgA ATT A	31	PCR: 56	74			
Heli-all-rl	Antisense	ATA gCT Tgg CCC gTT TTC TT	20	66.1 (PCR: 56)	57.3	58	45.00	
Heli-all-nes-probe	Marker/Probe	5' - FAM - ATg CAT ATT CCT CCA gCT CCC Tg - (T AMR A) - 3'	23	70.0 (PCR: 56)	51.3	70	52.17	

**Adobe Reader - [SOP\_BfR\_species-detection\_071016[1].pdf]**

File Bearbeiten Anzeige Dokument Werkzeuge Fenster Hilfe

Download Minimieren SOP\_BfR\_species-detection\_071016.pdf

Table A.1 GenBank® accession-No. of target sequences

detection of	plant species	target gene	GenBank® accession-No.	Abbreviations (detection systems)
sweet chestnut	<i>Castanea sativa</i>	<i>phenylalanine ammonia-lyase (PAL)</i>	no sequence entry available	Cas_PAL
lavender	<i>Lavandula sp.</i>	<i>Hydroxymethylglutaryl coenzyme A reductase</i>	no sequence entry available	Lav_HMG2
sunflower	<i>Helianthus annuus</i>	<i>HAPROFILN allergen</i>	J15210	Heli-all-nes
acacia	<i>Acacia sp.</i>	<i>alcohol dehydrogenase 1 (adh1)</i>	no sequence entry available	Aca_adh1

**BfR**  
 BfR erkennen - Gesundheit schützen  
 Website: <http://www.bfr.bund.de/>  
 Country: Germany

Methods" (WP3 SOM); WP3 Administration  
 Species Origin Methods" (WP3 SOM); Member of the Scientific Committee

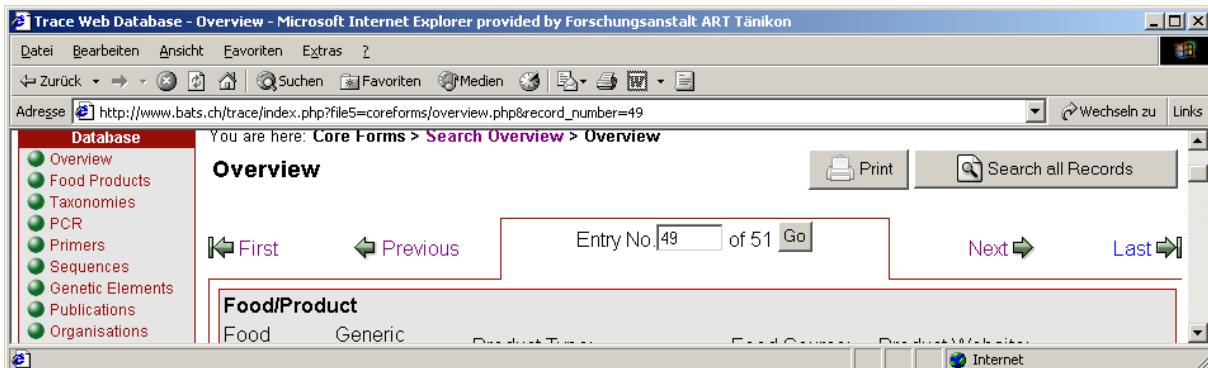
**Figure 6: Confidential record after the login:** The sequence information of the primers and the data in the PDF-table is visible after the login.

## 1.2 Navigation

Improvement of the navigation between the records:  
 The header-row shows special navigation-options like:

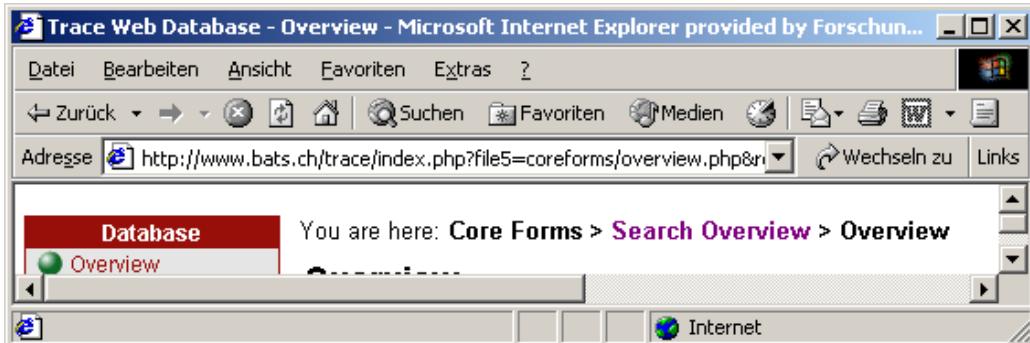
- First record
- Previous record
- Next record
- Last record

Or the user can insert the exact data-set number, if the number is already known.



**Figure 7:** The header-row containing 5 navigation elements to navigate between the records of the TRACE molecular biology database.

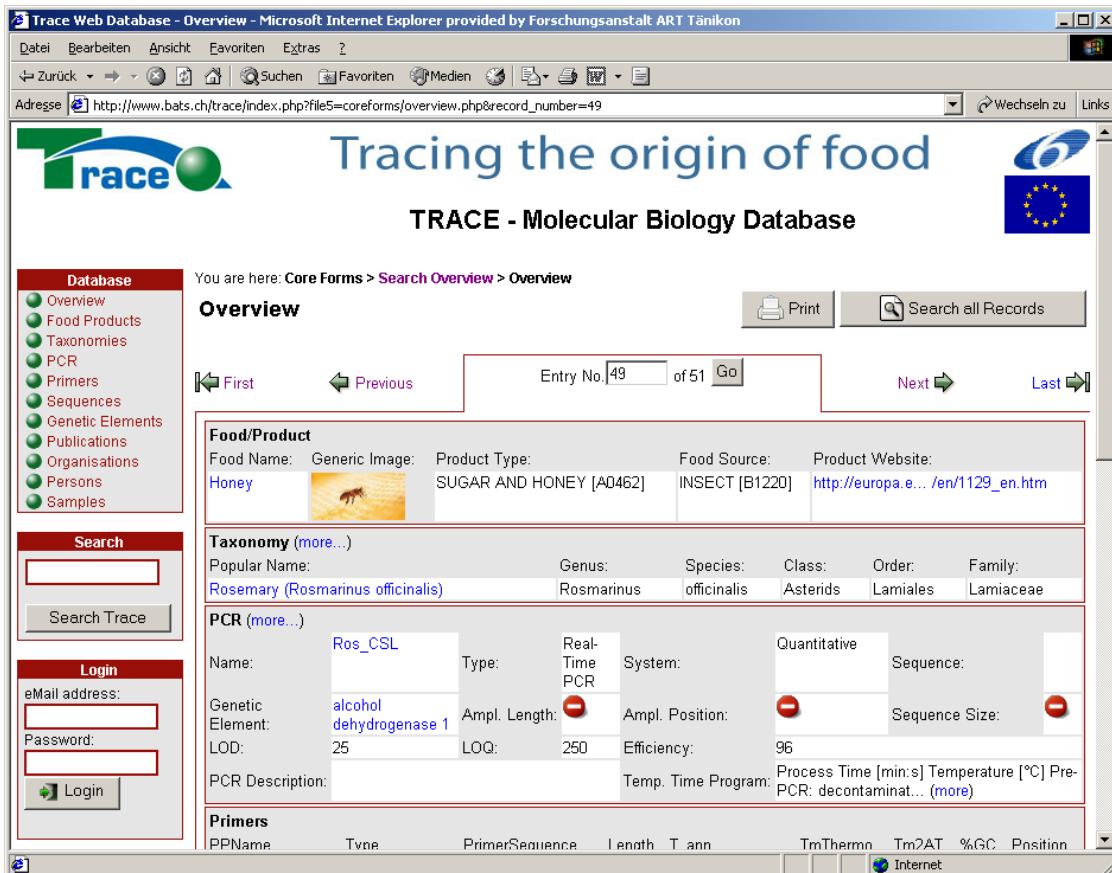
At the top left of the dataset, a bread-crumb-trail always shows the database-user his current position in the website by saying: You are here: followed by a hierarchical path of the websites document structure.



**Figure 8:** The bread-crumb-trail shows the database-user his current position in the website by saying.

### 1.3 Functional boxes

A further helpful usability-improvement for the database-user is the separation of the TRACE-information into functional and logical boxes, divided by red lines, e.g. for taxonomic information, molecular information, information on foods, information about the institution and contacts, information about publications. In addition, we marked the separation of the descriptive surrounding information (title of the box, name of the attributes, navigation) in dark grey from the data itself in white boxes. This helps the user to see, which data (white fields) has been filled in by the TRACE-partners into the grey forms of the database.



The screenshot shows the TRACE database interface. On the left, there's a vertical sidebar with a 'Database' section containing links for Overview, Food Products, Taxonomies, PCR, Primers, Sequences, Genetic Elements, Publications, Organisations, Persons, and Samples. Below it is a 'Search' section with a search bar and a 'Search Trace' button. At the bottom is a 'Login' section with fields for eMail address and Password, and a 'Login' button. The main content area has a header 'Tracing the origin of food' and 'TRACE - Molecular Biology Database'. It displays an 'Overview' page for entry number 49 of 51. The page includes sections for 'Food/Product' (Food Name: Honey, Product Type: SUGAR AND HONEY [A0462], Food Source: INSECT [B1220], Product Website: [http://europa.e.../en/1129\\_en.htm](http://europa.e.../en/1129_en.htm)), 'Taxonomy (more...)' (Popular Name: Rosemary (Rosmarinus officinalis), Genus: Rosmarinus, Species: officinalis, Class: Asterids, Order: Lamiales, Family: Lamiaceae), 'PCR (more...)' (Name: Ros CSL, Type: Real-Time PCR, System: Quantitative, Sequence: alcohol dehydrogenase 1, Ampl. Length: 25, Ampl. Position: 250, Efficiency: 96, Process Time [min:s] Temperature [°C] Pre-PCR: decontaminat... (more)), and 'Primers' (PPName, Type, PrimerSequence, Length, Tm ann, TmThermn, TmZAT, %GC, Position, Internet). Navigation buttons like First, Previous, Next, and Last are also present.

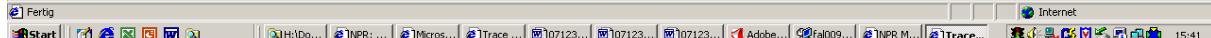
**Figure 9: Separation of the TRACE-information into functional and logical boxes.**

#### 1.4 Easy-to-print function

Many database-users still want to print out important data. Therefore we implemented an easy-to-print function for single records and for the whole database itself. After choosing the PRINT-button, the user gets a new webpage showing the chosen record in a print-optimised design, without any navigation and with an activated printer-dialogue.

**Overview**

First Previous Entry No. 49 of 51 Go

<b>Food/Product</b>	Food Name: Honey	Generic Image: 	Product Type: SUGAR AND HONEY [A0462]	Food Safety Category: INSECT
<b>Taxonomy (more...)</b>		Popular Name: Rosemary (Rosmarinus officinalis)	Genus: Rosmarinus	Species: officinalis
<b>PCR (more...)</b>				
Name: Ros CSL	Type: Real-Time PCR	System: Cepheid SmartCycler II		
Genetic Element: alcohol dehydrogenase 1	Ampl. Length: 74	Ampl. Position: 5' - 2000 Bp		
LOD: 25	LOQ: 250	Efficiency:		
PCR Description:	Temp. Time Program: 30°C / 10 min, 95°C / 10 min, 40 cycles of 95°C / 15 sec, 60°C / 1 min, 72°C / 1 min, 4°C / 10 min			
<b>Primers</b>				
PPName: Ros CSL-f	Type: PrimerSequence	Sense: gCg TAT gGg gCC AAC Ag		
PPName: Ros CSL-r	Type: PrimerSequence	Antisense: ACT gCC CTT gAA gAA gAA ATg g		
PPName: Ros CSL-probe	Type: Marker/Probe	5'- FAM ) - TGG CAG ATT CAT CAT TCT CCT TCA TTA GGA CC - (T AMR		
<b>Publications</b>				
Short Title: SOP PlantSpecies by PCR	Type: SOP	Date: September 2007	Download: <a href="#">SOP_BfR_species-detection_071016.pdf</a>	
<b>Organisation (more...)</b>				
Acronym: BfR	 Risiken erkennen – Gesundheit schützen			Website: <a href="http://www.bfr.bund.de/">http://www.bfr.bund.de/</a>
Name: BfR-Federal Institute for Risk Assessment, Berlin				Country: Germany
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Mr. Hermann Broll	h.broll@bfr.bund.de	+49-30-8412 3639	Leader of the TRACE Workpackage 3: "Species Origin Methods" (WP3 SOM); Member of the Scientific Committee	
<b>Devices</b>				
Electrophor.	RT-device	DNA-Sequencer	ThermoCyl.	SouthernBlot
DNA+protein	ABI 7700+LC	ABI 310	PE 2400	yes
Other: ELISA plate reader				
<b>Samples</b>				
Fertig				

**Figure 10: Printer-optimised webpage** showing the chosen record in a printer-optimised design, without any navigation and with an activated printer-dialogue.

## 2 Database description of tables and attributes

### 2.1 Entity Relationship Model

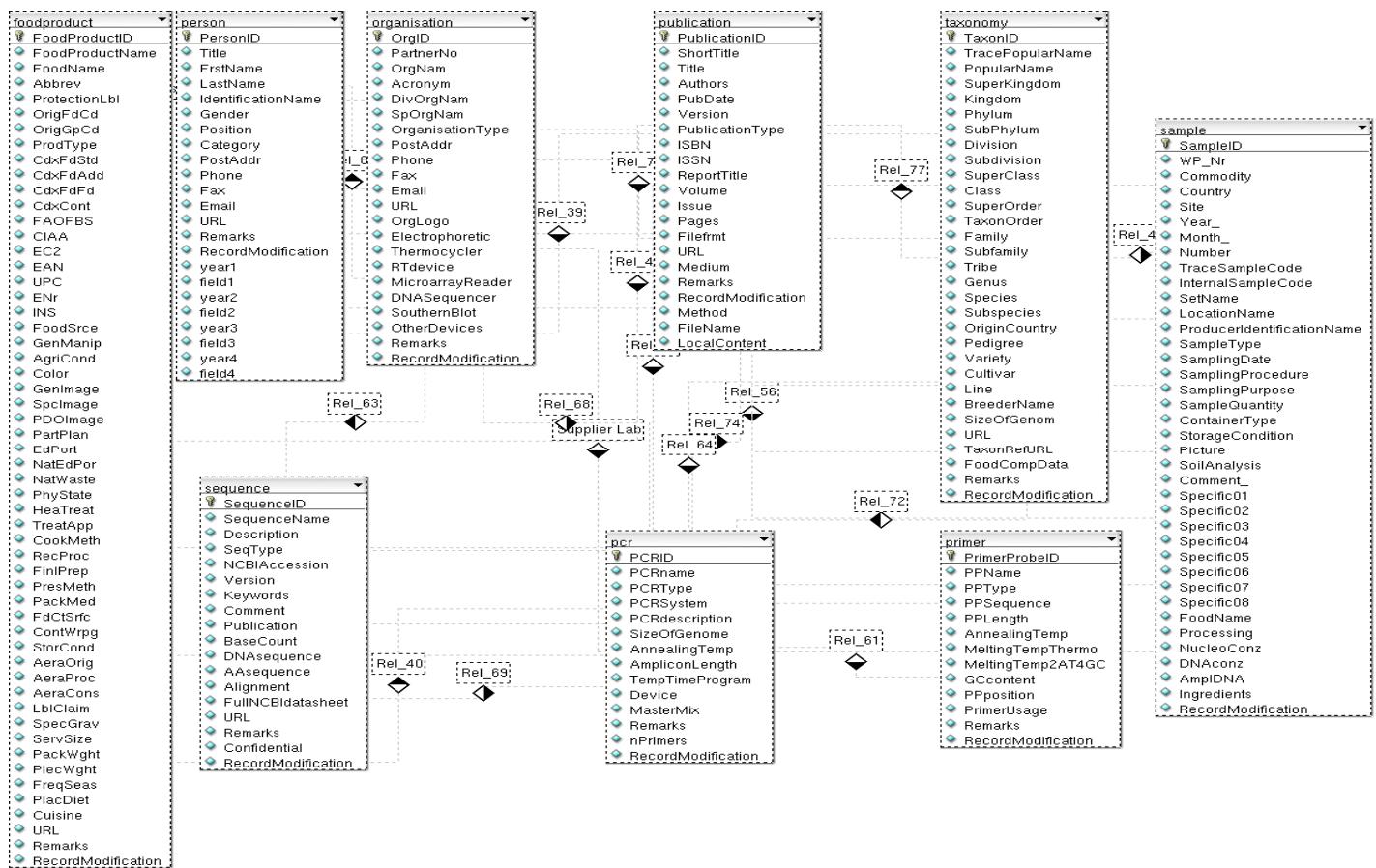


Figure 11: Small Entity Relationship Model of the Trace Molecular Database

For the whole Entity Relationship Model is too large following a small version with the most important tables.

## 2.2 Table extraction

Attribute	Description
ExtractionID	Primary Key
ExtractionName	The extraction name may have a maximum of 255 characters.
ExtractionDescription	The extraction description is a text field.
ExtractionCompany	The extraction company may have a maximum of 255 characters.
Remarks	The extraction remarks is a string of max. 255 characters.
TissueType	The extraction tissue type may have a maximum of 50 characters.
TimePerSample	The extraction time per sample may have a maximum of 50 characters.
SampleSize	The extraction sample size may have a maximum of 50 characters.
MeasuringMethod	The extraction method may have a maximum of 255 characters.
Purity	The extraction purity may have a maximum of 50 characters.
Yield	The extraction yield may have a maximum of 50 characters.
MethodID	The extraction method id is a smallint. See table method.
PublicationID	The extraction PublicationID is a smallint. See table publication.
Confidential	This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

The screenshot shows a Microsoft Management Studio (SSMS) window displaying the schema of a database table named 'extraction'. The table has 14 columns, each with a name and a corresponding data type. The columns are:

Feld	Typ
<u>ExtractionID</u>	int(6)
<b>ExtractionName</b>	varchar(255)
<b>ExtractionDescription</b>	text
<b>ExtractionCompany</b>	varchar(255)
<b>Remarks</b>	text
<b>TissueType</b>	varchar(50)
<b>TimePerSample</b>	varchar(50)
<b>SampleSize</b>	varchar(50)
<b>MeasuringMethod</b>	varchar(255)
<b>Purity</b>	varchar(50)
<b>Yield</b>	varchar(50)
<b>MethodID</b>	int(6)
<b>PublicationID</b>	int(6)
<b>Confidential</b>	char(1)
<b>RecordModification</b>	timestamp(14)

Table 1: Database table "extraction"

## 2.3 Table foodproduct

Attribute	Description
FoodProductID	Primary Key
FoodProductName	Name of Foodproduct
FoodName	This field contains the preferred food name and additional synonyms in various languages. Food Names should start with an upper case first character in the first word, e.g. Grapefruit,... Scientific Names must use Latin (la) as language flag and should adhere to the following format: Genus species Author [, Year], e.g. Gadus morhua Linnaeus, 1758.
Abbrev	This field is used for applications with limited screen/paper space.
OrigFdCd	The food code, ID, or abbreviation used to identify the food in the original publication.
OrigGpCd	The proprietary classification code is used in the original publication. The proprietary classification system should be provided separately under ORIGFDGP within the primary source description.
ProdType	FDA product type thesaurus of Langual facet A.
CdxFdStd	Codex Alimentarius Food Standards code.
CdxFdAdd	Standards for Food Additives of a foodproduct.
CdxFdFd	CODEX Classification of Foods and Feeds
CdxCont	CODEX Food Categorization System for Contaminants
FAOFBS	FAO Food Balance Sheet Classification
CIAA	CIAA Food Categorization
EC2	Eurocode2
EAN	European Article Number (EAN). For European Articles only.
UPC	Universal Product Code (UPC)
Enr	E-Number. If food is food additive, code according to the European E-Number system for additive standardisation.
INS	INS-Code. If the food is a food additive, code according to the International Numbering System for food additives according to CODEX Alimentarius
Manufact	Manufacturer of a foodproduct. Describes the direct manufacturer of producer of the food. e.g. farmer is considered a manufacturer. See Organisation table.
Distrib	Distributor. Between producer and retailer. See Organisation table.
FoodSrce	Food Source. Langual facet B.
GenManip	Genetically Modified or not.
AgriCond	Agricultural Production Conditions. Brief description of soil conditions, watering schemes, feeding, harvesting, slaughtering, ripeness, etc.

Attribute	Description
Color	Color values are currently not further specified. More detailed recommendations are planned in future versions of the Eurofoods Recommendations.
GenImage	Generic Image of a foodproduct. The file names of generic images showing foods similar to the food sample in question.
SpcImage	Specific Image of a foodproduct. The file names of specific images of the food sample, i.e. the food that was actually analysed.
PDOImage	PDO Image (Production Label) of a foodproduct.
PartPlan	Part of Plant or Animal of a foodproduct. See Langual facet C of Eurofood Recommendation.
EdPort	Percentage Edible Portion of a foodproduct. May also be considered a component.
NatEdPor	Nature of Edible Portion of a foodproduct. Which parts of the food are edible, e.g. flesh, root, leaf, etc.?
NatWaste	Nature of Waste of a foodproduct. Which parts of the food are not edible, e.g. rind, bone, stone, peel, etc.?
PhyState	Physical State Shape or Form of a foodproduct. See Langual facet E of Eurofood Recommendation.
HeaTreat	Extent of Heat Treatment of a foodproduct. See Langual facet F of Eurofood Recommendation.
TreatApp	Treatment Applied of a foodproduct. See Langual facet H of Eurofood Recommendation.
CookMeth	Cooking Method of a foodproduct. See Langual facet G of Eurofood Recommendation.
RecProc	Recipe Procedure of a foodproduct. If food is a recipe.
PublicationID	Recipe Bibliographic Reference (PublicationID)of a foodproduct. Link to the publication table (Publication ID) Describes the publication holding the recipe.
FinlPrep	Final Preparation of a foodproduct. Final preparation of food before consumption, e.g. heating a frozen dinner or canned food.
PresMeth	Preservation Method of a foodproduct. See Langual facet J of Eurofood Recommendation.
PackMed	Packing Medium of a foodproduct. See Langual facet K of Eurofood Recommendation.
FdCtSrfc	Food Contact Surface of a foodproduct. See Langual facet N of Eurofood Recommendation.
ContWrpg	Container or Wrapping of a foodproduct. See Langual facet M of Eurofood Recommendation.
StorCond	Storage Conditions of a foodproduct. Storage conditions and duration before arrival at lab.

Attribute	Description
AeraOrig	Area of Origin of a foodproduct. Origin of the main raw material or area where food was produced if food is a mixed product. See Langual facet R of Eurofood Recommendation.
AeraProc	Area of Processing of a foodproduct. Use if different from AREAORIG. See Langual facet R of Eurofood Recommendation.
AeraCons	Area of Consumption of a foodproduct. See Langual facet R of Eurofood Recommendation.
LblClaim	Customer Group Label Claim of a foodproduct. See Langual facet P of Eurofood Recommendation.
SpecGrav	Specific Gravity of a foodproduct. May also be considered a component. It is the density of the food devided by the density of water at the same temperature. Specific Gravity is used to convert to convert to and from standard volumetrix or household measures.
ServSize	Typical Serving Size in grams of a foodproduct.
PackWght	Typical Package Weight in grams of a foodproduct.
PiecWght	Typical Weight per Piece in grams of a foodproduct.
FreqSeas	Frequency and Season of a foodproduct. How often and in which season is the food preferably consumed?
PlacDiet	Place of Food in Diet of a foodproduct. How does the food relate to other foods in the diet? Is it a major source of some nutrient?
Cuisine	Cuisine of a foodproduct. Possible future Langual facet Q of the Eurofood Recommendation. The special diet a food belongs to (e.g. Mediterranean cuisine).
URL	URL of a foodproduct.
Remarks	Remarks of a foodproduct. Any further remarks.
TaxonID	See table taxonomy
SampleID	SampleID of a foodproduct. See table sample.
Confidential	Whether a food product record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

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Feld	Typ
<u>FoodProductID</u>	int(6)
<u>FoodProductName</u>	varchar(255)
<u>FoodName</u>	varchar(255)
<u>Abbrev</u>	varchar(32)
<u>ProtectionLbl</u>	varchar(50)
<u>CountryID</u>	int(6)
<u>OrigFdCd</u>	varchar(255)
<u>OrigGpCd</u>	varchar(255)
<u>ProdType</u>	varchar(255)
<u>CdxFdStd</u>	varchar(255)
<u>CdxFdAdd</u>	varchar(255)
<u>CdxFdFd</u>	varchar(255)
<u>CdxCont</u>	varchar(255)
<u>FAOFOBS</u>	varchar(255)
<u>CIAA</u>	varchar(255)
<u>EC2</u>	varchar(255)
<u>EAN</u>	varchar(255)
<u>UPC</u>	varchar(255)
<u>ENr</u>	varchar(255)
<u>INS</u>	varchar(255)
<u>Manufact</u>	int(6)
<u>Distrib</u>	int(6)
<u>FoodSrce</u>	varchar(255)
<u>GenManip</u>	tinyint(1)
<u>AgriCond</u>	text
<u>Color</u>	varchar(255)
<u>GenImage</u>	varchar(255)
<u>SpclImage</u>	varchar(255)
<u>PDOImage</u>	varchar(255)
<u>PartPlan</u>	varchar(255)
<u>EdPort</u>	float
<u>NatEdPor</u>	varchar(255)
<u>NatWaste</u>	varchar(255)
<u>PhyState</u>	varchar(255)

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Feld	Typ
<u>GenImage</u>	varchar(255)
<u>SpclImage</u>	varchar(255)
<u>PDOImage</u>	varchar(255)
<u>PartPlan</u>	varchar(255)
<u>EdPort</u>	float
<u>NatEdPor</u>	varchar(255)
<u>NatWaste</u>	varchar(255)
<u>PhyState</u>	varchar(255)
<u>HeaTreat</u>	varchar(255)
<u>TreatApp</u>	varchar(255)
<u>CookMeth</u>	varchar(255)
<u>RecProc</u>	text
<u>PublicationID</u>	int(6)
<u>FinlPrep</u>	varchar(255)
<u>PresMeth</u>	varchar(255)
<u>PackMed</u>	varchar(255)
<u>FdCtSrfc</u>	varchar(255)
<u>ContWrpg</u>	varchar(255)
<u>StorCond</u>	text
<u>AeraOrig</u>	varchar(255)
<u>AeraProc</u>	varchar(255)
<u>AeraCons</u>	varchar(255)
<u>LblClaim</u>	varchar(255)
<u>SpecGrav</u>	float
<u>ServSize</u>	float
<u>PackWght</u>	float
<u>PiecWght</u>	float
<u>FreqSeas</u>	varchar(255)
<u>PlacDiet</u>	varchar(255)
<u>Cuisine</u>	varchar(255)
<u>URL</u>	varchar(255)
<u>Remarks</u>	text
<u>Confidential</u>	char(1)
<u>RecordModification</u>	timestamp(14)

Table 2: Database table "foodproduct".

## 2.4 Table geneticelement

Attribute	Description
ElementID	Primary Key.
ElementName	Element name of an genetic element.
ElementCode	ElementCode of an genetic element.
ElementType	ElementType of an genetic element.
Size	Size of an genetic element.
Map	Map of an genetic element.
Sequence	Sequence of an genetic element.
TaxonID	TaxonID of an genetic element. See table taxonomy.
Trait	Trait of an genetic element.
ProteinProduct	ProteinProduct of an genetic element.
Expression	Expression of an genetic element.
Mechanism	Mechanism of an genetic element.
Remarks	Further remarks of an genetic element.
Confidential	Wether a food product record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

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Feld	Typ
<u>ElementID</u>	int(6)
<u>ElementCode</u>	varchar(255)
<u>ElementName</u>	varchar(255)
<u>ElementType</u>	varchar(50)
<u>Size</u>	varchar(255)
<u>Map</u>	varchar(50)
<u>Sequence</u>	varchar(50)
<u>TaxonID</u>	int(6)
<u>Trait</u>	varchar(255)
<u>ProteinProduct</u>	varchar(255)
<u>Expression</u>	varchar(255)
<u>Mechanism</u>	varchar(255)
<u>Remarks</u>	text
<u>Confidential</u>	char(1)
<u>RecordModification</u>	timestamp(14)

Table 3: Database table "geneticelement"

## 2.5 Table list\_country

Attribute	Description
CountryID	Primary Key
CountryName	Name of a country.
CountryCode	Country code (like a Top-Level-Domain code) of a country.
Remarks	Remarks concerning a country.
RecordModification	Date of last modification of the record. Timestamp.

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Feld	Typ
<u>CountryID</u>	int(6)
<u>CountryCode</u>	char(2)
<u>CountryName</u>	varchar(255)
<u>Remarks</u>	text

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Feld	Typ
<u>LanguageID</u>	int(6)
<u>LanguageName</u>	varchar(50)
<u>Remarks</u>	text
<u>RecordModification</u>	timestamp(14)

Internet

Table 4: Database table "list\_country"

## 2.6 Table list\_language

Attribute	Description
LanguageID	Primary Key.
LanguageName	Full name of a language
Remarks	Remarks concerning a language.
RecordModification	Date of last modification of the record. Timestamp.

Table 5: Database table "list\_language"

## 2.7 Table list\_probedye

Attribute	Description
ProbeDyeID	Primary Key.
ProbeDyeName	Name for a Probe Dye.
Excitation	Excitation for a Probe Dye.
Emission	Emission for a Probe Dye.
Company	Company for a Probe Dye.
Remarks	Remarks concerning a probedye.
RecordModification	Date of last modification of the record. Timestamp.

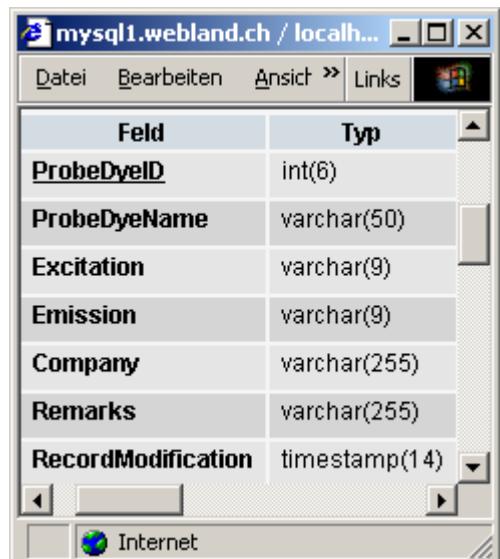


Table 6: Database table "list\_probedye"

## 2.8 Table method

Attribute	Description
MethodID	Primary Key
MethHdln	Method Headline according to the Method.
MethName	Method Name according to the Method.
GenDesc	GenDesc according to the Method. It contains the Scope and General Description.
PublicationID	PublicationID according to the Method. It contains the Bibliographic Reference. It's a Foreign Key: Link to Publication.
MethodType	MethodType according to the Method ID. Method Type is a selection from a defined list.
SampHand	Sample Handling according to the Method. It includes the description fo Sample Preparation, Extraction and clean-up at the Laboratory.
AnDetail	Analytical Details according to the Method. It includes the detection procedure, quantification procedure, confirmation procedure, quality control, use of reference materials.
SampleID	SampleID according to the Method. See table sample.
Accuracy	Accuracy according to the Method. It is the closeness of the arrangement between the result of a measurement and the true value of the measurement. It may be assessed by the use of reference material.
Applicab	Applicab according to the Method. It specifies the matrix, conentration range and, for Codex purposes, the reference to be given to "general" methods.
LOD	Limit of Detection according to the Method. The detection limit is conventionally defined as field blank $+3d$ , where $d$ is the standard deviation of the field blank value signal.
LoDet	Limit of Determination according to the Method. As for detection limit expect that $6d$ or $10d$ is required than $3d$ .
LOQ	Limit of Quantification (LOQ) according to the Method. As for detection limit, except that typically at least $10d$ is required.
Precision	Precision according to the Method. The closeness of the arrangement between independant test results obtained under prescribed conditions. The values obtained normally encompass both repeatabilities.
Repeat	Repeatability according to the Method. This is the value $r$ below which is the absolute difference between two single test results obtained under repeatability contidions.
Reproduc	Reproducability (inter-lab.) according to the Method. This is the value $r$ below which is the absolute difference between two single test results obtained under repeatability contidions.

Attribute	Description
Recovery	Recovery according to the Method. Proportion of the amount of analyte present or added to the test material which is extracted and presented for measurement.
Selectiv	Selectivity according to the Method.
Sensitiv	Sensitivity according to the Method.
Specific	Specificity according to the Method. The freedom of the analytical procedure from interference effects. It reflects the ability of instrumentation to measure only the signal of the determination.
Confidential	Confidential according to the Method.
Remarks	Remarks according to the Method. Contains any further remarks. Comment field to collect all uncategorized Information.
Range	Range according to the Method.
Linearity	Linearity according to the Method.
OrgID	Organisation ID according to the Method. See table organisation.
RecordModification	Date of last modification of the record. Timestamp.

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Feld	Typ
<b>MethodID</b>	int(6)
<b>MethHdln</b>	varchar(255)
<b>MethName</b>	varchar(255)
<b>GenDesc</b>	text
<b>PublicationID</b>	int(6)
<b>MethType</b>	varchar(50)
<b>SampHand</b>	text
<b>AnDetail</b>	text
<b>SampleID</b>	int(6)
<b>Accuracy</b>	varchar(255)
<b>Applicab</b>	text
<b>LOD</b>	varchar(50)
<b>LoDet</b>	varchar(255)
<b>LOQ</b>	varchar(50)
<b>Precision</b>	varchar(50)
<b>Repeat</b>	varchar(50)
<b>Reproduc</b>	varchar(50)
<b>Recovery</b>	varchar(50)
<b>Selectiv</b>	varchar(50)
<b>Sensitiv</b>	varchar(255)
<b>Specific</b>	text
<b>Confidential</b>	char(1)
<b>Remarks</b>	text
<b>Range</b>	varchar(50)
<b>Linearity</b>	varchar(255)
<b>OrgID</b>	int(6)
<b>RecordModification</b>	timestamp(14)

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Internet

Table 7: Database table "method".

## 2.9 Table organisation

Attribute	Description
OrgID	Organisation ID, Primary Key.
PartnerNo	TRACE partner number of an organisation.
Acronym	Acronym of an organisation.
Name	Full official name of the organisation.
OrganisationType	Type of the type the organisation, e.g. company.
CountryID	CountryID an organisation resides in. See table country.
OrgLogo	Logo of an organisation withing the <img...> Tag.
Phone	Phone number of an organisation. Telephone and Fax numbers should be formatted from an international point of view. Use the form: +country-code area-code sub-area-code phone-number. The various blocks should be separated with a space character or hyphen.
Fax	Fax number of an organisation. Formatting issues are the same as for phone numbers.
Email	Internet E-Mail address of an organisation.
URL	URL address of an organisation. Always give complete URLs. Example: http://www.bats.ch/trace/
SpOrgName	Umbrella Organisation of an organisation. If applicable, give the name of the umbrella organisation.
PostAddr	Post address of an organisation. Postal address as would be put on a letter, i.e. PO box, address, ZIP-code, city, country, etc.
Remarks	Any further remarks of an organisation.
DivOrgNam	DivOrgNam of an organisation.
Electrophoretic	Electrophoretic of an organisation.
Thermocycler	Thermocycler of an organisation.
Rtdevice	RTdevice of an organisation.
MicroarrayReader	MicroarrayReader of an organisation.
DNASequencer	DNASequencer of an organisation.
SouthernBlot	SouthernBlot of an organisation.
OtherDevices	OtherDevices of an organisation.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

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Feld	Typ
<u>OrgID</u>	int(6)
<b>PartnerNo</b>	int(6)
<b>OrgNam</b>	varchar(255)
<b>Acronym</b>	varchar(50)
<b>DivOrgNam</b>	varchar(255)
<b>SpOrgNam</b>	varchar(255)
<b>OrganisationType</b>	varchar(50)
<b>PostAddr</b>	text
<b>CountryID</b>	int(6)
<b>Phone</b>	varchar(50)
<b>Fax</b>	varchar(50)
<b>Email</b>	varchar(255)
<b>URL</b>	varchar(255)
<b>OrgInfoTRACE</b>	varchar(255)
<b>OrgLogo</b>	varchar(255)
<b>Description</b>	text
<b>Expertise</b>	text
<b>Activities</b>	text
<b>Electrophoretic</b>	varchar(255)
<b>Thermocycler</b>	varchar(255)
<b>RTdevice</b>	varchar(255)
<b>MicroarrayReader</b>	varchar(255)
<b>DNASequencer</b>	varchar(255)
<b>SouthernBlot</b>	varchar(255)
<b>OtherDevices</b>	varchar(255)
<b>Remarks</b>	text
<b>Confidential</b>	char(1)
<b>RecordModification</b>	timestamp(14)

Table 8: Database table "organisation".

## 2.10 Table pcr

Attribute	Description
PCRID	Primary Key
PCRName	Name of an PCR.
PCRTypE	Type name of an PCR.
PCRSyStEm	System name of an PCR.
TaxonID	TaxonID name of an PCR. See table taxonomy.
PCRdescription	PCRdescription of an PCR.
ElementID	ElementID of an PCR. See table geneticelement.
SequenceID	SequenceID of an PCR. See table sequence.
SizeOfGenome	SizeOfGenome of an PCR.
AnnealingTemp	AnnealingTemp of an PCR.
AmpliconLength	AmpliconLength of an PCR.
TempTimeProgram	TempTimeProgram of an PCR.
Device	Device of an PCR.
MasterMix	MasterMix of an PCR.
Remarks	Remarks of an PCR.
OrgID	Organisation ID of an PCR. See table organisation.
MethodID	MethodID of an PCR. See table method.
PublicationID	PublicationID of an PCR. See table publication.
nPrimers	nPrimers of an PCR.
FoodProductID	FoodProductID of an PCR. See table foodproduct.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

Feld	Typ
<u>PCRID</u>	int(6)
<b>PCRname</b>	varchar(255)
<b>TaxonID</b>	int(6)
<b>PCRTypE</b>	varchar(50)
<b>PCRSyStem</b>	varchar(50)
<b>PCRdescription</b>	text
<b>ElementID</b>	int(6)
<b>SequenceID</b>	int(6)
<b>SizeOfGenome</b>	varchar(50)
<b>AnnealingTemp</b>	varchar(50)
<b>AmpliconLength</b>	varchar(255)
<b>AmpliconPosition</b>	varchar(20)
<b>LOD</b>	varchar(6)
<b>LOQ</b>	varchar(6)
<b>Efficiency</b>	varchar(6)
<b>TempTimeProgram</b>	text
<b>Device</b>	varchar(255)
<b>Reagents</b>	text
<b>ReferenceSample</b>	varchar(255)
<b>Remarks</b>	text
<b>OrgID</b>	int(6)
<b>MethodID</b>	int(6)
<b>nPrimers</b>	varchar(50)
<b>Confidential</b>	char(1)
<b>RecordModification</b>	timestamp(1)

Table 9: Database table "pcr".

## 2.11 Table person

Attribute	Description
PersonID	Primary Key.

Attribute	Description
Title	Title of a person, e.g. Dr. or Prof. or Mr.,....
FirstName	First name of a person.
LastName	Last name of a person.
Gender	Gender of a person. Simply „m“ for male and f for „female“.
Position	Position of a person.
PostAddr	Post address of a person.
CountryID	The countryID the person lives in. See table country.
Phone	Phone number of a person.
Fax	Fax number of a person.
Email	e-Mail address of a person.
URL	URL of a website the person is listed.
LanguageID	Language ID a person speaks. See table language.
Remarks	Any further remarks of a person.
OrgID	Organisation ID of a persons organisation. See table organisation.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

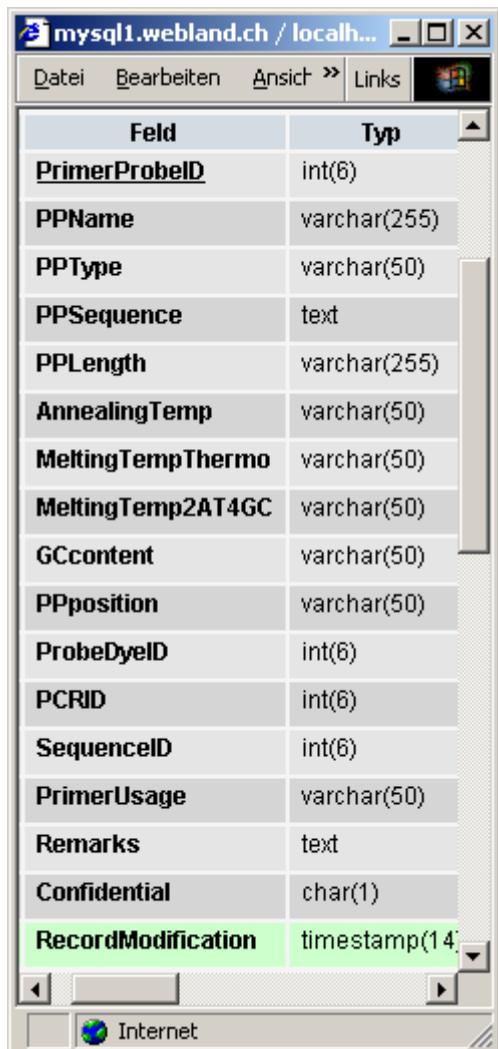
mysql1.webland.ch / local...	
Feld	Typ
<u>PersonID</u>	int(6)
<b>Title</b>	varchar(50)
<b>FrstName</b>	varchar(50)
<b>LastNames</b>	varchar(255)
<b>IdentificationName</b>	varchar(255)
<b>OrgID</b>	int(6)
<b>Gender</b>	char(1)
<b>Position</b>	varchar(255)
<b>Category</b>	varchar(50)
<b>PostAddr</b>	text
<b>CountryID</b>	int(6)
<b>Phone</b>	varchar(50)
<b>Fax</b>	varchar(50)
<b>Email</b>	varchar(255)
<b>URL</b>	varchar(255)
<b>LanguageID</b>	int(6)
<b>Remarks</b>	text
<b>RecordModification</b>	timestamp(14);
<b>Confidential</b>	char(1)

Table 10: Database table "person".

## 2.12 Table primer

Attribute	Description
PrimerProbeID	Primary Key
PPName	PPName according to the Primer.
PPType	PPType according to the Primer.
PPSequence	PPSequence according to the Primer.
PPLength	PPLength according to the Primer.
AnnealingTemp	AnnealingTemp according to the Primer.
MeltingTempThermo	MeltingTempThermo according to the Primer.
MeltingTemp2AT4GC	MeltingTemp2AT4GC according to the Primer.
Gccontent	GCcontent according to the Primer.

Attribute	Description
Pposition	PPposition according to the Primer.
ProbeDyeID	ProbeDyeID according to the Primer. See table probedeye.
PrimerUsage	PrimerUsage according to the Primer.
PCRID	PCRID according to the Primer. See table pcr.
SequenceID	SequenceID according to the Primer. See table sequence.
Remarks	Remarks according to the Primer.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.



The screenshot shows the MySQL Workbench interface with a database table named 'primer'. The table has 15 columns with the following definitions:

Feld	Typ
<u>PrimerProbeID</u>	int(6)
PPName	varchar(255)
PPType	varchar(50)
PPSequence	text
PPLength	varchar(255)
AnnealingTemp	varchar(50)
MeltingTempThermo	varchar(50)
MeltingTemp2AT4GC	varchar(50)
GCcontent	varchar(50)
PPposition	varchar(50)
ProbeDyeID	int(6)
PCRID	int(6)
SequenceID	int(6)
PrimerUsage	varchar(50)
Remarks	text
Confidential	char(1)
RecordModification	timestamp(14)

Table 11: Database table "primer".

## 2.13 Table proteindetection

Attribute	Description
ProteinDetectionID	Primary Key.
ProteinDetectionName	Protein Detection Name according to the Protein Detection.
Pdtype	PDtype according to the Protein Detection.
SamplePreparation	SamplePreparation according to a Protein Detection.
TestType	TestType according to a Protein Detection.
ElementID	ElementID according to a Protein Detection. See table geneticelement.
CaptureAntibody	CaptureAntibody according to a Protein Detection.
CaptABType	CaptABType according to a Protein Detection.
CaptABDescription	CaptABDescription according to the Protein Detection.
CaptABSourceTax	CaptABSourceTax according to a Protein Detection.
CaptABProducer	CaptABProducer for the Protein Detection.
DetectionAntibody	DetectionAntibody for the Protein Detection.
DetABType	DetABType of an Protein Detection.
DetABDescription	DetABDescription of an Protein Detection.
DetABSourceTax	DetABSourceTax of an Protein Detection.
DetABProducer	DetABProducer of an Protein Detection.
PositiveControl	PositiveControl of an Protein Detection.
SampleID	SampleID of the Protein Detection. See table sample.
MethodID	MethodID of an Protein Detection. See table method.
PublicationID	PublicationID of an Protein Detection. See table publication.
Remarks	Remarks according to the Protein Detection.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

Feld	Typ
ProteinDetectionID	int(6)
ProteinDetectionName	varchar(255)
PDtype	varchar(50)
SamplePreparation	varchar(50)
TestType	varchar(50)
ElementID	int(6)
CaptureAntibody	varchar(50)
CaptABType	varchar(50)
CaptABDescription	varchar(50)
CaptABSourceTax	varchar(50)
CaptABProducer	varchar(50)
DetectionAntibody	varchar(50)
DetABType	varchar(50)
DetABDescription	varchar(50)
DetABSourceTax	varchar(50)
DetABProducer	varchar(50)
PositiveControl	varchar(50)
SampleID	int(6)
MethodID	int(6)
PublicationID	int(6)
Remarks	text
Confidential	char(1)

Table 12: Database table "proteinindetection".

## 2.14 Table publication

Attribute	Description
PublicationID	Primary Key.
Title	Full title of an Publication.
ShortTitle	Short title of an Publication.
Authors	Authors of an Publication.

Attribute	Description
OrgID	OrgID of an Publication. See table organisation.
PubDate	PubDate of an Publication.
Version	Version of an Publication.
PublicationType	PublicationType of an Publication.
LanguageID	LanguageID of an Publication. See table language.
ISBN	ISBN of an Publication.
ISSN	ISSN of an Publication.
ReportTitle	ReportTitle of an Publication.
Volume	Volume of an Publication.
Issue	Issue of an Publication.
Pages	Pages of an Publication.
Filefrmt	Filefrmt of an Publication.
URL	URL of an Publication.
Medium	Medium of an Publication.
Remarks	Any further remarks of an Publication.
TaxonID	TaxonID of an Publication. See table taxonomy.
Method	Method of an Publication.
FileName	FileName of an Publication.
LocalContent	LocalContent of an Publication.
FileSize	FileSize of an Publication.
PCRID	PCRID of an Publication. See table pcr.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

The screenshot shows a Microsoft Management Console (MMC) window titled "mysql1.webland.ch / local...". The window displays a table of database fields and their types. The columns are labeled "Feld" (Field) and "Typ" (Type). The table contains 23 rows, each representing a field in the "publication" table. The fields and their types are:

Feld	Typ
<u>PublicationID</u>	int(6)
<b>ShortTitle</b>	varchar(255)
<b>Title</b>	varchar(255)
<b>Authors</b>	varchar(255)
<b>OrgID</b>	varchar(255)
<b>PubDate</b>	varchar(50)
<b>Version</b>	varchar(255)
<b>PublicationType</b>	varchar(50)
<b>LanguagelD</b>	int(6)
<b>ISBN</b>	varchar(50)
<b>ISSN</b>	varchar(50)
<b>ReportTitle</b>	varchar(255)
<b>Volume</b>	varchar(50)
<b>Issue</b>	varchar(50)
<b>Pages</b>	varchar(50)
<b>Filefrmt</b>	varchar(255)
<b>URL</b>	varchar(255)
<b>Medium</b>	varchar(255)
<b>Remarks</b>	text
<b>RecordModification</b>	timestamp(14)
<b>Method</b>	varchar(255)
<b>FileName</b>	varchar(50)
<b>PublicFileName</b>	varchar(50)
<b>LocalContent</b>	varchar(255)
<b>Confidential</b>	char(1)

Table 13: Database table "publication".

## 2.15 Table sample

Attribute	Description
SampleID	Primary Key.
WP_Nr	Trace Project Workpackage Number according to the Sample.
Commodity	Commodity according to the Sample ID. Commodity normally consists of one letter, e.g. w = water; h = honey; o = olive; c = cereal; b = beef; l = lamb; p = poultry.
Country	Country where the sample was collected. The country code consists of two letters that follow the ICANN Top Level Domains. Country code xx means, the country is not appropriated.
Site	Site according to the Sample ID. Site is a three letter short form, e.g. Car = Carpentras; Cin = Ciney; Lim = Limousin. XXX means "no appropriated".
Year	Year when the sample was collected. The field year consists of two letters starting with 01 = 2001; 02 = 2002. Be aware: 00 does not mean year 2000, but means "no appropriated".
Month	Month when a sample was collected. This field contains two numbers: 01 is January, 02 is February...
Number	Sample number assigned by the responsible person. This field consists of four numbers starting with 0001.
TraceSampleCode	Trace Sample Code of a sample. The Trace Sample Code consists of 15 letters and numbers in following order: Workpackage Number (1 number), Commodity (1 char), Country (2 chars), Site (3 chars), Year (2 numbers), Month (2 numbers) and Number (4 numbers).
ResponsiblePerson	Person ID of the responsible person for the sample. See table person.
InternalSampleCode	Internal Sample Code of the sample provider or the TRACE institute. They use it for their convenience.
SetName	Set Name of a sample. A Set Name is a name given to a set of samples corresponding to a specific process in the project.
LocationName	Location Name of a sample. The Location Name is the site where the sample was collected.
ProducerIdentificationName	Producer Identification Name of a sample. This can be a farmer, producer,...
CollectorIdentificationName	Collector Identification Name ID of a sample. This is the person in charge to collect the sample.
DonorIdentificationName	Donor Identification Name of a sample. The function of this person must be defined in Workpackage 3. Waiting for the definition...
FoodProductID	Food Product Name ID of the sample. This name is used in the Food Standards (see foodproduct table).

Attribute	Description
TaxonID	Trace Popular Name ID = TaxonID of an Sample. See table taxonomy.
SampleType	Sample Type of an Sample. Sample Type are for animals: skin, blood, muscle; for vegetals: fruit, oil, pollen leaves, buds, grain, root, seed; for mineral: water or soil; for food product: honey, meat.
SamplingDate	Date of sample collection.
SamplingProcedure	Sampling Procedure of an Sample. e.g. one sample and ? subsamples to provide the sample.
SamplingPurpose	Sampling Purpose of an Sample. This is either RNA or DNA extraction.
SampleQuantity	Sample Quantity of an Sample. This can be the weight, volume or number of plants collected.
ContainerType	Container Type of an Sample. This is the type of container, where the sample is stored.
StorageCondition	Storage Condition of an Sample.
Picture	Picture (just the link to a file) of an Sample.
SoilAnalysis	Soil Analysis of an Sample. This value just tells whether a soil analysis is planned or not.
Comment	Comment / Remarks of an Sample.
Specific01	First specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific02	Second specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific03	Third specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific04	Fourth specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific05	Fifth specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific06	Sixth specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific07	Seventh specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
Specific08	Eighth specific feature of an Sample. This field includes two parts. The first part is the name of the field and is finished with an ":". After this the content of the field starts.
FoodName	FoodName according to the Sample.
ExtractionID	ExtractionID according to the Sample. See table extraction.
Processing	Processing according to the Sample.
NucleoConz	NucleoConz according to the Sample.

Attribute	Description
DNAconz	DNAconz according to the Sample.
AmplIDNA	aDNA according to the Sample.
Ingredients	Ingredients according to the Sample.
PublicationID	Publication ID according to the Sample. See table publication.
Confidential	Whether a record is confidential or not. The database field consists of one char.
RecordModification	Date of last modification of the record. Timestamp.

Feld	Typ
<b>SampleID</b>	int(6)
<b>WP_Nr</b>	int(1)
<b>Commodity</b>	char(1)
<b>Country</b>	char(2)
<b>Site</b>	char(3)
<b>Year</b>	char(2)
<b>Month</b>	char(2)
<b>Number</b>	varchar(4)
<b>TraceSampleCode</b>	varchar(15)
<b>ResponsiblePerson</b>	int(6)
<b>InternalSampleCode</b>	varchar(12)
<b>SetName</b>	varchar(255)
<b>LocationName</b>	varchar(255)
<b>ProducerIdentificationName</b>	varchar(255)
<b>CollectorIdentificationName</b>	varchar(50)
<b>DonorIdentificationName</b>	varchar(50)
<b>FoodProductID</b>	int(6)
<b>TaxonID</b>	int(6)
<b>SampleType</b>	varchar(50)
<b>SamplingDate</b>	date
<b>SamplingProcedure</b>	varchar(10)
<b>SamplingPurpose</b>	varchar(255)
<b>SampleQuantity</b>	varchar(255)
<b>Gender</b>	char(1)
<b>AnimalRegistrationNumber</b>	varchar(15)
<b>DateBirth</b>	varchar(10)
<b>RecordModification</b>	timestamp(14)
<b>PublicationID</b>	int(6)
<b>Confidential</b>	char(1)

Table 14: Database table "sample".

## 2.16 Table sequence

Attribute	Description
SequenceID	Primary Key.
SequenceName	Sequence Name of an Sequence.
Description	Sequence description of an Sequence.
TaxonID	Taxon ID to the Sequence. See table taxonomy.
ElementID	Element ID to the Sequence. See table geneticelement.
SeqType	Seqence type to the Sequence.
NCBIAccession	NCBI Accession to the Sequence.
Version	Version to the Sequence.
Keywords	Keywords of the Sequence.
Comment	Comment of the Sequence.
Publication	Publication of the Sequence.
BaseCount	BaseCount of the Sequence.
DNAsequence	DNAsequence of the Sequence.
Aasequence	AAsequence of the Sequence.
Alignment	Alignment of the Sequence.
FullNCBIdatasheet	FullNCBIdatasheet of the Sequence.
URL	URL of the Sequence.
OrgID	Organisation ID of the Sequence. See table Organisation.
Remarks	Remarks of the Sequence.
Confidential	Whether a record is confidential or not. The database field consists of one char.
RecordModification	Date of last modification of the record. Timestamp.

Feld	Typ
<u>SequenceID</u>	int(6)
<b>SequenceName</b>	varchar(255)
<b>Description</b>	text
<b>TaxonID</b>	int(6)
<b>ElementID</b>	int(6)
<b>SeqType</b>	varchar(50)
<b>NCBIAccession</b>	varchar(30)
<b>Version</b>	varchar(50)
<b>Keywords</b>	varchar(255)
<b>Comment</b>	text
<b>Publication</b>	text
<b>BaseCount</b>	varchar(255)
<b>DNAsequence</b>	varchar(60)
<b>AAsequence</b>	varchar(60)
<b>Alignment</b>	varchar(50)
<b>FullNCBIdatasheet</b>	varchar(50)
<b>URL</b>	varchar(255)
<b>OrgID</b>	int(6)
<b>Remarks</b>	text
<b>Confidential</b>	char(1)
<b>RecordModification</b>	timestamp(14)

Table 15: Database table "sequence".

## 2.17 Table site

Attribute	Description
SiteID	Primary Key.
LocationName	Location Name according to the Site. The Location Name is, where the sample is selected or purchased (see general descriptor: location name)
TraceSiteCode	TraceSiteCode according to the Site. This Code is used in the Trace sample code (3 digits).
SiteCoordinator	SiteCoordinator according to a Site.

Attribute	Description
CountryID	CountryID according to a Site. See table country.
PoliticArea	PoliticArea according to a Site.
PoliticSubarea	PoliticSubarea according to a Site.
GeographicArea	GeographicArea according to a Site.
GeographicSubarea	GeographicSubarea according to the Site.
PostalCode	PostalCode according to a Site.
CityName	CityName for the Site.
LocalName	LocalName for the Site. This is a the local or field name.
Parcel	Parcel of an Site. This is the area identification where the sample was collected in the field.
GPS	GPS of an Site. These are the coordinates of sampling/rearing locations (preferably GPS, but postcode is acceptable) Format [d]y.y,[d]x.x or [d]y:yy,yy,[d]x:xx:xx where [d] is the optional direction NSE or W, y = lat, x = long, -x is west, +x is east. E.g. 52.038333,4.578611 or N52.038333, W4.578611 or 52:02:18,-4:34: 43 or N52:02:18,W4:34:43
Longitude	Specific description of the Longitude of an Site.
Latitude	Specific description of the Latitude of an Site.
Altitude	Altitude of an Site in meters above sea level.
Map	Map of the Site. This is a link to a picture or map.
PACNb	PACNb of an Site. This is a specific PAC number for EU subsidies.
Area	Area of an Site in Ha.
Soil	Soil type according to the Site.
AgriculturalSystem	AgriculturalSystem according to the Site. This is organic, integrated, conventional.
LandUse	LandUse according to the Site. This can be Arable land, Pasture, Olive, Forest.
Relief	Relief according to the Site.
Slope	Slope according to the Site.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

The screenshot shows a MySQL Workbench interface with a table named 'site'. The table has 25 columns, each with a name and a data type. The columns are:

Feld	Typ
<u>SitID</u>	int(6)
<b>LocationName</b>	varchar(255)
<b>TraceSiteCode</b>	varchar(255)
<b>SiteCoordinator</b>	varchar(255)
<b>CountryID</b>	varchar(255)
<b>PoliticArea</b>	varchar(255)
<b>PoliticSubarea</b>	varchar(255)
<b>GeographicArea</b>	varchar(255)
<b>GeographicSubarea</b>	varchar(255)
<b>PostalCode</b>	varchar(50)
<b>CityName</b>	varchar(255)
<b>LocalName</b>	varchar(255)
<b>Parcel</b>	varchar(255)
<b>GPS</b>	varchar(255)
<b>Longitude</b>	varchar(255)
<b>Latitude</b>	varchar(255)
<b>Altitude</b>	varchar(255)
<b>Map</b>	varchar(255)
<b>PACNb</b>	varchar(255)
<b>Area</b>	varchar(255)
<b>Soil</b>	varchar(255)
<b>AgriculturalSystem</b>	varchar(255)
<b>LandUse</b>	varchar(255)
<b>Relief</b>	varchar(255)
<b>Slope</b>	varchar(255)
<b>Confidential</b>	char(1)

Table 16: Database table "site".

## 2.18 Table taxonomy

Attribute	Description
TaxonID	Primary Key.
PopularName	Popular name of a taxonomy.
Genus	Genus of a taxonomy.
Species	Genus of a taxonomy.
SuperKingdom	Super kingdom of a taxonomy.
Kingdom	Kingdom of a taxonomy.
Class	Class of a taxonomy.
Order	Order of a taxonomy.
Family	Family of a taxonomy.
Phylum	Phylum of a taxonomy.
SubPhylum	SubPhylum of a taxonomy.
Division	Division of a taxonomy.
Subdivision	Subdivision of a taxonomy.
SuperClass	SuperClass of a taxonomy.
SuperOrder	SuperOrder mily of a taxonomy.
Subfamily	Subfamily of a taxonomy.
Tribe	Tribe of a taxonomy.
Subspecies	Subspecies of a taxonomy.
Variety	Variety of a taxonomy.
Cultivar	Cultivar of a taxonomy.
Line	Line of a taxonomy.
SizeOfGenom	SizeOfGenom of a taxonomy.
URL	URL of a taxonomy.
References	References of a taxonomy.
FoodCompData	FoodCompData of a taxonomy.
Remarks	Remarks of a taxonomy.
Confidential	Whether a record is confidential or not. This field contains one char. If a record is confidential, the value is "y".
RecordModification	Date of last modification of the record. Timestamp.

mysql1.webland.ch / localho...

---

Feld	Typ
<b>TaxonID</b>	int(6)
<b>TracePopularName</b>	varchar(255)
<b>PopularName</b>	varchar(255)
<b>SuperKingdom</b>	varchar(50)
<b>Kingdom</b>	varchar(50)
<b>Phylum</b>	varchar(50)
<b>SubPhylum</b>	varchar(50)
<b>Division</b>	varchar(255)
<b>Subdivision</b>	varchar(255)
<b>SuperClass</b>	varchar(50)
<b>Class</b>	varchar(255)
<b>SuperOrder</b>	varchar(50)
<b>TaxonOrder</b>	varchar(255)
<b>Family</b>	varchar(255)
<b>Subfamily</b>	varchar(255)
<b>Tribe</b>	varchar(255)
<b>Genus</b>	varchar(255)
<b>Species</b>	varchar(255)
<b>Subspecies</b>	varchar(255)
<b>OriginCountry</b>	varchar(255)
<b>Pedigree</b>	varchar(255)
<b>Variety</b>	text
<b>Cultivar</b>	varchar(50)
<b>Line</b>	varchar(50)
<b>BreederName</b>	varchar(255)
<b>SizeOfGenom</b>	varchar(50)
<b>URL</b>	varchar(255)
<b>TaxonRefURL</b>	varchar(255)
<b>FoodCompData</b>	varchar(50)
<b>Remarks</b>	text
<b>Confidential</b>	char(1)
<b>RecordModification</b>	timestamp(14)

---

Internet

*Table 17: Database table "taxonomy".*

## 3 Trace Web Database - API

This documentation is for the API and the database tables. The API has one function for each database table column. In each table section you will find the file name and some general functions. After these you find a function for each table column. The function name corresponds the table and column name, e.g. function get\_extraction\_ExtractionName(...) means table extraction, column ExtractionName. After the function name you will find a short general description of the function. If there is additional information about the data of a column, it is provided after the general description.

Not documented are the ID-Fields, RecordModification and some Remark fields in list\_tables.

### 3.1 API extraction

```
function get_extraction_countAllExtractions()  
/*  
 * This function returns the number of all Extractions in Database  
 */  
  
function get_extraction_ExtractionName($ExtractionID, $allow_access)  
/*  
 * This function returns the extraction name of an extraction. The extraction  
 * name may have a maximum of 255 characters.  
 */  
  
function get_extraction_ExtractionDescription($ExtractionID, $allow_access)  
/*  
 * This function returns the extraction descripton of an extraction.  
 * The extraction description is a text field.  
 */  
  
function get_extraction_ExtractionCompany($ExtractionID, $allow_access)  
/*  
 * This function returns the extraction company of an extraction. The extraction  
 * company may have a maximum of 255 caracters.  
 */  
  
function get_extraction_Remarks($ExtractionID, $allow_access)  
/*  
 * This function returns the remarks for an extraction. The extraction  
 * remarks is a string of max. 255 characters.  
 */  
  
function get_extraction_TissueType($ExtractionID, $allow_access)  
/*  
 * This function returns the tissue type of an extraction. The extraction  
 * tissue type may have a maximum of 50 caracters.  
 */  
  
function get_extraction_TimePerSample($ExtractionID, $allow_access)  
/*  
 * This function returns the Time Per Sample of an extraction. The extraction  
 * time per sample may have a maximum of 50 caracters.  
 */  
  
function get_extraction_SampleSize($ExtractionID, $allow_access)  
/*  
 * This function returns the extraction sample size of an extraction. The  
 * extraction sample size may have a maximum of 50 caracters.  
 */
```

```
function get_extraction_MeasuringMethod($ExtractionID, $allow_access)
/*
* This function returns the extraction method of an extraction. The extraction
* method may have a maximum of 255 caracters.
*/

function get_extraction_Purity($ExtractionID, $allow_access)
/*
* This function returns the extraction purity of an extraction. The extraction
* purity may have a maximum of 50 caracters.
*/

function get_extraction_Yield($ExtractionID, $allow_access)
/*
* This function returns the extraction yield of an extraction. The extraction
* yield may have a maximum of 50 caracters.
*/

function get_extraction_MethodID($ExtractionID, $allow_access)
/*
* This function returns the extraction method ID of an extraction. The
* extraction method id is a smallint. See table method.
*/

function get_extraction_PublicationID($ExtractionID, $allow_access)
/*
* This function returns the extraction PublicationID of an extraction. The
* extraction PublicationID is a smallint. See table Publication
*/

function get_extraction_Confidential($ExtractionID)
/*
* This function returns wether a extraction record is confidential or not.
* This field contains one char. If a record is confidential, the value is "y".
*/
```

## 3.2 API foodproduct

```
function get_FoodProduct_RecordNumberforFoodProductID($FoodProductID)
/*
* This function returns the record number for a FoodProductID.
*/

function get_FoodProduct_FoodProductIDforRecordNumber($record_number)
/*
* This function returns the FoodProductID for a record number.
*/

function get_FoodProduct_FoodProductIDs()
/*
* This function returns all FoodProductIDs
*/

function get_FoodProduct_countAllFoodProducts()
/*
* This function returns the number of all FoodProducts in Database
*/

function get_FoodProduct_FoodProductName($FoodProductID, $allow_access)
/*
* This function returns the Food ProductName of a foodproduct.
*/
```

```
function get_FoodProduct_FoodName($FoodProductID, $allow_access)
/*
* This function returns the Food Name of a foodproduct.
* This field contains the preferred food name and additional synonyms in various
* languages. Food Names should start with an upper case first character in the
* first word, e.g. Grapefruit,... Scientific Names must use Latin (la) as language flag
* and should adhere to the following format: Genus species Author [, Year], e.g.
* Gadus morhua Linnaeus, 1758.
*/

function get_FoodProduct_Abbrev($FoodProductID, $allow_access)
/*
* This function returns the Abbreviated Food Name of a foodproduct.
* This field is used for applications with limited screen/paper space.
*/

function get_FoodProduct_OrigFdCd($FoodProductID, $allow_access)
/*
* This function returns the Original Food Code of a foodproduct.
* The food code, ID, or abbreviation used to identify the food in the original
* publication.
*/

function get_FoodProduct_OrigGpCd($FoodProductID, $allow_access)
/*
* This function returns the Original Food Group Code of the type a foodproduct is.
* The proprietary classification code is used in the original publication. The
* proprietary classification system should be provided separately under ORIGFDGP
* within the primary source description.
*/

function get_FoodProduct_ProdType($FoodProductID, $allow_access)
/*
* This function returns the Product Type a foodproduct.
* FDA product type thesaurus of Langual facet A.
*/

function get_FoodProduct_CdxFdStd($FoodProductID, $allow_access)
/*
* This function returns the CODEX Food Standards of a foodproduct.
* Codex Alimentarius Food Standards code.
*/

function get_FoodProduct_CdxFdAdd($FoodProductID, $allow_access)
/*
* This function returns the CODEX Food Categorization System for the General
* Standards for Food Additives of a foodproduct.
*/

function get_FoodProduct_CdxFdFd($FoodProductID, $allow_access)
/*
* This function returns the CODEX Classification of Foods and Feeds of a
* foodproduct.
*/

function get_FoodProduct_CdxCont($FoodProductID, $allow_access)
/*
* This function returns the CODEX Food Categorization System for Contaminants
* of a foodproduct.
*/

function get_FoodProduct_FAOFBS($FoodProductID, $allow_access)
```

```

/*
 * This function returns the FAO Food Balance Sheet Classification of a foodproduct.
 */

function get_FoodProduct_CIAA($FoodProductID, $allow_access)
/*
 * This function returns the CIAA Food Categorization of a foodproduct.
 */

function get_FoodProduct_EC2($FoodProductID, $allow_access)
/*
 * This function returns the Eurocode2 of a foodproduct.
 */

function get_FoodProduct_EAN($FoodProductID, $allow_access)
/*
 * This function returns the European Article Number (EAN) of a foodproduct.
 * For European Articles only.
 */

function get_FoodProduct_UPC($FoodProductID, $allow_access)
/*
 * This function returns the Universal Product Code (UPC) of a foodproduct.
 */

function get_FoodProduct_ENr($FoodProductID, $allow_access)
/*
 * This function returns the E-Number of a foodproduct.
 * If food is food additive, code according to the European E-Number system for
 * additive standardisation.
 */

function get_FoodProduct_INS($FoodProductID, $allow_access)
/*
 * This function returns the INS-Code of a foodproduct.
 * If the food is a food additive, code according to the International Numbering
 * System for food additives according to CODEX Alimentarius
 */

function get_FoodProduct_Manufact($FoodProductID, $allow_access)
/*
 * This function returns the Manufacturer of a foodproduct.
 * Link to Organisation table (OrganisationID). Describes the direct
 * manufacturer of producer of the food. e.g. farmer is considered a
 * manufacturer.
 */

function get_FoodProduct_Distrib($FoodProductID, $allow_access)
/*
 * This function returns the Distributor of a foodproduct.
 * Between producer and retailer. Link to Organisation Table (Organisation
 * ID).
 */

function get_FoodProduct_FoodSrce($FoodProductID, $allow_access)
/*
 * This function returns the Food Source of a foodproduct.
 * Langual facet B.
 */

function get_FoodProduct_GenManip($FoodProductID, $allow_access)
/*
 * This function returns wether a foodproduct is genetically Modified or not.
 */

```

```
*/  
  
function get_FoodProduct_AgriCond($FoodProductID, $allow_access)  
/*  
* This function returns the Agricultural Production Conditions of a foodproduct.  
* Brief description of soil conditions, watering schemes, feeding, harvesting,  
* slaughtering, ripeness, etc.  
*/  
  
function get_FoodProduct_Color($FoodProductID, $allow_access)  
/*  
* This function returns the Color of a foodproduct.  
* Color values are currently not further specified. More detailed recommendations  
* are planned in future versions of the Eurofoods Recommentations.  
*/  
  
function get_FoodProduct_GenImage($FoodProductID, $allow_access)  
/*  
* This function returns the Generic Image of a foodproduct.  
* The file names of generic images showing foods similar to the food sample in  
* question.  
*/  
  
function get_FoodProduct_SpcImage($FoodProductID, $allow_access)  
/*  
* This function returns the Specific Image of a foodproduct.  
* The file names of specific images of the food sample, i.e. the food that was  
* actually analysed.  
*/  
  
function get_FoodProduct_PDOImage($FoodProductID, $allow_access)  
/*  
* This function returns the PDO Image (Production Label) of a foodproduct.  
*/  
  
function get_FoodProduct_PartPlan($FoodProductID, $allow_access)  
/*  
* This function returns the Part of Plant or Animal of a foodproduct.  
* See Languual facet C of Eurofood Recommandation.  
*/  
  
function get_FoodProduct_EdPort($FoodProductID, $allow_access)  
/*  
* This function returns the Percentage Edible Portion of a foodproduct.  
* May also be considered a component.  
*/  
  
function get_FoodProduct_NatEdPor($FoodProductID, $allow_access)  
/*  
* This function returns the Nature of Edible Portion of a foodproduct.  
* Which parts of the food are edible, e.g. flesh, root, leaf, etc.?  
*/  
  
function get_FoodProduct_NatWaste($FoodProductID, $allow_access)  
/*  
* This function returns the Nature of Waste of a foodproduct.  
* Which parts of the food are not edible, e.g. rind, bone, stone, peel, etc.?  
*/  
  
function get_FoodProduct_PhysState($FoodProductID, $allow_access)  
/*  
* This function returns the Physical State Shape or Form of a foodproduct.  
* See Languual facet E of Eurofood Recommandation.
```

\*/

```
function get_FoodProduct_HeaTreat($FoodProductID, $allow_access)
/*
* This function returns the Extent of Heat Treatment of a foodproduct.
* See Langual facet F of Eurofood Recommendation.
*/

function get_FoodProduct_TreatApp($FoodProductID, $allow_access)
/*
* This function returns the Treatment Applied of a foodproduct.
* See Langual facet H of Eurofood Recommendation.
*/

function get_FoodProduct_CookMeth($FoodProductID, $allow_access)
/*
* This function returns the Cooking Method of a foodproduct.
* See Langual facet G of Eurofood Recommendation.
*/

function get_FoodProduct_RecProc($FoodProductID, $allow_access)
/*
* This function returns the Recipe Procedure of a foodproduct.
* If food is a recipe.
*/

function get_FoodProduct_PublicationID($FoodProductID, $allow_access)
/*
* This function returns the Recipe Bibliographic Reference (PublicationID)
* of a foodproduct.
* Link to the publication table (Publication ID) Describes the publication holding the
* recipe.
*/

function get_FoodProduct_FinlPrep($FoodProductID, $allow_access)
/*
* This function returns the Final Preparation of a foodproduct.
* Final preparation of food before consumption, e.g. heating a frozen dinner or
* canned food.
*/

function get_FoodProduct_PresMeth($FoodProductID, $allow_access)
/*
* This function returns the Preservation Method of a foodproduct.
* See Langual facet J of Eurofood Recommendation.
*/

function get_FoodProduct_PackMed($FoodProductID, $allow_access)
/*
* This function returns the Packing Medium of a foodproduct.
* See Langual facet K of Eurofood Recommendation.
*/

function get_FoodProduct_FdCtSrfc($FoodProductID, $allow_access)
/*
* This function returns the Food Contact Surface of a foodproduct.
* See Langual facet N of Eurofood Recommendation.
*/

function get_FoodProduct_ContWrpg($FoodProductID, $allow_access)
/*
* This function returns the Container or Wrapping of a foodproduct.
* See Langual facet M of Eurofood Recommendation.
```

```
*/  
  
function get_FoodProduct_StorCond($FoodProductID, $allow_access)  
/*  
* This function returns the Storage Conditions of a foodproduct.  
* Storage conditions and duration before arrival at lab.  
*/  
  
function get_FoodProduct_AeraOrig($FoodProductID, $allow_access)  
/*  
* This function returns the Area of Origin of a foodproduct.  
* Origin of the main raw material or area where food was produced if food is a  
* mixed product.  
* See Langual facet R of Eurofood Recommendation.  
*/  
  
function get_FoodProduct_AeraProc($FoodProductID, $allow_access)  
/*  
* This function returns the Area of Procesing of a foodproduct.  
* Use if different from AREAORIG.  
* See Langual facet R of Eurofood Recommendation.  
*/  
  
function get_FoodProduct_AeraCons($FoodProductID, $allow_access)  
/*  
* This function returns the Area of Consumption of a foodproduct.  
* See Langual facet R of Eurofood Recommendation.  
*/  
  
function get_FoodProduct_LblClaim($FoodProductID, $allow_access)  
/*  
* This function returns the Customer Group Label Claim of a foodproduct.  
* See Langual facet P of Eurofood Recommendation.  
*/  
  
function get_FoodProduct_SpecGrav($FoodProductID, $allow_access)  
/*  
* This function returns the Specific Gravity of a foodproduct.  
* May also be considered a component. It is the density of the food devided by the  
* densitiy of water at the same temperature. Specific Gravity is used to convert to  
* convert to and from standard volumetrix or household measures.  
*/  
  
function get_FoodProduct_ServSize($FoodProductID, $allow_access)  
/*  
* This function returns the Typical Serving Size in grams of a foodproduct.  
*/  
  
function get_FoodProduct_PackWght($FoodProductID, $allow_access)  
/*  
* This function returns the Typical Package Weight in grams of a foodproduct.  
*/  
  
function get_FoodProduct_PiecWght($FoodProductID, $allow_access)  
/*  
* This function returns the Typical Weight per Piece in grams of a foodproduct.  
*/  
  
function get_FoodProduct_FreqSeas($FoodProductID, $allow_access)  
/*  
* This function returns the Frequency and Season of a foodproduct.  
* How often and in which season is the food preferably consumed?  
*/
```

```

function get_FoodProduct_PlacDiet($FoodProductID, $allow_access)
/*
 * This function returns the Place of Food in Diet of a foodproduct.
 * How does the food relate to other foods in the diet? Is it a major source of
 * some nutrient?
 */

function get_FoodProduct_Cuisine($FoodProductID, $allow_access)
/*
 * This function returns the Cuisine of a foodproduct.
 * Possible future Langual facet Q of the Eurofood Recommendation. The special
 * diet a food belongs to (e.g. Mediteranean cuisine).
 */

function get_FoodProduct_URL($FoodProductID, $allow_access)
/*
 * This function returns the URL of a foodproduct.
 */

function get_FoodProduct_Remarks($FoodProductID, $allow_access)
/*
 * This function returns the Remarks of a foodproduct.
 * Any further remarks.
 */

function get_FoodProduct_FoodproductIDsforTaxonID($TaxonID)
/*
 * This function returns the Taxonomy ID of a foodproduct.
 */

function get_FoodProduct_TaxonID($FoodProductID, $allow_access)
/*
 * This function returns the TaxonID of a foodproduct.
 */

function get_FoodProduct_SampleID($FoodProductID, $allow_access)
/*
 * This function returns the SampleID of a foodproduct.
 */

function get_FoodProduct_Confidential($FoodProductID)
/*
 * This function returns wether a food product record is confidential or not.
 * This field contains one char. If a record is confidential, the value is "y".
 */

```

### 3.3 API geneticelement

```

function get_geneticelement_RecordNumberforElementID($ElementID)
/*
 * This function returns the record number for a PublicationID.
 */

function get_geneticelement_countAllGeneticElements()
/*
 * This function returns the number of all GeneticElements in Database
 */

function get_geneticelement_ElementIDs()
/*
 * This function returns all ElementIDs
 */

```

```
function get_geneticelement_ElementIDforRecordNumber($record_number)
/*
* This function returns the ElementID for a record number.
*/

function get_geneticelement_ElementName($ElementID, $allow_access)
/*
* This function returns the element name of an genetic element.
*/

function get_geneticelement_ElementCode($ElementID, $allow_access)
/*
* This function returns the ElementCode of an genetic element.
*/

function get_geneticelement_ElementType($ElementID, $allow_access)
/*
* This function returns the ElementType of an genetic element.
*/

function get_geneticelement_Size($ElementID, $allow_access)
/*
* This function returns the Size of an genetic element.
*/

function get_geneticelement_Map($ElementID, $allow_access)
/*
* This function returns the Map of an genetic element.
*/

function get_geneticelement_Sequence($ElementID, $allow_access)
/*
* This function returns the Sequence of an genetic element.
*/

function get_geneticelement_TaxonID($ElementID)
/*
* This function returns the TaxonID of an genetic element.
*/

function get_geneticelement_Trait($ElementID, $allow_access)
/*
* This function returns the element name of an genetic element.
*/

function get_geneticelement_ProteinProduct($ElementID, $allow_access)
/*
* This function returns the ProteinProduct of an genetic element.
*/

function get_geneticelement_Expression($ElementID, $allow_access)
/*
* This function returns the Expression of an genetic element.
*/

function get_geneticelement_Mechanism($ElementID, $allow_access)
/*
* This function returns the Mechanism of an genetic element.
*/

function get_geneticelement_Remarks($ElementID, $allow_access)
/*
```

```
* This function returns the element name of an genetic element.  
*/
```

```
function get_geneticelement_Confidential($ElementID)  
/*  
* This function returns the confidential String for a ElementID.  
*/
```

### **3.4 API list\_country**

```
function get_listCountry_CountryName($CountryID)  
/*  
* This function returns the name of a country.  
*/  
  
function get_listCountry_CountryCode($CountryID)  
/*  
* This function returns the coutnry code (like a Top-Level-Domain code)  
* of a country.  
*/  
  
function get_listCountry_Remarks($CountryID)  
/*  
* This function returns the remarks concerning a country.  
*/
```

### **3.5 API list\_language**

```
function get_listLanguage_LanguageName($LanguageID)  
/*  
* Returns the name of a language according to the Language ID  
*/
```

### **3.6 API list\_probeDye**

```
function get_listProbeDye_ProbeDyeName($ProbeDyeID)  
/*  
* This function returns the Name for a Probe Dye.  
*/  
  
function get_listProbeDye_Excitation($ProbeDyeID)  
/*  
* This function returns the Excitation for a Probe Dye.  
*/  
  
function get_listProbeDye_Emission($ProbeDyeID)  
/*  
* This function returns the Emission for a Probe Dye.  
*/  
  
function get_listProbeDye_Company($ProbeDyeID)  
/*  
* This function returns the Company for a Probe Dye.  
*/
```

### **3.7 API method**

```
function get_Method_RecordNumberforMethodID($MethodID)  
/*  
* This function returns the record number for a MethodID.  
*/
```

```
function get_Method_countAllMethods()
/*
 * This function returns the number of all Method in Database
 */

function get_Method_MethHdln($MethodID, $allow_access)
/*
 * This function returns the Method Headline according to the Method ID.
 */

function get_Method_MethName($MethodID, $allow_access)
/*
 * This function returns the Method Name according to the Method ID.
 */

function get_Method_GenDesc($MethodID, $allow_access)
/*
 * This function returns the GenDesc according to the Method ID.
 * It contains the Scope and General Description.
 */

function get_Method_PublicationID($MethodID, $allow_access)
/*
 * This function returns the PublicationID according to the Method ID.
 * It contains the Bibliographic Reference. It's a Foreign Key: Link to Publication.
 */

function get_Method_MethodType($MethodID, $allow_access)
/*
 * This function returns the MethodType according to the Method ID.
 * Method Type is a selection from a defined list.
 */

function get_Method_SampHand($MethodID, $allow_access)
/*
 * This function returns the Sample Handling according to the Method ID.
 * It includes the description fo Sample Preparation, Extraction and clean-up at the
 * Laboratory.
 */

function get_Method_AnDetail($MethodID, $allow_access)
/*
 * This function returns the Analytical Details according to the Method ID.
 * It includes the detection procedure, quantification procedure, confirmation
 * procedure, quality control, use of reference materials.
 */

function get_Method_SampleID($MethodID, $allow_access)
/*
 * This function returns the SampleID according to the Method ID.
 */

function get_Method_Accuracy($MethodID, $allow_access)
/*
 * This function returns the Accuracy according to the Method ID.
 * It is the closeness of the arrangement between the result of a measurement and
 * the true value of the measurement. It may be assessed by the use of reference
 * material.
 */

function get_Method_Applicab($MethodID, $allow_access)
/*
```

```
* This function returns the Applicab according to the Method ID.
* It specifies the matrix, concentration range and, for Codex purposes, the
* reference to be given to "general" methods.
*/
function get_Method_LOD($MethodID, $allow_access)
/*
* This function returns the Limit of Detection according to the Method ID.
* The detection limit is conventionally defined as field blank +3d, where d is the
* standard deviation of the field blank value signal.
*/
function get_Method_LoDet($MethodID, $allow_access)
/*
* This function returns the Limit of Determination according to the Method ID.
* As for detection limit expect that 6d or 10d is required than 3d.
*/
function get_Method_LOQ($MethodID, $allow_access)
/*
* This function returns the Limit of Quantification (LOQ) according to the Method ID.
* As for detection limit, except that typically at least 10d is required.
*/
function get_Method_Precision($MethodID, $allow_access)
/*
* This function returns the Precision according to the Method ID.
* The closeness of the arrangement between independant test results obtained
* under prescribed conditions. The values obtained normally encompass both
* repeatabilities.
*/
function get_Method_Repeat($MethodID, $allow_access)
/*
* This function returns the Repeatability according to the Method ID.
* This is the value r below which is the absolute difference between two single test
* results obtained under repeatability conditions.
*/
function get_Method_Reproduc($MethodID, $allow_access)
/*
* This function returns the Reproducability (inter-lab.) according to the Method ID.
* This is the value r below which is the absolute difference between two single test
* results obtained under repeatability conditions.
*/
function get_Method_Recovery($MethodID, $allow_access)
/*
* This function returns the Recovery according to the Method ID.
* Proportion of the amount of analyte present or added to the test material
* which is extracted and presented for measurement.
*/
function get_Method_Selectiv($MethodID, $allow_access)
/*
* This function returns the Selectivity according to the Method ID.
*/
function get_Method_Sensitiv($MethodID, $allow_access)
/*
* This function returns the Selectivity according to the Method ID.
*/
```

```
function get_Method_Specific($MethodID, $allow_access)
/*
 * This function returns the Specificity according to the Method ID.
 * The freedom of the analytical procedure from interference effects. It reflects the
 * ability of instrumentation to measure only the signal of the determination.
 */

function get_Method_Confidential($MethodID)
/*
 * This function returns the Confidential according to the Method ID.
 */

function get_Method_Remarks($MethodID, $allow_access)
/*
 * This function returns the Remarks according to the Method ID.
 * Contains any further remarks. Comment field to collect all uncategorized
 * Information.
 */

function get_Method_Range($MethodID, $allow_access)
/*
 * This function returns the Range according to the Method ID.
 */

function get_Method_Linearity($MethodID, $allow_access)
/*
 * This function returns the Linearity according to the Method ID.
 */

function get_Method_OrgID($MethodID, $allow_access)
/*
 * This function returns the Organisation ID according to the Method ID.
 */
```

### 3.8 API organisation

```
function get_Organisation_RecordNumberforOrgID($OrgID)
/*
 * This function returns the record number for a Organisation ID.
 */

function get_Organisation_OrgIDforRecordNumber($record_number)
/*
 * This function returns the Organisation ID for a record number.
 */

function get_Organisation_OrgIDs()
/*
 * This function returns all Organisatino IDs
 */

function get_Organisation_countAllOrganisations()
/*
 * This function returns the number of all Organisations in Database
 */

function get_Organisation_Acronym($OrgID)
/*
 * This function returns the Acronym of an organisation.
 */

function get_Organisation_Name($OrgID)
/*
```

```
* This function returns the full official name of the organisation.  
*/  
  
function get_Organisation_PartnerNo($OrgID)  
/*  
* This function returns the TRACE partner number of an organisation.  
*/  
  
function get_Organisation_OrganisationType($OrgID)  
/*  
* This function returns the type of the type the organisation.  
*/  
  
function get_Organisation_CountryID($OrgID)  
/*  
* This function returns the country an organisation resides in.  
*/  
  
function get_Organisation_OrgLogo($OrgID)  
/*  
* This function returns the logo of an organisation withing the <img...>  
* Tag.  
*/  
  
function get_Organisation_Phone($OrgID)  
/*  
* This function returns the phone number of an organisation.  
* Telephone and Fax numbers should be formatted from an international point  
* of view. Use the form: +country-code area-code sub-area-code phone-number.  
* The various blocks should be separated with a space character or hyphen.  
*/  
  
function get_Organisation_Fax($OrgID)  
/*  
* This function returns the phone number of an organisation.  
* Formatting issues are the same as for phone numbers.  
*/  
  
function get_Organisation_EMail($OrgID)  
/*  
* This function returns the Internet E-Mail address of an organisation.  
*/  
  
function get_Organisation_URL($OrgID)  
/*  
* This function returns the URL address of an organisation.  
* Always give complete URLs. Example: http://www.bats.ch/trace/  
*/  
  
function get_Organisation_SpOrgName($OrgID)  
/*  
* This function returns the Umbrella Organisation of an organisation.  
* If applicable, give the name of the umbrella organisation.  
*/  
  
function get_Organisation_PostAddr($OrgID)  
/*  
* This function returns the post address of an organisation.  
* Postal address as would be put on a letter, i.e. PO box, address, ZIP-  
* code, city, country, etc.  
*/  
  
function get_Organisation_Remarks($OrgID)
```

```
/*
 * This function returns any further remarks of an organisation.
 */

function get_Organisation_DivOrgNam($OrgID)
/*
 * This function returns the DivOrgNam of an organisation.
 */

function get_Organisation_Electrophoretic($OrgID)
/*
 * This function returns the Electrophoretic of an organisation.
 */

function get_Organisation_Thermocycler($OrgID)
/*
 * This function returns the Thermocycler of an organisation.
 */

function get_Organisation_RTdevice($OrgID)
/*
 * This function returns the RTdevice of an organisation.
 */

function get_Organisation_MicroarrayReader($OrgID)
/*
 * This function returns the MicroarrayReader of an organisation.
 */

function get_Organisation_DNASequencer($OrgID)
/*
 * This function returns the DNASequencer of an organisation.
 */

function get_Organisation_SouthernBlot($OrgID)
/*
 * This function returns the SouthernBlot of an organisation.
 */

function get_Organisation_OtherDevices($OrgID)
/*
 * This function returns the OtherDevices of an organisation.
 */

function get_Organisation_Confidential($OrgID)
/*
 * This function returns whether a record is confidential or not.
 * This field contains one char. If a record is confidential, the value is "y".
 */
```

### 3.9 API overview

```
function get_Overview_countAllRecords()
/*
 * This function returns the number of all Overview Records in Database
 */

function get_Overview_OrgID($record_number)
/*
 * This function returns OrgID for the record
 */

function get_Overview_PCRID($record_number)
```

```
/*
 * This function returns PCRID for the record
 */

function get_Overview_TaxonID($record_number)
/*
 * This function returns TaxonID for the record
 */

function get_Overview_ElementID($record_number)
/*
 * This function returns ElementID for the record
 */
```

### 3.10 API pcr

```
function get_PCR_RecordNumberforPCRID($PCRID)
/*
 * This function returns the record number for a PCRID.
 */

function get_PCR_PCRIDforRecordNumber($record_number)
/*
 * This function returns the PCRID for a record number.
 */

function get_PCR_PCRIDsforOrgID($OrgID)
/*
 * This function returns all PCRIDs for a Organisation ID
 */

function get_PCR_PCRIDsforTaxonID($TaxonID)
/*
 * This function returns all PCRIDs for a TaxonID
 */

function get_PCR_PCRIDsforElementID($ElementID)
/*
 * This function returns all PCRIDs for an ElementID
 */

function get_PCR_PCRIDs()
/*
 * This function returns all PCRIDs
 */

function get_PCR_countAllPCRs()
/*
 * This function returns the number of all PCRs in Database
 */

function get_PCR_PCRName($PCRID, $allow_access)
/*
 * This function returns the name of an PCR.
 */

function get_PCR_PCRTYPE($PCRID, $allow_access)
/*
 * This function returns the type name of an PCR.
 */

function get_PCR_PCRSystem($PCRID, $allow_access)
/*
```

```
* This function returns the system name of an PCR.  
*/  
  
function get_PCR_TaxonID($PCRID, $allow_access)  
/*  
* This function returns the TaxonID name of an PCR.  
*/  
  
function get_PCR_PCRdescription($PCRID, $allow_access)  
/*  
* This function returns the PCRdescription of an PCR.  
*/  
  
function get_PCR_ElementID($PCRID, $allow_access)  
/*  
* This function returns the ElementID of an PCR.  
*/  
  
function get_PCR_SequenceID($PCRID, $allow_access)  
/*  
* This function returns the SequenceID of an PCR.  
*/  
  
function get_PCR_SizeOfGenome($PCRID, $allow_access)  
/*  
* This function returns the SizeOfGenome of an PCR.  
*/  
  
function get_PCR_AnnealingTemp($PCRID, $allow_access)  
/*  
* This function returns the AnnealingTemp of an PCR.  
*/  
  
function get_PCR_AmpliconLength($PCRID, $allow_access)  
/*  
* This function returns the AmpliconLength of an PCR.  
*/  
  
function get_PCR_TempTimeProgram($PCRID, $allow_access)  
/*  
* This function returns the TempTimeProgram of an PCR.  
*/  
  
function get_PCR_Device($PCRID, $allow_access)  
/*  
* This function returns the Device of an PCR.  
*/  
  
function get_PCR_MasterMix($PCRID, $allow_access)  
/*  
* This function returns the MasterMix of an PCR.  
*/  
  
function get_PCR_Remarks($PCRID, $allow_access)  
/*  
* This function returns the Remarks of an PCR.  
*/  
  
function get_PCR_OrgID($PCRID, $allow_access)  
/*  
* This function returns the Organisation ID of an PCR.  
*/
```

```
function get_PCR_MethodID($PCRID, $allow_access)
/*
* This function returns the MethodID of an PCR.
*/

function get_PCR_PublicationID($PCRID, $allow_access)
/*
* This function returns the PublicationID of an PCR.
*/

function get_PCR_nPrimers($PCRID, $allow_access)
/*
* This function returns the nPrimers of an PCR.
*/

function get_PCR_FoodProductID($PCRID, $allow_access)
/*
* This function returns the FoodProductID of an PCR.
*/

function get_PCR_Confidential($PCRID)
/*
* This function returns wether a record is confidential or not.
* This field contains one char. If a record is confidential, the value is "y".
*/
```

### 3.11 API person

```
function get_Person_RecordNumberforPersonID($PersonID)
/*
* This function returns the record number for a PersonID.
*/

function get_Person_PersonIDsforOrgID($OrgID)
/*
* This function returns all PersonIDs for a OrgID
*/

function get_Person_PersonIDforRecordNumber($record_number)
/*
* This function returns the PersonID for a record number.
*/

function get_Person_PersonIDs()
/*
* This function returns all PersonIDs
*/

function get_Person_countAllPersons()
/*
* This function returns the number of all Persons in Database
*/

function get_Person_Title($PersonID, $allow_access)
/*
* This function returns the title of a person.
*/

function get_Person_FirstName($PersonID, $allow_access)
/*
* This function returns the first name of a person.
*/
```

```
function get_Person_LastName($PersonID, $allow_access)
/*
* This function returns the last name of a person.
*/

function get_Person_Gender($PersonID, $allow_access)
/*
* This function returns the gender of a person.
*/

function get_Person_Position($PersonID, $allow_access)
/*
* This function returns the position of a person.
*/

function get_Person_PostAddr($PersonID, $allow_access)
/*
* This function returns the post address of a person.
*/

function get_Person_CountryID($PersonID, $allow_access)
/*
* This function returns the name of the country the person lives in.
*/

function get_Person_Phone($PersonID, $allow_access)
/*
* This function returns the phone number of a person.
*/

function get_Person_Fax($PersonID, $allow_access)
/*
* This function returns the fax number of a person.
*/

function get_Person_Email($PersonID, $allow_access)
/*
* This function returns the e-Mail address of a person.
*/

function get_Person_URL($PersonID, $allow_access)
/*
* This function returns the URL of a website the person is listed.
*/

function get_Person_LanguageID($PersonID, $allow_access)
/*
* This function returns the language ID a person speaks.
*/

function get_Person_Remarks($PersonID, $allow_access)
/*
* This function returns the remarks of a person.
*/

function get_Person_OrgID($PersonID, $allow_access)
/*
* This function returns the organisation ID of a persons organisation.
*/

function get_Person_Confidential($PersonID)
/*
* This function returns wether a record is confidential or not.
```

\* This field contains one char. If a record is confidential, the value is "y".  
\*/

### 3.12 API primer

```
function get_Primer_PrimerProbeIDs()  
/*  
 * This function returns all PrimerProbeIDs  
 */  
  
function get_Primer_PrimerIDforRecordNumber($record_number)  
/*  
 * This function returns the PrimerID for a record number.  
 */  
  
function get_Primer_RecordNumberforPrimerID($PrimerID)  
/*  
 * This function returns the record number for a PrimerID.  
 */  
  
function get_Primer_countAllPrimers()  
/*  
 * This function returns the number of all Primers in Database  
 */  
  
function get_Primer_numberOfPrimers($PCRID)  
/*  
 * This function returns the number of primers for a PCR ID.  
 */  
  
function get_Primer_PrimerProbeIDsforPCRID($PCRID)  
/*  
 * This function returns all PrimerProbeIDs for a PCRID  
 */  
  
function get_Primer_PPName($PrimerProbeID, $allow_access)  
/*  
 * This function returns the PPName according to the Primer ID.  
 */  
  
function get_Primer_PPType($PrimerProbeID, $allow_access)  
/*  
 * This function returns the PPType according to the Primer ID.  
 */  
  
function get_Primer_PPSequence($PrimerProbeID, $allow_access)  
/*  
 * This function returns the PPSequence according to the Primer ID.  
 */  
  
function get_Primer_PPLength($PrimerProbeID, $allow_access)  
/*  
 * This function returns the PPLength according to the Primer ID.  
 */  
  
function get_Primer_AnnealingTemp($PrimerProbeID, $allow_access)  
/*  
 * This function returns the AnnealingTemp according to the Primer ID.  
 */  
  
function get_Primer_MeltingTempThermo($PrimerProbeID, $allow_access)  
/*  
 * This function returns the MeltingTempThermo according to the Primer ID.
```

```
*/  
  
function get_Primer_MeltingTemp2AT4GC($PrimerProbeID, $allow_access)  
/*  
* This function returns the MeltingTemp2AT4GC according to the Primer ID.  
*/  
  
function get_Primer_GCcontent($PrimerProbeID, $allow_access)  
/*  
* This function returns the GCcontent according to the Primer ID.  
*/  
  
function get_Primer_PPposition($PrimerProbeID, $allow_access)  
/*  
* This function returns the PPposition according to the Primer ID.  
*/  
  
function get_Primer_ProbeDyeID($PrimerProbeID, $allow_access)  
/*  
* This function returns the ProbeDyeID according to the Primer ID.  
*/  
  
function get_Primer_PrimerUsage($PrimerProbeID, $allow_access)  
/*  
* This function returns the PrimerUsage according to the Primer ID.  
*/  
  
function get_Primer_PCRID($PrimerProbeID, $allow_access)  
/*  
* This function returns the PCRID according to the Primer ID.  
*/  
  
function get_Primer_SequenceID($PrimerProbeID, $allow_access)  
/*  
* This function returns the SequenceID according to the Primer ID.  
*/  
  
function get_Primer_Remarks($PrimerProbeID, $allow_access)  
/*  
* This function returns the Remarks according to the Primer ID.  
*/  
  
function get_Primer_Confidential($PrimerProbeID)  
/*  
* This function checks whether the recordset of the given PrimerProbeID is  
* confidential or not.  
*/
```

### **3.13 API protein detection**

```
function get_ProteinDetection_countAllProteinDetections()  
/*  
* This function returns the number of all Protein Detections in Database  
*/  
  
function get_ProteinDetection_ProteinDetectionName($ProteinDetectionID, $allow_access)  
/*  
* This function returns the Protein Detection Name according to the Protein  
* Detection ID.  
*/  
  
function get_ProteinDetection_PDtype($ProteinDetectionID, $allow_access)  
/*
```

```
* This function returns the PDtype according to the Protein Detection ID.  
*/  
  
function get_ProteinDetection_SamplePreparation($ProteinDetectionID, $allow_access)  
/*  
* This function returns the SamplePreparation according to a  
* Proteindetection ID  
*/  
  
function get_ProteinDetection_TestType($ProteinDetectionID, $allow_access)  
/*  
* This function returns the TestType according to a Proteindetection  
* ID.  
*/  
  
function get_ProteinDetection_ElementID($ProteinDetectionID, $allow_access)  
/*  
* This function returns the ElementID according to a Proteindetection ID  
*/  
  
function get_ProteinDetection_CaptureAntibody($ProteinDetectionID, $allow_access)  
/*  
* This function returns the CaptureAntibody according to a  
* Proteindetection ID.  
*/  
  
function get_ProteinDetection_CaptABType($ProteinDetectionID, $allow_access)  
/*  
* This function returns CaptABType according to a Proteindetection ID.  
*/  
  
function get_ProteinDetection_CaptABDescription($ProteinDetectionID, $allow_access)  
/*  
* This function returns the CaptABDescription according to the  
* Proteindetection ID.  
*/  
  
function get_ProteinDetection_CaptABSourceTax($ProteinDetectionID, $allow_access)  
/*  
* This function returns the CaptABSourceTax according to a Proteindetection  
* ID.  
*/  
  
function get_ProteinDetection_CaptABProducer($ProteinDetectionID, $allow_access)  
/*  
* This function returns the CaptABProducer for the Protein Detection.  
*/  
  
function get_ProteinDetection_DetectionAntibody($ProteinDetectionID, $allow_access)  
/*  
* This function returns the DetectionAntibody for the Protein Detection.  
*/  
  
function get_ProteinDetection_DetABType($ProteinDetectionID, $allow_access)  
/*  
* This function returns the DetABType of an Protein Detection.  
*/  
  
function get_ProteinDetection_DetABDescription($ProteinDetectionID, $allow_access)  
/*  
* This function returns the DetABDescription of an Protein Detection.  
*/
```

```

function get_ProteinDetection_DetABSourceTax($ProteinDetectionID, $allow_access)
/*
* This function returns the DetABSourceTax of an Protein Detection.
*/

function get_ProteinDetection_DetABProducer($ProteinDetectionID, $allow_access)
/*
* This function returns the DetABProducer of an Protein Detection.
*/

function get_ProteinDetection_PositiveControl($ProteinDetectionID, $allow_access)
/*
* This function returns the PositiveControl of an Protein Detection.
*/

function get_ProteinDetection_SampleID($ProteinDetectionID, $allow_access)
/*
* This function returns the SampleID of the Protein Detection. See table
* sample.
*/

function get_ProteinDetection_MethodID($ProteinDetectionID, $allow_access)
/*
* This function returns the MethodID of an Protein Detection. See table
* method.
*/

function get_ProteinDetection_PublicationID($ProteinDetectionID, $allow_access)
/*
* This function returns the PublicationID of an Protein Detection. See table
* publication.
*/

function get_ProteinDetection_Remarks($ProteinDetectionID, $allow_access)
/*
* This function returns the Remarks according to the Protein Detection ID.
*/

function get_ProteinDetection_Confidential($ProteinDetectionID)
/*
* This function returns wether a record is confidential or not.
* This field contains one char. If a record is confidential, the value is "y".
*/

```

### 3.14 API publication

```

function get_Publication_RecordNumberforPublicationID($PublicationID)
/*
* This function returns the record number for a PublicationID.
*/

function get_Publication_PublicationIDforRecordNumber($record_number)
/*
* This function returns the PublicationID for a record number.
*/

function get_Publication_countAllPublications()
/*
* This function returns the number of all Publications in Database
*/

function get_Publication_PublicationIDs()
/*

```

```
* This function returns all PublicationIDs
*/
function get_Publication_PublicationIDsforPCRID($PCRID)
/*
* This function returns all PublicationIDs for a PCRID
*/
function get_Publication_PublicationIDsforOrgID($OrgID)
/*
* This function returns all PublicationIDs for a PCRID
*/
function get_Publication_Title($PublicationID, $allow_access)
/*
* This function returns the title of an Publication.
*/
function get_Publication_ShortTitle($PublicationID, $allow_access)
/*
* This function returns the short title of an Publication.
*/
function get_Publication_Authors($PublicationID, $allow_access)
/*
* This function returns the Authors of an Publication.
*/
function get_Publication_OrgID($PublicationID, $allow_access)
/*
* This function returns the OrgID of an Publication.
*/
function get_Publication_PubDate($PublicationID, $allow_access)
/*
* This function returns the PubDate of an Publication.
*/
function get_Publication_Version($PublicationID, $allow_access)
/*
* This function returns the Version of an Publication.
*/
function get_Publication_PublicationType($PublicationID, $allow_access)
/*
* This function returns the PublicationTypeID of an Publication.
*/
function get_Publication_LanguageID($PublicationID, $allow_access)
/*
* This function returns the LanguageID of an Publication.
*/
function get_Publication_ISBN($PublicationID, $allow_access)
/*
* This function returns the ISBN of an Publication.
*/
function get_Publication_ISSN($PublicationID, $allow_access)
/*
* This function returns the ISSN of an Publication.
*/
```

```
function get_Publication_ReportTitle($PublicationID, $allow_access)
/*
* This function returns the ReportTitle of an Publication.
*/

function get_Publication_Volume($PublicationID, $allow_access)
/*
* This function returns the Volume of an Publication.
*/

function get_Publication_Issue($PublicationID, $allow_access)
/*
* This function returns the Issue of an Publication.
*/

function get_Publication_Pages($PublicationID, $allow_access)
/*
* This function returns the Pages of an Publication.
*/

function get_Publication_Filefrmt($PublicationID, $allow_access)
/*
* This function returns the Filefrmt of an Publication.
*/

function get_Publication_URL($PublicationID, $allow_access)
/*
* This function returns the title of an Publication.
*/

function get_Publication_Medium($PublicationID, $allow_access)
/*
* This function returns the Medium of an Publication.
*/

function get_Publication_Remarks($PublicationID, $allow_access)
/*
* This function returns the Remarks of an Publication.
*/

function get_Publication_TaxonID($PublicationID, $allow_access)
/*
* This function returns the TaxonID of an Publication.
*/

function get_Publication_Method($PublicationID, $allow_access)
/*
* This function returns the Method of an Publication.
*/

function get_Publication_FileName($PublicationID, $allow_access)
/*
* This function returns the FileName of an Publication.
*/

function get_Publication_LocalContent($PublicationID, $allow_access)
/*
* This function returns the LocalContent of an Publication.
*/

function get_Publication_FileSize($PublicationID, $allow_access)
/*
* This function returns the FileSize of an Publication.
*/
```

```
*/  
  
function get_Publication_PCRID($PublicationID, $allow_access)  
/*  
 * This function returns the PCRID of an Publication.  
 */  
  
function get_Publication_Confidential($PublicationID)  
/*  
 * This function returns wether a record is confidential or not.  
 * This field contains one char. If a record is confidential, the value is "y".  
 */  
  
3.15 API sample  
  
function get_Sample_RecordNumberforSampleID($SampleID)  
/*  
 * This function returns the record number for a PCRID.  
 */  
  
function get_Sample_SampleIDforRecordNumber($record_number)  
/*  
 * This function returns the SampleID for a record number.  
 */  
  
function get_Sample_SampleIDs()  
/*  
 * This function returns all SampleIDs  
 */  
  
function get_Sample_SampleIDsforTaxonID($TaxonID)  
/*  
 * This function returns all SampleIDs for a TaxonID  
 */  
  
function get_Sample_SampleIDsforFoodProductID($FoodProductID)  
/*  
 * This function returns all SampleIDs for a FoodProductID  
 */  
  
function get_Sample_countAllSamples()  
/*  
 * This function returns the number of all Samples in Database  
 */  
  
function get_Sample_WP_Nr($SampleID, $allow_access)  
/*  
 * This function returns the Trace Project Workpackage Number according to  
 * the Sample ID.  
 */  
  
function get_Sample_Commodity($SampleID, $allow_access)  
/*  
 * This function returns the Commodity according to the Sample ID. Commodity  
 * normally consists of one letter, e.g. w = water; h = honey; o = olive;  
 * c = cereal; b = beef; l = lamb; p = poultry.  
 */  
  
function get_Sample_Country($SampleID, $allow_access)  
/*  
 * This function returns the country where the sample was collected.  
 * The country code consists of two letters that follow the ICANN  
 * Top Level Domains. Country code xx means, the country is not appropriated.  
 */
```

```
*/  
  
function get_Sample_Site($SampleID, $allow_access)  
/*  
* This function returns the Site according to the Sample ID. Site is a three  
* letter short form, e.g. Car = Carpentras; Cin = Ciney; Lim = Limousin.  
* XXX means "no appropriated".  
*/  
  
function get_Sample_Year($SampleID, $allow_access)  
/*  
* This function returns the Year when the sample was collected. The field  
* year consists of two letters starting with 01 = 2001; 02 = 2002. Be aware:  
* 00 does not mean year 2000, but means "no appropriated".  
*/  
  
function get_Sample_Month($SampleID, $allow_access)  
/*  
* This function returns the Month when a sample was collected. This field  
* contains two numbers: 01 is January, 02 is February...  
*/  
  
function get_Sample_Number($SampleID, $allow_access)  
/*  
* This function returns the sample number assigned by the responsible  
* person. This field consists of four numbers starting with 0001.  
*/  
  
function get_Sample_TraceSampleCode($SampleID, $allow_access)  
/*  
* This function returns the Trace Sample Code of an sample. The Trace Sample  
* Code consists of 15 letters and numbers in following order: Workpackage  
* Number (1 number), Commodity (1 char), Country (2 chars), Site (3 chars),  
* Year (2 numbers), Month (2 numbers) and Number (4 numbers).  
*/  
  
function get_Sample_ResponsiblePerson($SampleID, $allow_access)  
/*  
* This function returns the Person ID of the responsible person for the  
* sample.  
*/  
  
function get_Sample_InternalSampleCode($SampleID, $allow_access)  
/*  
* This function returns the Internal Sample Code of the sample provider or  
* the TRACE insitute. They use it for their convenience.  
*/  
  
function get_Sample_SetName($SampleID, $allow_access)  
/*  
* This function returns the Set Name of an sample. A Set Name is a name  
* given to a set of samples corresponding to a specific process in the  
* project.  
*/  
  
function get_Sample_LocationName($SampleID, $allow_access)  
/*  
* This function returns the Location Name of an sample. The Location Name is  
* the site where the sample was collected.  
*/  
  
function get_Sample_ProducerIdentificationName($SampleID, $allow_access)  
/*
```

```
* This function returns the Producer Identification Name of an sample. This
* can be a farmer, producer,....
*/
function get_Sample_CollectorIdentificationName($SampleID, $allow_access)
/*
* This function returns the Collector Identification Name ID of an sample.
* This is the person in charge to collect the sample. See person table.
*/
function get_Sample_DonorIdentificationName($SampleID, $allow_access)
/*
* This function returns the Donor Identification Name ID of an sample. The
* function of this person must be defined in Workpackage 3. Waiting for the
* definition...
*/
function get_Sample_FoodProductID($SampleID, $allow_access)
/*
* This function returns the Food Product Name ID of the sample. This name is
* used in the Food Standards (see foodproduct table).
*/
function get_Sample_TaxonID($SampleID, $allow_access)
/*
* This function returns the Trace Popular Name ID = TaxonID of an Sample. See table
* taxonomy.
*/
function get_Sample_SampleType($SampleID, $allow_access)
/*
* This function returns the Sample Type of an Sample. Sample Type are for
* animals: skin, blood, muscle; for vegetals: fruit, oil, pollen leaves,
* buds, grain, root, seed; for mineral: water or soil; for food product:
* honey, meat.
*/
function get_Sample_SamplingDate($SampleID, $allow_access)
/*
* This function returns the Date of sample collection.
*/
function get_Sample_SamplingProcedure($SampleID, $allow_access)
/*
* This function returns the Sampling Procedure of an Sample. e.g. one sample
* and ? subsamples to provide the sample.
*/
function get_Sample_SamplingPurpose($SampleID, $allow_access)
/*
* This function returns the Sampling Purpose of an Sample. This is either
* RNA or DNA extraction.
*/
function get_Sample_SampleQuantity($SampleID, $allow_access)
/*
* This function returns the Sample Quantity of an Sample. This can be the
* weight, volume or number of plants collected.
*/
function get_Sample_ContainerType($SampleID, $allow_access)
/*
* This function returns the Container Type of an Sample. This is the type of
```

```
* container, where the sample is stored.  
*/  
  
function get_Sample_StorageCondition($SampleID, $allow_access)  
/*  
* This function returns the Storage Condition of an Sample.  
*/  
  
function get_Sample_Picture($SampleID, $allow_access)  
/*  
* This function returns the Picture (just the link to a file) of an Sample.  
*/  
  
function get_Sample_SoilAnalysis($SampleID, $allow_access)  
/*  
* This function returns the Soil Analysis of an Sample. This value just  
* tells whether a soil analysis is planned or not.  
*/  
  
function get_Sample_Comment($SampleID, $allow_access)  
/*  
* This function returns the Comment / Remarks of an Sample.  
*/  
  
function get_Sample_Specific01($SampleID, $allow_access)  
/*  
* This function returns the first specific feature of  
* an Sample. This field includes two parts. The first part is the name of  
* the field and is finished with an ":". After this the content of the fidld  
* starts.  
*/  
  
function get_Sample_Specific02($SampleID, $allow_access)  
/*  
* This function returns the first specific feature of  
* an Sample. This field includes two parts. The first part is the name of  
* the field and is finished with an ":". After this the content of the fidld  
* starts.  
*/  
  
function get_Sample_Specific03($SampleID, $allow_access)  
/*  
* This function returns the first specific feature of  
* an Sample. This field includes two parts. The first part is the name of  
* the field and is finished with an ":". After this the content of the fidld  
* starts.  
*/  
  
function get_Sample_Specific04($SampleID, $allow_access)  
/*  
* This function returns the first specific feature of  
* an Sample. This field includes two parts. The first part is the name of  
* the field and is finished with an ":". After this the content of the fidld  
* starts.  
*/  
  
function get_Sample_Specific05($SampleID, $allow_access)  
/*  
* This function returns the first specific feature of  
* an Sample. This field includes two parts. The first part is the name of  
* the field and is finished with an ":". After this the content of the fidld  
* starts.  
*/
```

```
function get_Sample_Specific06($SampleID, $allow_access)
/*
* This function returns the first specific feature of
* an Sample. This field includes two parts. The first part is the name of
* the field and is finished with an ":". After this the content of the fidld
* starts.
*/
function get_Sample_Specific07($SampleID, $allow_access)
/*
* This function returns the first specific feature of
* an Sample. This field includes two parts. The first part is the name of
* the field and is finished with an ":". After this the content of the fidld
* starts.
*/
function get_Sample_Specific08($SampleID, $allow_access)
/*
* This function returns the first specific feature of
* an Sample. This field includes two parts. The first part is the name of
* the field and is finished with an ":". After this the content of the fidld
* starts.
*/
function get_Sample_FoodName($SampleID, $allow_access)
/*
* This function returns the FoodName according to the Sample ID.
*/
function get_Sample_ExtractionID($SampleID, $allow_access)
/*
* This function returns the ExtractionID according to the Sample ID.
*/
function get_Sample_Processing($SampleID, $allow_access)
/*
* This function returns the Processing according to the Sample ID.
*/
function get_Sample_NucleoConz($SampleID, $allow_access)
/*
* This function returns the NucleoConz according to the Sample ID.
*/
function get_Sample_DNAconz($SampleID, $allow_access)
/*
* This function returns the DNAconz according to the Sample ID.
*/
function get_Sample_AmplDNA($SampleID, $allow_access)
/*
* This function returns the aDNA according to the Sample ID.
*/
function get_Sample_Ingredients($SampleID, $allow_access)
/*
* This function returns the Ingredients according to the Sample ID.
*/
function get_Sample_PublicationID($SampleID, $allow_access)
/*
* This function returns the Publication ID according to the Sample ID.
```

```
*/  
  
function get_Sample_Confidential($SampleID)  
/*  
 * This function returns according to the Sample ID whether a record is  
 * confidential or not. The database field consists of one char.  
 */
```

### 3.16 API sequence

```
function get_Sequence_SequenceIDs()  
/*  
 * This function returns all SequenceIDs  
 */  
  
function get_Sequence_SequenceIDforRecordNumber($record_number)  
/*  
 * This function returns the SequenceID for a record number.  
 */  
  
function get_Sequence_RecordNumberforSequenceID($SequenceID)  
/*  
 * This function returns the record number for a SequenceID.  
 */  
  
function get_Sequence_countAllSequences()  
/*  
 * This function returns the number of all Sequences in Database  
 */  
  
function get_Sequence_SequenceName($SequenceID, $allow_access)  
/*  
 * This function returns the Sequence Name of an Sequence ID.  
 */  
  
function get_Sequence_Description($SequenceID, $allow_access)  
/*  
 * This function returns the sequence description of an sequence ID.  
 */  
  
function get_Sequence_TaxonID($SequenceID, $allow_access)  
/*  
 * This function returns the fitting Taxon ID to the Sequence ID.  
 */  
  
function get_Sequence_ElementID($SequenceID, $allow_access)  
/*  
 * This function returns the fitting Element ID to the Sequence ID.  
 */  
  
function get_Sequence_SeqType($SequenceID, $allow_access)  
/*  
 * This function returns the fitting seqence type to the Sequence ID.  
 */  
  
function get_Sequence_NCBIAccession($SequenceID, $allow_access)  
/*  
 * This function returns the NCBI Accession to the Sequence ID.  
 */  
  
function get_Sequence_Version($SequenceID, $allow_access)  
/*  
 * This function returns the Version to the Sequence ID.
```

```
*/  
  
function get_Sequence_Keywords($SequenceID, $allow_access)  
/*  
* This function returns the Keywords of the Sequence ID.  
*/  
  
function get_Sequence_Comment($SequenceID, $allow_access)  
/*  
* This function returns the Comment of the Sequence ID.  
*/  
  
function get_Sequence_Publication($SequenceID, $allow_access)  
/*  
* This function returns the Publication of the Sequence ID.  
*/  
  
function get_Sequence_BaseCount($SequenceID, $allow_access)  
/*  
* This function returns the BaseCount of the Sequence ID.  
*/  
  
function get_Sequence_DNAsequence($SequenceID, $allow_access)  
/*  
* This function returns the DNAsequence of the Sequence ID.  
*/  
  
function get_Sequence_AAsequence($SequenceID, $allow_access)  
/*  
* This function returns the AAsequence of the Sequence ID.  
*/  
  
function get_Sequence_Alignment($SequenceID, $allow_access)  
/*  
* This function returns the Alignment of the Sequence ID.  
*/  
  
function get_Sequence_FullNCBIdatasheet($SequenceID, $allow_access)  
/*  
* This function returns the FullNCBIdatasheet of the Sequence ID.  
*/  
  
function get_Sequence_URL($SequenceID, $allow_access)  
/*  
* This function returns the URL of the Sequence ID.  
*/  
  
function get_Sequence_OrgID($SequenceID, $allow_access)  
/*  
* This function returns the Organisation ID of the Sequence ID.  
*/  
  
function get_Sequence_Remarks($SequenceID, $allow_access)  
/*  
* This function returns the Remarks of the Sequence ID.  
*/  
  
function get_Sequence_Confidential($SequenceID)  
/*  
* This function returns the confidential String for a SequenceID.  
*/
```

### 3.17 API site

```
function get_Site_countAllSites()  
/*  
* This function returns the number of all Sites in Database  
*/  
  
function get_Site_LocationName($SiteID, $allow_access)  
/*  
* This function returns the Location Name according to the Site ID. The  
* Location Name is, where the sample is selected or purchased (see general  
* descriptor: location name)  
*/  
  
function get_Site_TraceSiteCode($SiteID, $allow_access)  
/*  
* This function returns the TraceSiteCode according to the Site ID. This  
* Code is used in the Trace sample code (3 digits).  
*/  
  
function get_Site_SiteCoordinator($SiteID, $allow_access)  
/*  
* This function returns the SiteCoordinator according to a Site ID  
*/  
  
function get_Site_CountryID($SiteID, $allow_access)  
/*  
* This function returns the CountryID according to a Site  
* ID.  
*/  
  
function get_Site_PoliticArea($SiteID, $allow_access)  
/*  
* This function returns the PoliticArea according to a Site ID  
*/  
  
function get_Site_PoliticSubarea($SiteID, $allow_access)  
/*  
* This function returns the PoliticSubarea according to a  
* Site ID.  
*/  
  
function get_Site_GeographicArea($SiteID, $allow_access)  
/*  
* This function returns GeographicArea according to a Site ID.  
*/  
  
function get_Site_GeographicSubarea($SiteID, $allow_access)  
/*  
* This function returns the GeographicSubarea according to the  
* Site ID.  
*/  
  
function get_Site_PostalCode($SiteID, $allow_access)  
/*  
* This function returns the PostalCode according to a Site  
* ID.  
*/  
  
function get_Site_CityName($SiteID, $allow_access)  
/*  
* This function returns the CityName for the Site.  
*/
```

```
function get_Site_LocalName($SiteID, $allow_access)
/*
 * This function returns the LocalName for the Site. This is
 * a the local or field name.
 */

function get_Site_Parcel($SiteID, $allow_access)
/*
 * This function returns the Parcel of an Site. This is the area
 * identification where the sample was collected in the field.
 */

function get_Site_GPS($SiteID, $allow_access)
/*
 * This function returns the GPS of an Site. These are the
 * coordinates of sampling/rearing locations (preferably GPS, but postcode
 * is acceptable) Format [d]y.y,[d]x.x or [d]y:yy:yy,[d]x:xx:xx where [d] is
 * the optional direction NSE or W, y = lat, x = long, -x is west, +x is
 * east. E.g. 52.038333,4.578611 or N52.038333, W4.578611 or 52:02:18,-4:34:
 * 43 or N52:02:18,W4:34:43
 */

function get_Site_Longitude($SiteID, $allow_access)
/*
 * This function returns the specific description of the Longitude of an
 * Site.
 */

function get_Site_Latitude($SiteID, $allow_access)
/*
 * This function returns the specific description of the Latitude of an Site.
 */

function get_Site_Altitude($SiteID, $allow_access)
/*
 * This function returns the Altitude of an Site in meters above sea level.
 */

function get_Site_Map($SiteID, $allow_access)
/*
 * This function returns the Map of the Site. This is a link to a picture or
 * map.
 */

function get_Site_PACNb($SiteID, $allow_access)
/*
 * This function returns the PACNb of an Site. This is a specific PAC number
 * for EU subsidies
 */

function get_Site_Area($SiteID, $allow_access)
/*
 * This function returns the Area of an Site in Ha.
 */

function get_Site_Soil($SiteID, $allow_access)
/*
 * This function returns the Soil type according to the Site.
 */

function get_Site_AgriculturalSystem($SiteID, $allow_access)
/*
```

```

* This function returns the AgriculturalSystem according to the Site ID.
* This is organic, integrated, conventional.
*/
function get_Site_LandUse($SiteID, $allow_access)
/*
* This function returns the LandUse according to the Site ID. This can be
* Arable land, Pasture, Olive, Forest.
*/
function get_Site_Relief($SiteID, $allow_access)
/*
* This function returns the Relief according to the Site ID.
*/
function get_Site_Slope($SiteID, $allow_access)
/*
* This function returns the Slope according to the Site ID.
*/
function get_Site_Confidential($SiteID)
/*
* This function returns wether a record is confidential or not.
* This field contains one char. If a record is confidential, the value is "y".
*/

```

### 3.18 API taxonomy

```

function get_Taxonomy_RecordNumberforTaxonID($TaxonID)
/*
* This function returns the record number for a TaxonID.
*/
function get_Taxonomy_TaxonIDforRecordNumber($record_number)
/*
* This function returns the TaxonID for a record number.
*/
function get_Taxonomy_TaxonIDs()
/*
* This function returns all TaxonIDs
*/
function get_Taxonomy_TaxonIDsForSameTribe($TaxonID, $allow_access)
/*
* This function returns all TaxonIDs with the same tribe of the given
* TaxonID
*/
function get_Taxonomy_countAllTaxonomys()
/*
* This function returns the number of all Taxonomys in Database
*/
function get_Taxonomy_PopularName($TaxonID, $allow_access)
/*
* This function returns the popular name of a taxonomy.
*/
function get_Taxonomy_Genus($TaxonID, $allow_access)
/*
* This function returns the genus of a taxonomy.
*/

```

```
function get_Taxonomy_Species($TaxonID, $allow_access)
/*
* This function returns the genus of a taxonomy.
*/

function get_Taxonomy_SuperKingdom($TaxonID, $allow_access)
/*
* This function returns the super kingdom of a taxonomy.
*/

function get_Taxonomy_Kingdom($TaxonID, $allow_access)
/*
* This function returns the kingdom of a taxonomy.
*/

function get_Taxonomy_Class($TaxonID, $allow_access)
/*
* This function returns the class of a taxonomy.
*/

function get_Taxonomy_Order($TaxonID, $allow_access)
/*
* This function returns the order of a taxonomy.
*/

function get_Taxonomy_Family($TaxonID, $allow_access)
/*
* This function returns the family of a taxonomy.
*/

function get_Taxonomy_Phylum($TaxonID, $allow_access)
/*
* This function returns the Phylum of a taxonomy.
*/

function get_Taxonomy_SubPhylum($TaxonID, $allow_access)
/*
* This function returns the SubPhylum of a taxonomy.
*/

function get_Taxonomy_Division($TaxonID, $allow_access)
/*
* This function returns the Division of a taxonomy.
*/

function get_Taxonomy_Subdivision($TaxonID, $allow_access)
/*
* This function returns the Subdivision of a taxonomy.
*/

function get_Taxonomy_SuperClass($TaxonID, $allow_access)
/*
* This function returns the SuperClass of a taxonomy.
*/

function get_Taxonomy_SuperOrder($TaxonID, $allow_access)
/*
* This function returns the SuperOrder mily of a taxonomy.
*/

function get_Taxonomy_Subfamily($TaxonID, $allow_access)
/*
```

```
* This function returns the Subfamily of a taxonomy.  
*/  
  
function get_Taxonomy_Tribe($TaxonID, $allow_access)  
/*  
* This function returns the Tribe of a taxonomy.  
*/  
  
function get_Taxonomy_Subspecies($TaxonID, $allow_access)  
/*  
* This function returns the Subspecies of a taxonomy.  
*/  
  
function get_Taxonomy_Variety($TaxonID, $allow_access)  
/*  
* This function returns the Variety of a taxonomy.  
*/  
  
function get_Taxonomy_Cultivar($TaxonID, $allow_access)  
/*  
* This function returns the Cultivar of a taxonomy.  
*/  
  
function get_Taxonomy_Line($TaxonID, $allow_access)  
/*  
* This function returns the Line of a taxonomy.  
*/  
  
function get_Taxonomy_SizeOfGenom($TaxonID, $allow_access)  
/*  
* This function returns the SizeOfGenom of a taxonomy.  
*/  
  
function get_Taxonomy_URL($TaxonID, $allow_access)  
/*  
* This function returns the family of a taxonomy.  
*/  
  
function get_Taxonomy_References($TaxonID, $allow_access)  
/*  
* This function returns the References of a taxonomy.  
*/  
  
function get_Taxonomy_FoodCompData($TaxonID, $allow_access)  
/*  
* This function returns the FoodCompData of a taxonomy.  
*/  
  
function get_Taxonomy_Remarks($TaxonID, $allow_access)  
/*  
* This function returns the Remarks of a taxonomy.  
*/  
  
function get_Taxonomy_Confidential($TaxonID)  
/*  
* This function returns whether a record is confidential or not.  
* This field contains one char. If a record is confidential, the value is "y".  
*/
```

## 4 How to import Data

This howto describes how additional data can be imported in the Trace Molecular Database. It is describes on the example of Sample data.

### 4.1 General Description

First download the data to import from the Trace Intranet. Open the file. Compare the column names in the Excelfile and in the Database. Correct the column names in the Excelfile. Export the Excelfile to a csv-file and import it in the Database

### 4.2 Import FoodProduct Data

#### 4.1.1 Overview

The Sample Data Excel-Files have following data structure:

Excel File Column Name	Molecular DB Column Name	Import Notice
	FoodProductID	Must be created manually
FoodProductName	FoodProductName	
FoodName	FoodName	
	Abbrev	
Protection Label	ProtectionLbl	
Country	CountryID	Substitute with CountryID from table list_country
	OrigFdCd	
	OrigGpCd	
ProductType	ProdType	In ExcelFile before ProtectionLabel
	CdxFdStd	
	CdxFdAdd	
	CdxFdFd	
	CdxCont	
	FAOFBs	
	CIAA	
	EC2	
	EAN	
	UPC	
	ENr	
	INS	
	Manufact	
	Distrib	

Excel File Column Name	Molecular DB Column Name	Import Notice
	FoodSrce	
	GanManip	
	AgriCond	
	Color	
GeneralPicture	GenImage	
SpecificPicture	SpcImage	
	PDOImage	
	PartPlan	
	EdPort	
	NetEdPor	
	NatWaste	
	PhyState	
	HeaTreat	
	TreatApp	
	CookMeth	
	RecProc	
	PublicationID	
	FinlPrep	
	PresMeth	
	PackMed	
	FdCtSrfc	
	ContWrpg	
	StorCond	
	AeraOrig	
	AeraProc	
	AeraCons	
	LblClaim	
	SpecGrav	
	ServSize	
	PackWght	
	PiecWght	
	FreqSeas	
	PlacDiet	
	Cuisine	
Label web-link	URL	In Excelfile before GeneralPicture
	Remarks	

Excel File Column Name	Molecular DB Column Name	Import Notice
	TaxonID	
	SampleID	
	RecordModification	

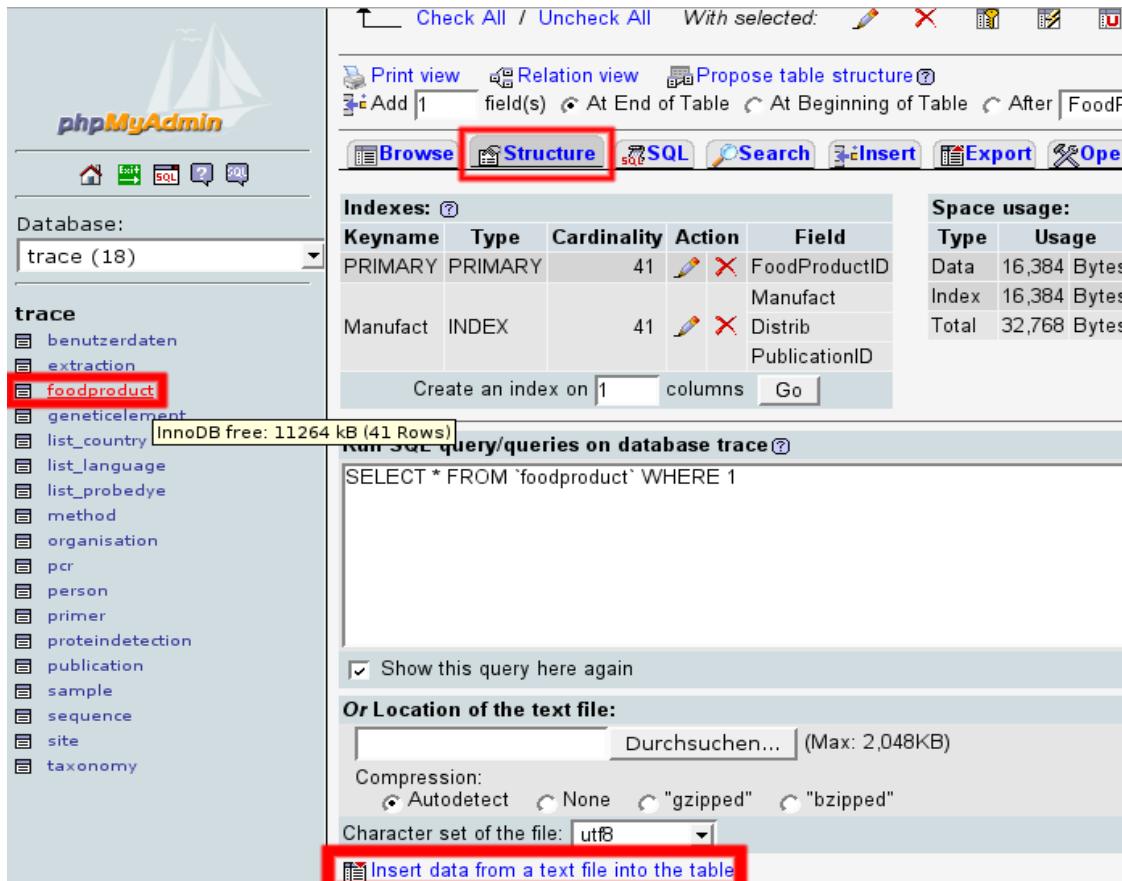
Table 18: Importing scheme for foodproduct data

## 4.1.2 Importing FoodProduct Data Step by Step

Following, importing foodproduct data is described step by step.

1. Fill in the FoodProduct-ID in the column. The FoodPruductID must be unique. For finding out which number to fill in, log in the TMDB PHPMyAdmin and find out the largest FoodProductID number. Add one and acending numbers in the next field.
2. Change the order of the column “ProductType” and “Protection Label” and “Country”. “Protection Label” must be first, “Country” second and “ProductType” third.
3. Add one column between “FoodName” and “Protection Label”.
4. Subsstitute Country with CountryID from table “list\_country”.
5. Add two columns between “Country” and “ProductType”.
6. Change the order of the column “Label web-link” and “GeneralPicture” and “SpecificPicture”. “GeneralPicture” must be first, “SpecificPicture” second and “Label web-link” third.
7. Add 17 columns between “ProductType” and “GeneralPicture”.
8. Add 28 columns between “SpecificPicture” and “Label web-link”.
9. Delete first row. That is the headline row.
10. Save table as foodproduct.csv. A csv (comma sperated values) file can be imported by PHPMyAdmin in a MySQL database. The values should be sperated by a “;” (semicolon) not only a “,” (comma).
11. Open PHPMyAdmin and select the table “foodproduct”.

12. Go to the very end of the page and click on “Insert data from a text file into the table”.



The screenshot shows the phpMyAdmin interface for the 'trace' database. The left sidebar lists tables: benutzerdaten, extraction, foodproduct (highlighted with a red box), geneticelement, list\_country, list\_language, list\_probedeye, method, organisation, pcr, person, primer, proteindetection, publication, sample, sequence, site, taxonomy. The main area shows the 'Structure' tab for the 'foodproduct' table. It displays indexes: PRIMARY (PRIMARY, FoodProductID), Manufact (INDEX, Manufact), Distrib (INDEX, Distrib), PublicationID. Below is a query editor with the SQL command: 'SELECT \* FROM `foodproduct` WHERE 1'. At the bottom, there's a section for 'Or Location of the text file:' with a browse button ('Durchsuchen...'), compression options ('Autodetect', 'None', 'gzipped', 'bzipped'), character set ('utf8'), and a red box highlighting the 'Insert data from a text file into the table' button.

Figure 13: Insert data in table foodproduct from text file

13. Enter the name of the csv-file (here: foodproduct.csv). Be aware that you entered the correct value in the field “Fields terminated by”. The value must be the same separator from number 10.

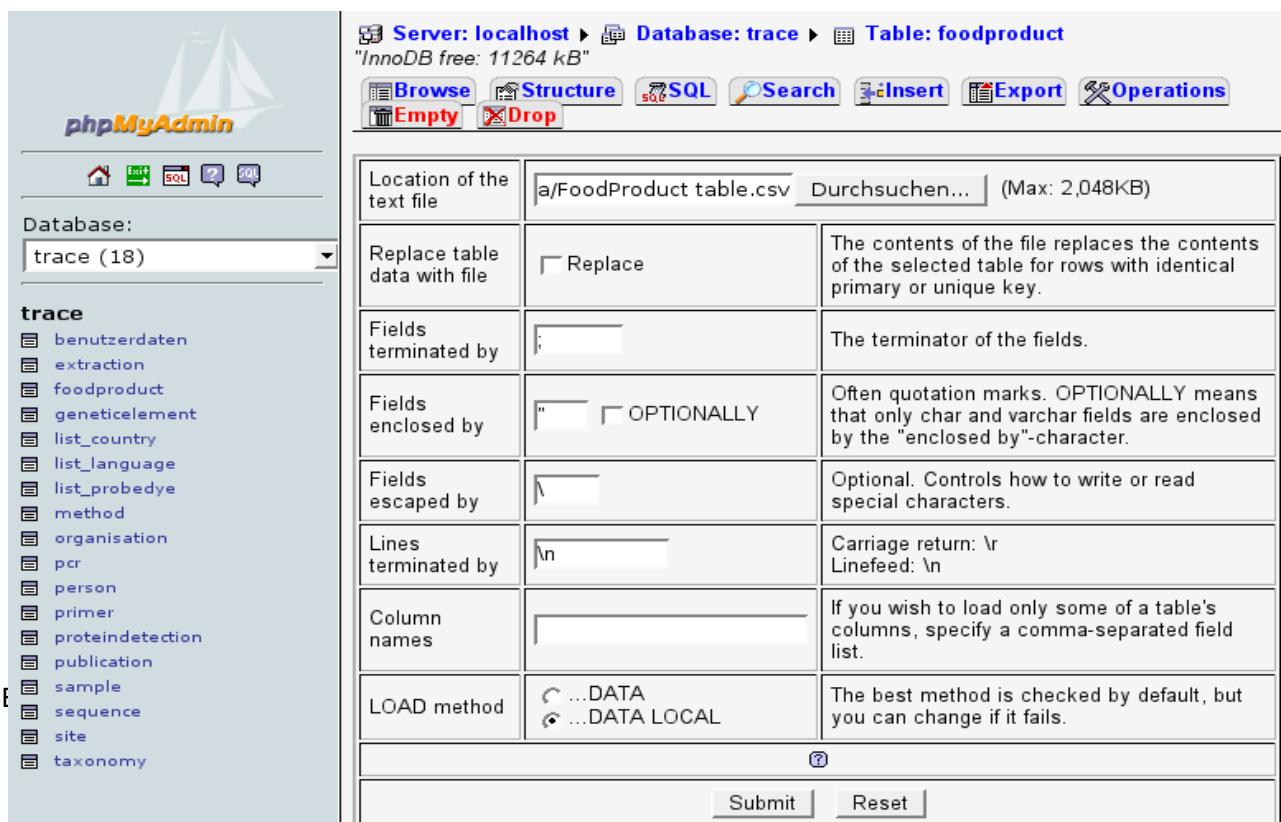
You finished importing data. Please Browse the table to verify you entered the data correct.

## 4.3 Import Sample Data

### 4.1.3 Overview

The Sample Data Excel-Files have following data structure:

Sample Data Section	Excel File Column Name	Molecular DB Column Name	Import Notice
		SampleID	must be declared manually
SampleCodes	WP_Nr	WP_Nr	
	Commodity	Commodity	
	Country	Country	
	Site	Site	
	Year	Year	
	Month	Month	
	Nr	Number	
	TraceSampleCode	TraceSampleCode	
	Responsible	ResponsiblePerson	Substitute by PersonID from Person table
General Description	TraceSampleCode	TraceSampleCode	
	InternalSampleCode	InternalSampleCode	
	SetName	SetName	
	LocationName	LocationName	
	ProducerIdentificationName	ProducerIdentificationName	Substitute by PersonID from Person table



The screenshot shows the phpMyAdmin interface for importing data into the 'foodproduct' table of the 'trace' database. The table structure is as follows:

Table: foodproduct			
Location of the text file	/a/FoodProduct table.csv Durchsuchen... (Max: 2.048KB)		
Replace table data with file	<input type="checkbox"/> Replace	The contents of the file replaces the contents of the selected table for rows with identical primary or unique key.	
Fields terminated by	:	The terminator of the fields.	
Fields enclosed by	" <input type="checkbox"/> OPTIONAL	Often quotation marks. OPTIONAL means that only char and varchar fields are enclosed by the "enclosed by"-character.	
Fields escaped by	\	Optional. Controls how to write or read special characters.	
Lines terminated by	\n	Carriage return: \r Linefeed: \n	
Column names	<input type="checkbox"/>		If you wish to load only some of a table's columns, specify a comma-separated field list.
LOAD method	<input type="radio"/> ...DATA <input checked="" type="radio"/> ...DATA LOCAL		The best method is checked by default, but you can change if it fails.
<input type="button" value="Submit"/> <input type="button" value="Reset"/>			

Figure 14: Import screen for csv files

Sample Data Section	Excel File Column Name	Molecular DB Column Name	Import Notice
	CollectorIdentificationName	CollectorIdentificationName	
	DonorIdentificationName	DonorIdentificationName	
	Food/ProductName	FoodProductID	Substitute by FoodProductID from Foodproduct Table
	TracePopularName	TaxonID	Substitute by TaxonID from Taxonomy Table
	SampleType	SampleType	
	SamplingDate	SamplingDate	Change Date format to YYYY-MM-DD
	SamplingProcedure	SamplingProcedure	
	SamplingPurpose	SamplingPurpose	
	SampleQuantity	SampleQuantity	
	ContainerType	ContainerType	
	StorageCondition	StorageCondition	
	Picture	Picture	
	SoilAnalysis	SoilAnalysis	
	Comment	Comment	
Specific Description	<i>differs depending on Commodity</i>	Specific01	Put Field Name in front data, separated with ":"
		Specific02	Put Field Name in front data, separated with ":"
		Specific03	Put Field Name in front data, separated with ":"
		Specific04	Put Field Name in front data, separated with ":"
		Specific05	Put Field Name in front data, separated with ":"
		Specific06	Put Field Name in front data, separated with ":"
		Specific07	Put Field Name in front data, separated with ":"
		Specific08	Put Field Name in front data, separated with ":"

Table 19: Importing scheme for sample data

#### 4.1.4 Importing Sample Data Step by Step

Following, importing sample data is described step by step.

1. Sample data is split over several tables. So first step is to unite all tables in one table. Following must be considered: many cells are blocked and linked to other cells in the table. You can't disable this. The solution is to export every single table (start with table "sample code", then "general description" and at

last “specific description”) in an csv-file. Open these files and copy the content in one table. Copy first all “sample code” column. After these columns the “general...” columns und at least the “specific...” columns.

2. Create in this new table a column called “SampleID”. This column must be in front of the other columns (in front of “WP\_Nr”).
3. Fill in the column “SampleID” IDs. For finding out which number to fill in, log in the TMDB (Trace Molecular Database) PHPMyAdmin and find out the largest SampleID number. Add one and ascending numbers in the next field.
4. Substitute the Name of the Responsible Person by the PersonID (table person) you can find in the TMDB.
5. Delete the column that follows the “ResponsiblePerson”. This column is called “**TraceSampleCode**” and is double. Do not delete the first column called “TraceSampleCode”, for the fields must correspond the scheme of Table 2.
6. Substitute the Name of the Food/ProductName by the FoodProductID (table foodproduct) you can find in the TMDB.
7. Substitute the Name of the TracePopularName by the TaxonID (table taxonomy) you can find in the TMDB.
8. Replace the SamplingDate by a date in following form: YYYY-MM-DD (Year [4 digits], Month [2 digits], Day [2 digits] according to ISO 8601). Be aware that you have to copy the date in, not just link it, because links can't be exported in csv-files.
9. Delete the column that follows the “Comment”. This column is called “TraceSampleCode” and is double. Do not delete the first column called “TraceSampleCode”, for the fields must correspond the scheme of Table 2.
10. Correct all following columns. The cells must have following form: “field name: data”. So add in every cell the field name in front of the data, separated by a doublepoint (“:”). If the cell or even column contains no data, delete it.  
Example: the column is named “AnimalRegistrationNumber” and the value of the cell is “54RA111258”. The cell must be corrected to the value: “AnimalRegistrationNumber: 54RA111258”. This is necessary, because the specific description differs from sample to sample depending on the commodity.
11. Delete first row, that is the headline row.
12. Go on as described for table foodproduct in Figure 9: Insert data in table foodproduct from text file on page 69. Well, please select correct table (you are importing sample data...).
13. Check the imported data by browsing it.

## 5 Web based frontend for the database

There exists a web based frontend for maintaining the data in the database. This webfrontend is called PHPMyAdmin and is a OpenSource project. With this tool you can add tables, columns, records or delete them. You can import and export data or just browse it. For further information is available on the website <http://www.phpmyadmin.net>.

Access to the Web based frontend for maintaining data can be given by the administrator of Center BATS.

The Following Screenshots show the functionality of PHPMyAdmin.

**WEBLAND.CH**  
REALIZE IT.

**Home**

trace (18)

**trace**

- benutzerdaten
- extraction
- foodproduct
- geneticelement
- list\_country
- list\_language
- list\_probedye
- method
- organisation
- pcr
- person
- primer
- proteindetection
- publication
- sample
- sequence
- site
- taxonomy

**Database trace running on mysql1.webland.ch**

Table	Action	Records	Type	Size	Overhead
benutzerdaten		7	InnoDB	32.0 KB	-
extraction		9	InnoDB	16.0 KB	-
foodproduct		59	InnoDB	16.0 KB	-
geneticelement		15	InnoDB	80.0 KB	-
list_country		157	InnoDB	48.0 KB	-
list_language		23	InnoDB	32.0 KB	-
list_probedye		57	InnoDB	16.0 KB	-
method		2	InnoDB	16.0 KB	-
organisation		58	InnoDB	112.0 KB	-
pcr		9	InnoDB	96.0 KB	-
person		233	InnoDB	144.0 KB	-
primer		19	InnoDB	32.0 KB	-
proteindetection		0	InnoDB	32.0 KB	-
publication		9	InnoDB	32.0 KB	-
sample		270	InnoDB	160.0 KB	-
sequence		48	InnoDB	112.0 KB	-
site		123	InnoDB	16.0 KB	-
taxonomy		150	InnoDB	128.0 KB	-
<b>18 table(s)</b>	<b>Sum</b>	<b>1,248</b>	--	<b>1.1 MB</b>	<b>0 Bytes</b>

Check All / Uncheck All      With selected:

◆ Print view  
◆ Data Dictionary

[Query window](#)

[Done](#)

Figure 15: PHPMyAdmin entry site

The Screenshot above shows the entry site of PHPMyAdmin. On this site you can delete or edit tables or add new tables.

**WEBLAND.CH**  
REALIZE IT.

**Home**

trace (18)

**trace**

- [benutzerdaten](#)
- [extraction](#)
- [browse](#)
- [SQL](#)
- [Search](#)
- [foodpr...](#)
- [geneticelement](#)
- [list\\_country](#)
- [list\\_language](#)
- [list\\_probebye](#)
- [method](#)
- [organisation](#)
- [pcr](#)
- [person](#)
- [primer](#)
- [proteindetection](#)
- [publication](#)
- [sample](#)
- [sequence](#)
- [site](#)
- [taxonomy](#)

**Database trace - Table list\_country running on mysql1.webland.ch**

Structure Browse SQL Search Insert Export Operations Empty Drop

InnoDB free: 8192 kB

Field	Type	Attributes	Null	Default	Extra	Action				
CountryID	smallint(6)		No		auto_increment					
CountryCode	char(2)		Yes	NULL						
CountryName	varchar(255)		Yes	NULL						
Remarks	text		Yes	NULL						
RecordModification	timestamp(14)		Yes	NULL						

Check All / Uncheck All With selected:

**Indexes : [Documentation]**

Keyname	Type	Cardinality	Action	Field	Type	Usage	Statements
PRIMARY	PRIMARY	157		CountryID	Data	16,384 Bytes	Format
CountryCode	UNIQUE	157		CountryCode	Index	32,768 Bytes	Next Autoindex
CountryName	UNIQUE	157		CountryName	Total	49,152 Bytes	

Create an index on  columns

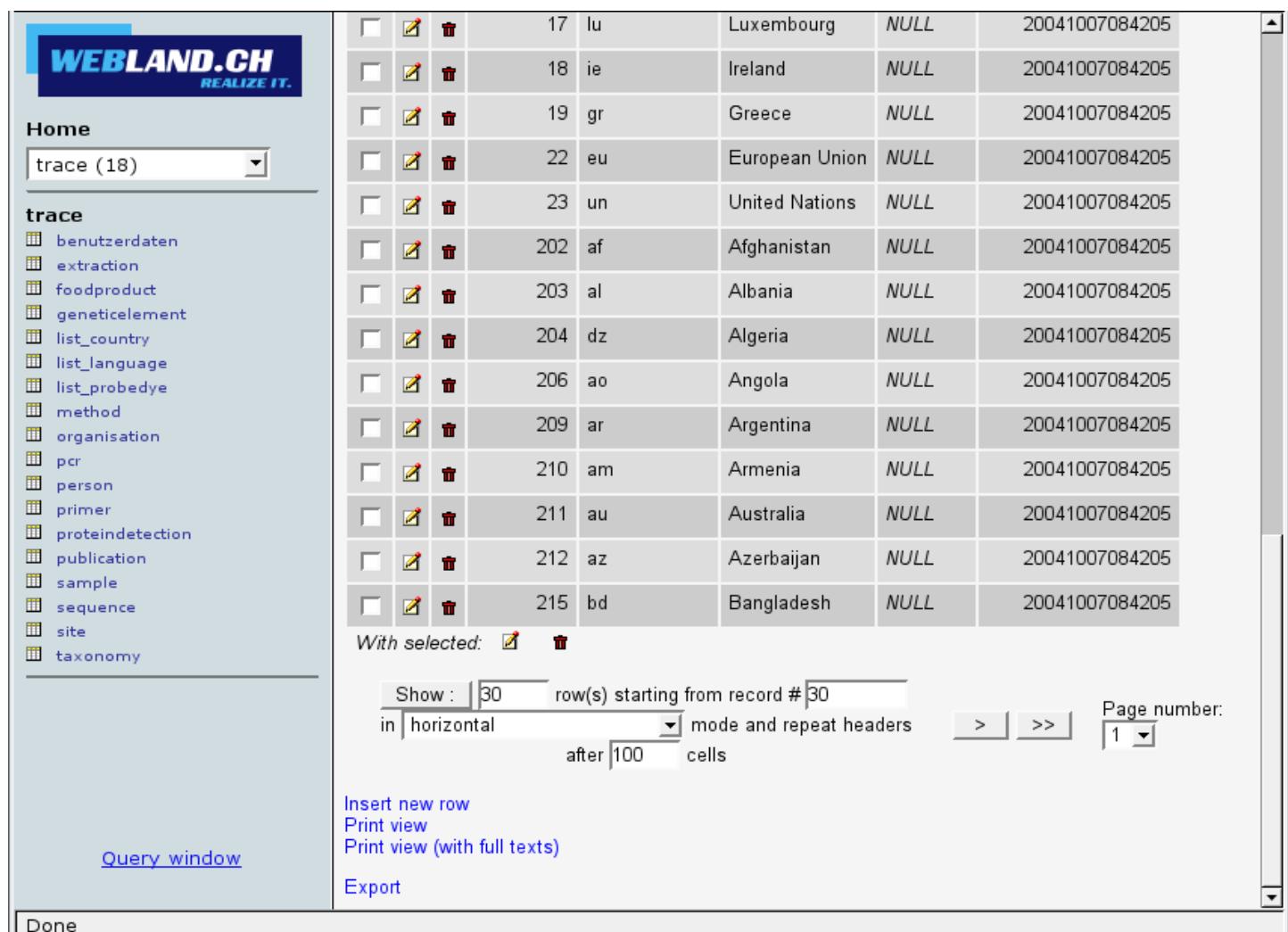
• Print view  
 • Add new field :  At End of Table   
 • Propose table structure [Documentation]  
 Run SQL query/queries on database trace [Documentation]  
 SELECT \* FROM `list\_country` WHERE 1

Query window

[http://mysql1.webland.ch/tbl\\_properties\\_structure.php?lang=en-iso-8859-1&server=1&db=trace&table=benutzerdaten](http://mysql1.webland.ch/tbl_properties_structure.php?lang=en-iso-8859-1&server=1&db=trace&table=benutzerdaten)

Figure 16: PHPMyAdmin table view

The screenshot above shows the table view. In this view, you can edit table properties: deleting or adding columns. This site grants you access to all other features of the table.



WEBLAND.CH  
REALIZE IT.

**Home**

trace (18)

**trace**

- benutzerdaten
- extraction
- foodproduct
- geneticelement
- list\_country
- list\_language
- list\_probebye
- method
- organisation
- pcr
- person
- primer
- proteindetection
- publication
- sample
- sequence
- site
- taxonomy

**Query window**

<input type="checkbox"/>			17	lu	Luxembourg	NULL
<input type="checkbox"/>			18	ie	Ireland	NULL
<input type="checkbox"/>			19	gr	Greece	NULL
<input type="checkbox"/>			22	eu	European Union	NULL
<input type="checkbox"/>			23	un	United Nations	NULL
<input type="checkbox"/>			202	af	Afghanistan	NULL
<input type="checkbox"/>			203	al	Albania	NULL
<input type="checkbox"/>			204	dz	Algeria	NULL
<input type="checkbox"/>			206	ao	Angola	NULL
<input type="checkbox"/>			209	ar	Argentina	NULL
<input type="checkbox"/>			210	am	Armenia	NULL
<input type="checkbox"/>			211	au	Australia	NULL
<input type="checkbox"/>			212	az	Azerbaijan	NULL
<input type="checkbox"/>			215	bd	Bangladesh	NULL

With selected:

Show :  row(s) starting from record #   
 in  mode and repeat headers  
 after  cells

> >> Page number:

[Insert new row](#)  
[Print view](#)  
[Print view \(with full texts\)](#)  
[Export](#)

Done

Figure 17: PHPMyAdmin browsing a table

The screenshot above shows the feet when browsing a table. In this view you can edit records. On the very end of this page you find the link “Insert new row”.

**WEBLAND.CH**  
REALIZE IT.

Home

trace (18)

**trace**

- benutzerdaten
- extraction
- foodproduct
- geneticelement
- list\_country**
- list\_language
- list\_probabye
- method
- organisation
- pcr
- person
- primer
- proteindetection
- publication
- sample
- sequence
- site
- taxonomy

[Query window](#)

**Database trace - Table list\_country running on mysql1.webland.ch**

Structure Browse SQL Search Insert Export Operations Empty Drop

InnoDB free: 8192 kB

Field	Type	Function	Null	Value
CountryID	smallint(6)			
CountryCode	char(2)		<input checked="" type="checkbox"/>	
CountryName	varchar(255)		<input checked="" type="checkbox"/>	
Remarks	text		<input checked="" type="checkbox"/>	
RecordModification	timestamp(14)	NOW	<input type="checkbox"/>	

Insert as a new row    -- And --

Go back to previous page  
Or  
 Insert another new row

Done

Figure 18: PHPMyAdmin adding a record

Following this link leads you to the page shown on the screenshot above, where you can add one or more records.

The next twelve pages show the security-concept, the usability-concept and the user-questionnaire of the TRACE molecular biology database.

# Installation & Security

of the TRACE Molecular Biology Database  
Version 0.5, 31.12.2007

Authors: Jakob Lindenmeyer, Tobias Krais

## 1 Installation of the TRACE molecular biology database

The TRACE molecular biology database web application was tested on following systems:

Application Name	Configuration I	Configuration II	Configuration III
PHP Version	4.4.7	5.2.3	5.2.5
MySQL Version	3.23.49	5.0.45	5.0.22
Operating System	Windows Server	Linux	Windows Server
Webserver	Microsoft IIS	Apache	Microsoft IIS

The installation package contains a dump of the MySQL database and a compressed file containing the web database files. The installation package is available for download under the following addresses:

Dump of the MySQL database:

<https://ssl12.webland.ch/www172/downloads/trace.sql.zip>

Compressed file containing the web database files:

<https://ssl12.webland.ch/www172/downloads/webfiles.zip>

All files are protected by username and password, which can be requested by authorised TRACE partners from TRACE partner no. 41.

1. To install the web database, the administrator has to create an empty database (we name it "trace") on the administrators MySQL server. He then he has to import the dump of the database. If the database already exists, then the administrator has to just import the new data and the old data will be deleted.
2. To install the web application, the administrator has to extract the compressed file to a folder of the target web server. This folder can be chosen freely. It must not be a root folder of a domain.
3. Finally the file "secure/API/connection\_info.php" has to be configured according to the target database settings.

## 2 Security issues

### 2.1 User management

Some information of the web application can only be accessed if the user is logged in.

#### 2.1.1 User security

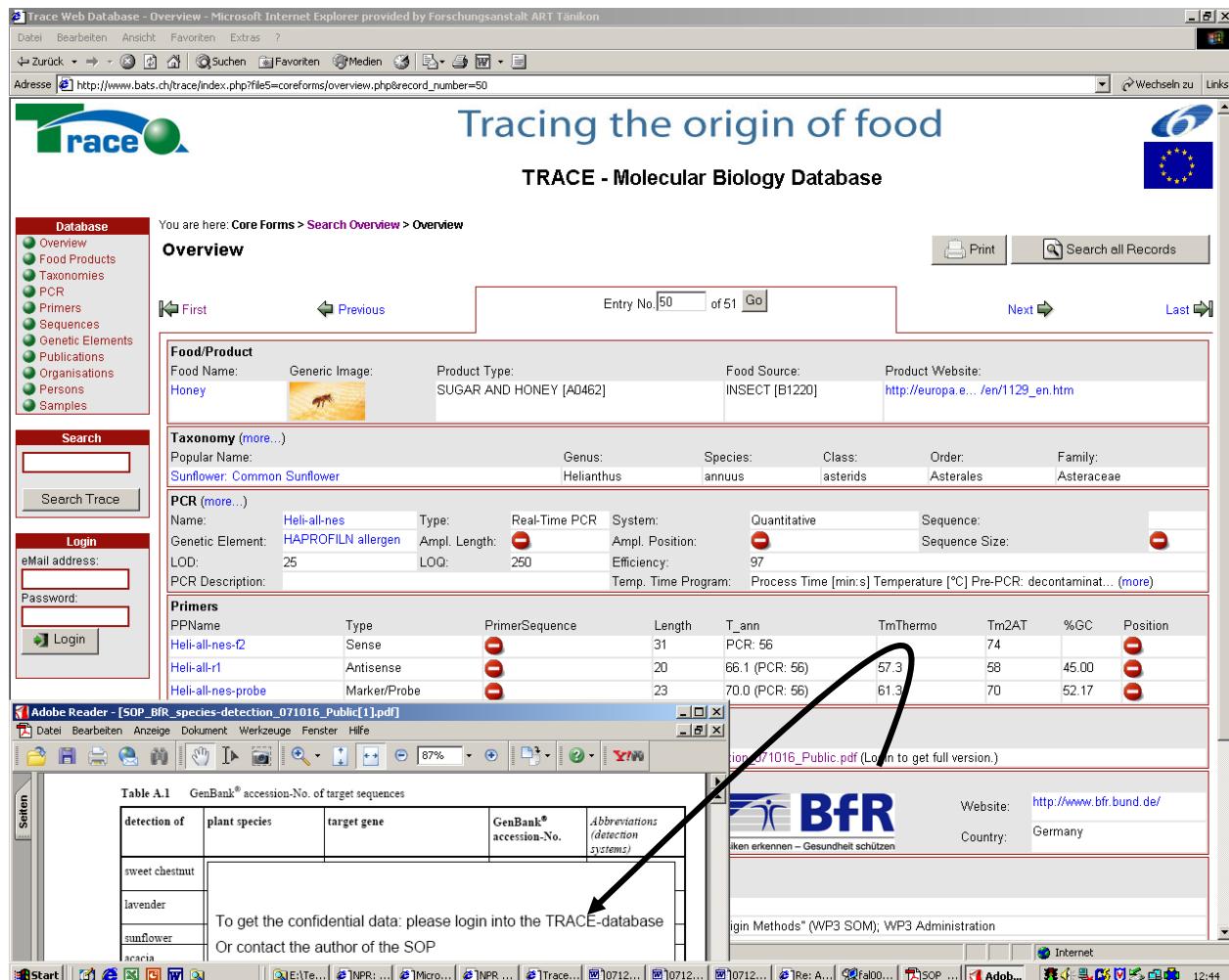
The TRACE molecular biology database is not located on a HTTPS secured server by default. HTTPS ciphers all information that is transmitted between the client browser and the server. For the default connection to the TRACE web interface is not ciphered with HTTPS, the login process is vulnerable for so called “man in the middle attacks”. If an attacker can listen to the traffic between the client browser and the server, it can record the password and all other information transferred to the user.

The TRACE web database is also accessible with an HTTPS secured connection. It can be accessed with the URL <https://ssl12.weblan.ch/www172/trace/>. Why is this URL not made the default, or even the only way to access the trace web database? This URL is only a HTTPS proxy server. Thus the web database will always be accessible via the default connection.

Once the password is transmitted to the server, it is encrypted as an MD5 checksum. The MD5 checksum algorithm can only be calculated in one direction. This means in practice, that the password “Hj48&klö” has the MD5 checksum “49ffb558d39a4bf476e7ad01dda3757b”. No one can recalculate the password if only the checksum is known. Thus decryption it not possible. The password is stored as an MD5 checksum in the database. This offers best server side password security. The password is not stored within the user session.

After first time login a user has to change the password due to security reasons.

## 2.1.2 Login procedure



**Trace Web Database - Overview** Microsoft Internet Explorer provided by Forschungsanstalt ART Tänikon

Datei Bearbeiten Ansicht Favoriten Extras ?

Zurück → Zurück ← Suchen Favoriten Medien Datei Wechseln zu Links

Adresse http://www.bats.ch/trace/index.php?file5=coreforms/overview.php&record\_number=50

**Tracing the origin of food**

**TRACE - Molecular Biology Database**

You are here: Core Forms > Search Overview > Overview

**Overview**

Entry No. 50 of 51 Go

**Food/Product**

Food Name:	Generic Image: Honey	Product Type:	SUGAR AND HONEY [A0462]	Food Source:	INSECT [B1220]	Product Website:	<a href="http://europa.e.../en/1129_en.htm">http://europa.e.../en/1129_en.htm</a>
------------	----------------------	---------------	-------------------------	--------------	----------------	------------------	---

**Taxonomy (more...)**

Popular Name:	Sunflower: Common Sunflower	Genus:	Helianthus	Species:	annus	Class:	asterids	Order:	Asterales	Family:	Asteraceae
---------------	-----------------------------	--------	------------	----------	-------	--------	----------	--------	-----------	---------	------------

**PCR (more...)**

Name:	Heli-all-nes	Type:	Real-Time PCR	System:	Quantitative	Sequence:	
Genetic Element:	HAPROFIL allergen	Ampl. Length:	250	Ampl. Position:		Sequence Size:	
LOD:	25	LOQ:	250	Efficiency:	97		
PCR Description:				Temp. Time Program:	Process Time [min:s] Temperature [°C] Pre-PCR: decontaminat... (more)		

**Primers**

PPName	Type	PrimerSequence	Length	T <sub>ann</sub>	TmThermo	Tm2AT	%GC	Position
Heli-all-nes-f2	Sense	●	31	PCR: 56	74	58	45.00	●
Heli-all-r1	Antisense	●	20	66.1 (PCR: 56)	57.3	70	52.17	●
Heli-all-nes-probe	Marker/Probe	●	23	70.0 (PCR: 56)	61.3			

**Adobe Reader - [SOP\_BFR\_species-detection\_071016\_Public[1].pdf]**

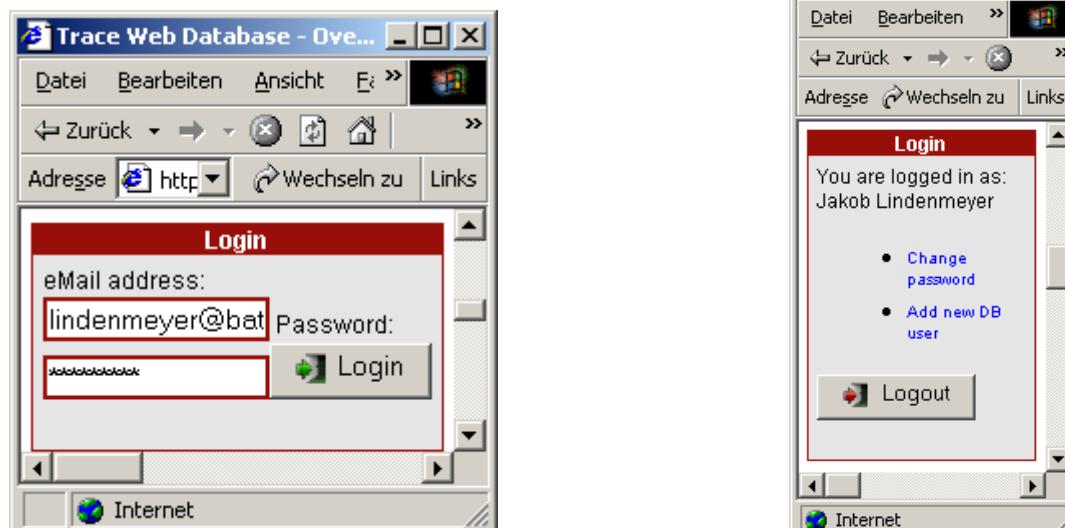
Table A.1 GenBank® accession-No. of target sequences

detection of	plant species	target gene	GenBank® accession-No.	Abbreviations (detection systems)
sweet chestnut				
lavender				
sunflower				
acacia				

To get the confidential data: please login into the TRACE-database  
Or contact the author of the SOP

**BfR** <http://www.bfr.bund.de/>  
Country: Germany

**Figure 1: Public data-set before the login:** The confidential information is covered by a no-access-sign and the PDF-table does not contain any data.



**Trace Web Database - Overview**

Datei Bearbeiten Ansicht E: Zurück → Zurück ← Suchen Favoriten Medien Datei Wechseln zu Links

Adresse http://www.bats.ch/trace/index.php?file5=coreforms/overview.php&record\_number=50

**Login**

eMail address:  
**lindenmeyer@bats.ch**

Password:  
**XXXXXXXXXX**

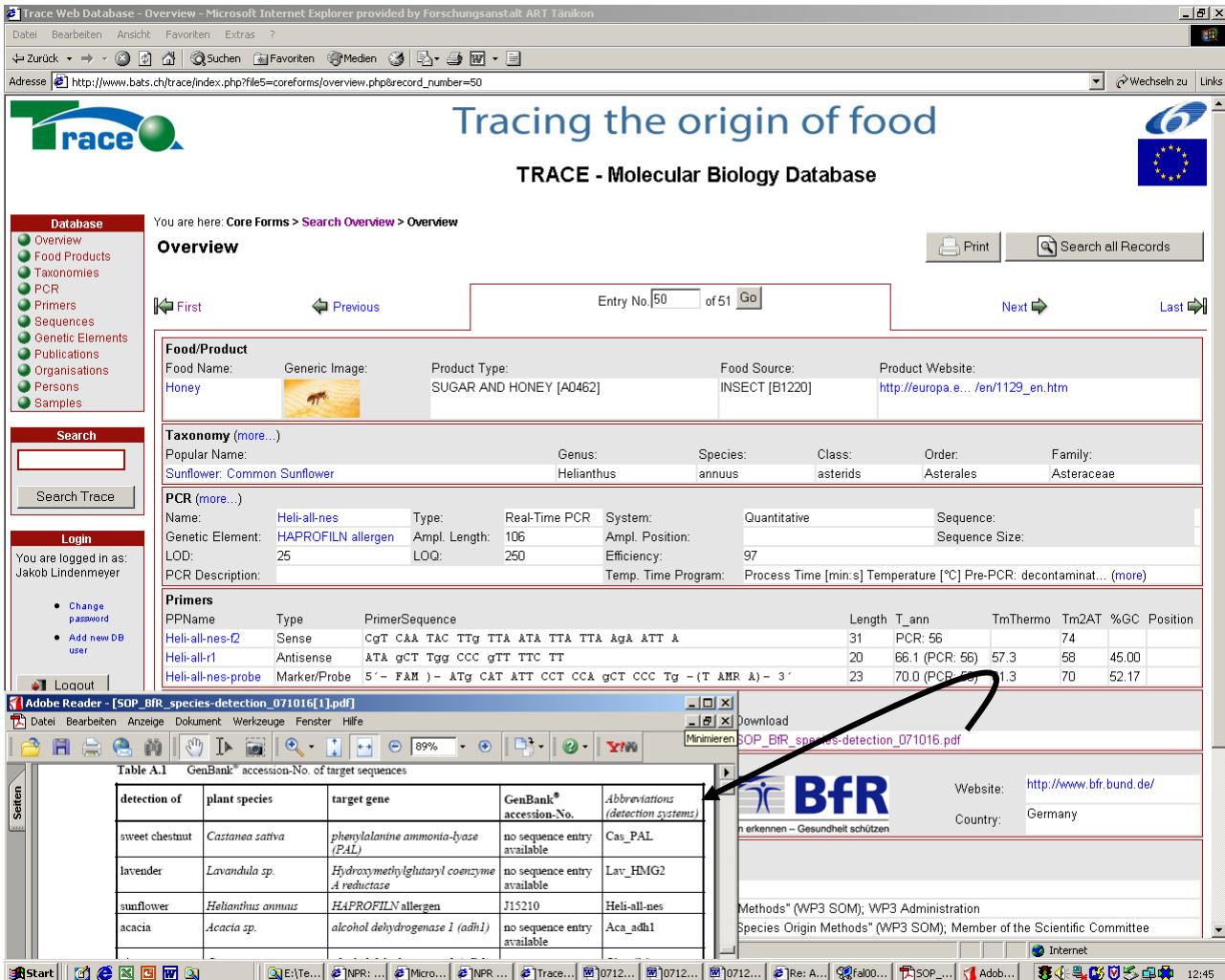
**Login**

You are logged in as:  
**Jakob Lindenmeyer**

- Change password
- Add new DB user

**Logout**

**Figure 2: Login-window before (left) and after (right) the login-process.**



The screenshot shows a Microsoft Internet Explorer window displaying the TRACE database. On the left, there's a sidebar with links for Database Overview, Food Products, Taxonomies, PCR, Primers, Sequences, Genetic Elements, Publications, Organisations, Persons, and Samples. Below that is a Search bar and a Login section where the user is logged in as Jakob Lindenmeyer. The main content area has a title "Tracing the origin of food" and "TRACE - Molecular Biology Database". It shows an "Overview" page with sections for Food/Product (Food Name: Honey, Product Type: SUGAR AND HONEY [A0462], Food Source: INSECT [B1220], Product Website: [http://europa.e.../en/1129\\_en.htm](http://europa.e.../en/1129_en.htm)), Taxonomy (Popular Name: Sunflower; Common Sunflower, Genus: Helianthus, Species: annuus, Class: asterids, Order: Asterales, Family: Asteraceae), PCR (Name: Heli-all-nes, Type: Real-Time PCR, System: Quantitative, Sequence: HAPROFIL allergen, Ampl. Length: 106, Ampl. Position: 25, LOD: 25, LOQ: 250, Efficiency: 97, Temp. Time Program: Process Time [min:s] Temperature [°C] Pre-PCR: decontaminat... (more)), and Primers (Table A.1: GenBank® accession-No. of target sequences). A black arrow points from the "Logout" link in the sidebar to the "Heli-all-nes" PCR entry. Another black arrow points from the "Logout" link to the PDF viewer window titled "SOP\_BfR\_species-detection\_071016[1].pdf". The PDF viewer shows the same PCR information as the database.

detection of	plant species	target gene	GenBank® accession-No.	abbreviations (detection systems)
sweet chestnut	<i>Castanea sativa</i>	<i>phenylalanine ammonia-lyase (PAL)</i>	no sequence entry available	Cas_PAL
lavender	<i>Lavandula sp.</i>	<i>Hydroxymethylglutaryl coenzyme A reductase</i>	no sequence entry available	Lav_HMG2
sunflower	<i>Helianthus annuus</i>	<i>HAPROFIL allergen</i>	J15210	Heli-all-nes
acacia	<i>Acacia sp.</i>	<i>alcohol dehydrogenase 1 (adh1)</i>	no sequence entry available	Aca_adh1

**Figure 3: Confidential data-set after the login:** The sequence information of the primers and the data in the PDF-table is visible after the login.

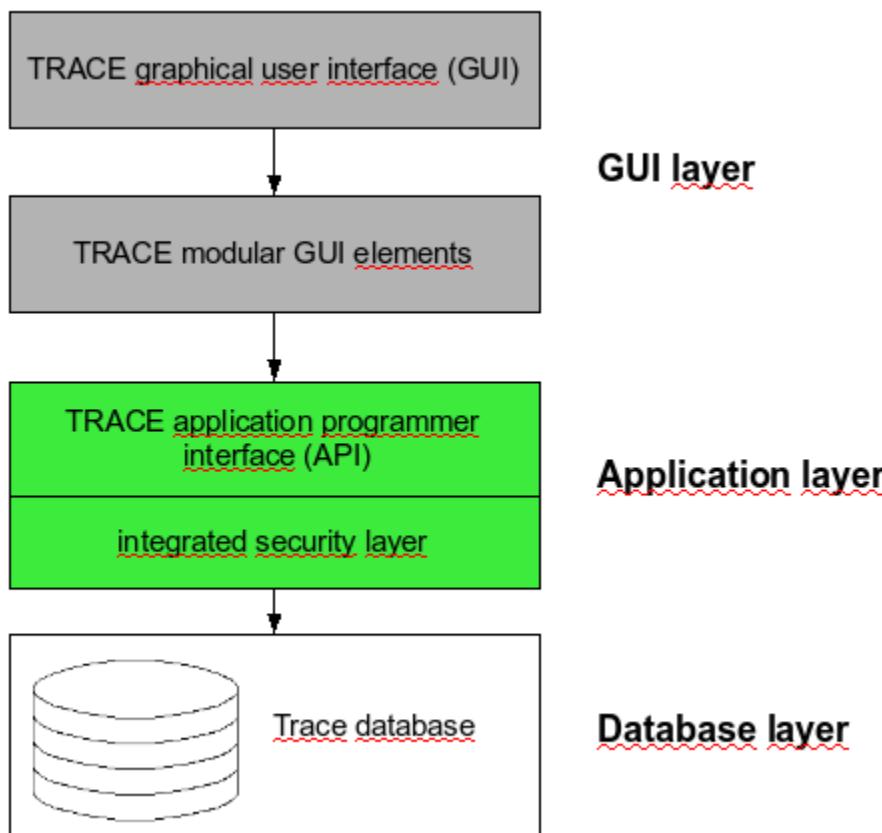
### 2.1.3 User roles

There exist two different user roles. A normal user is allowed to view secured data within the web database. He can also change his password. An administrator is additionally allowed to add new users.

Users can only be deleted within the MySQL database. phpMyAdmin is an opensource tool written in PHP intended to handle the administration of MySQL, the database management system chosen for the TRACE molecular biology database. The administration is done over the HTTP-protocol through a webbrowser. Like this users can create and drop databases, create and alter tables, add and edit fields, manage keys on fields, manage privileges, export data into various formats without knowing all the SQL statements. phpMyAdmin runs under the GPL License. phpMyAdmin is therefore a suitable alternative for a webbased data-import into the TRACE-database by the database-administrator and the coordinator.

## 2.2 Database security model

The TRACE web database programming code is divided into three main layers with

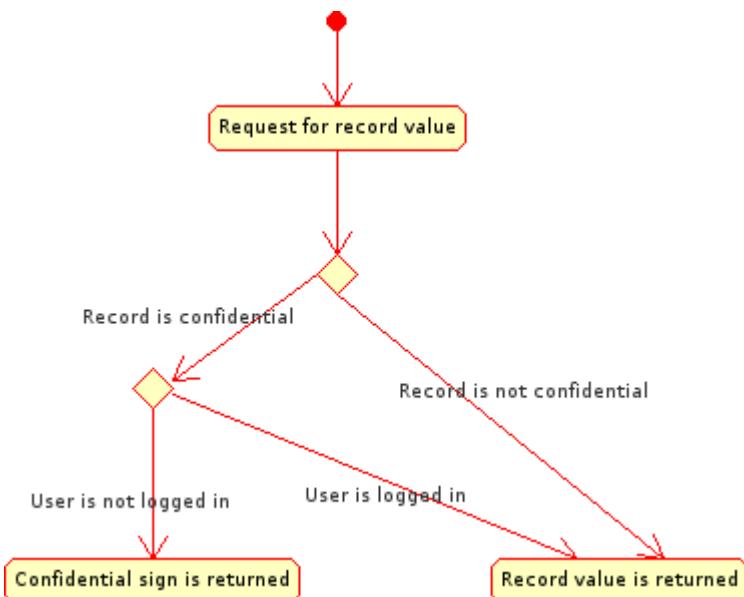


several sub layers. The upper GUI-layer simply adds content to one another like a puzzle, e.g. the overview form. The advantage is less redundancy, better maintainability and rapid application development. The lower GUI-layer contains all the areas itself, e.g. the organisation-box of the overview form. The application layer consists of the API (Application Programmer Interface). The API is the only way to access the database. For each database field exists one function.

**Figure 4: Security model of the TRACE molecular biology database:** Database-, application- and GUI-layers.

This application architecture is secured by its design. For each database field exists one function to access the database field content. This function checks if the content may be shown to the user. Thus a security check is done on one place and not on many. This defines a very high security standard.

The disadvantage of this design is a slower performance, e.g. by opening the overview over all samples (several hundred records). This takes some seconds to build up the overview table.



**Figure 5: Flow diagram of a user-request for a confidential record.**

Each table has a field named Confidential. This field consists of one character. Has a record with this field the character value “y” then the record is confidential and is only displayed after the login.

If there is now coming a request to the API to return the value another field of this record, the API checks whether the record is confidential or not. If it is, the API checks if the user is logged in (that means the user is allowed to view all the data in the database). If the user is not logged in, a confidential sign is returned. In all other cases the correct value is returned.

User logins are stored in session cookies. This guarantees that internet bots (like bots from search engines, e.g. the Googlebot) have no access to sensible data. Bots can't handle sessions. The API is stored in a sub folder of the password protected folder called “secure”. These files can only be accessed with a valid password for this folder. This is necessary to protect the API from inclusion from outside the web database. Only other files from [www.bats.ch/trace/](http://www.bats.ch/trace/) can include the API.

## 2.3 File download

Files that should not be shown to the public are stored in a password protected subfolder of the project, named “secure”. Only persons who have a valid administrator password can access the data. All files which are intended for download are stored in subfolders of the secure-folder. The password and login name differ from the general user login of the online database. If somebody wants to download files, he would need the password of the folder. To solve this problem, we created a kind of “single sign on” for the online database. If the user is logged in the web database, he can see a download link. This link is a link to a PHP-file. And this PHP-file fakes the download for requested file in an unsecured folder. It is only faked for this specific request and not really copied. From this folder it is possible to download the requested file. The user will see a download location that does not exist. So if the user remembers the download location and later on wants to download the file again by typing the location in the address line of the browser, the browser will not find the file any more.

# Usability-testing

of the TRACE Molecular Biology Database

Version 0.5, 31.12.2007

Authors: Jakob Lindenmeyer, Tobias Krais

## 1 Testing of client and server

3 different users were supervised by using the TRACE molecular biology database on different operating system and using different browsers. The experiences by this usability-testing were then used to make the following improvements of the TRACE molecular biology database:

Application	Configuration I	Configuration II	Configuration III
Operating system	Microsoft Windows XP	MacOS X	Linux
Browser	Internet Explorer 7	Safari 2	Mozilla Firefox 2

TRACE molecular biology database web application was tested on these systems:

Application Name	Configuration I	Configuration II	Configuration III
PHP Version	4.4.7	5.2.3	5.2.5
MySQL Version	3.23.49	5.0.45	5.0.22
Operating System	Windows Server	Linux	Windows Server
Webserver	Microsoft IIS	Apache	Microsoft IIS

## 2 Navigation

Improvement of the navigation between the records:

The header-row shows special navigation-options like:

- First record
- Previous record
- Next record
- Last record

Or the user can insert the exact data-set number, if the number is already known.

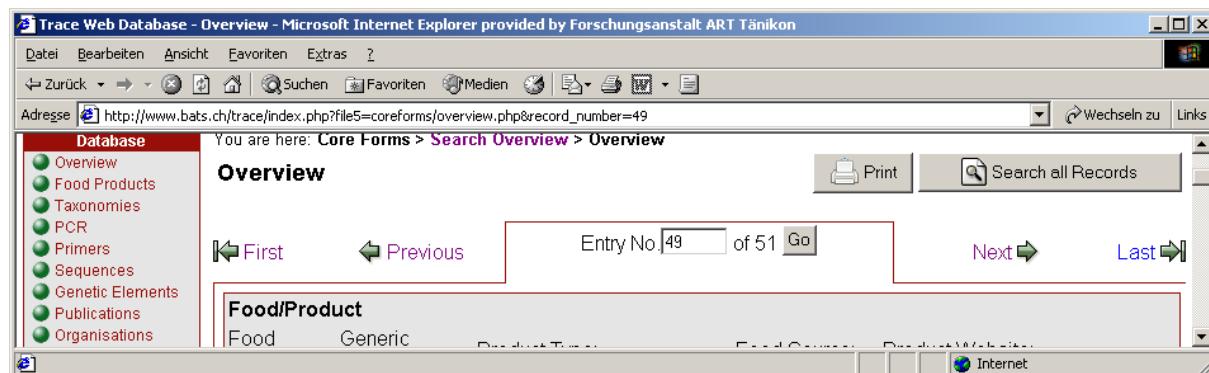
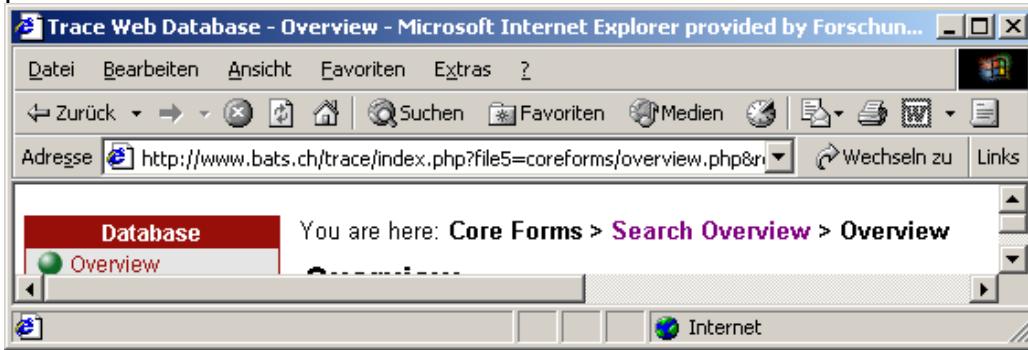


Figure 1: The header-row containing 5 navigation elements to navigate between the records of the TRACE molecular biology database.

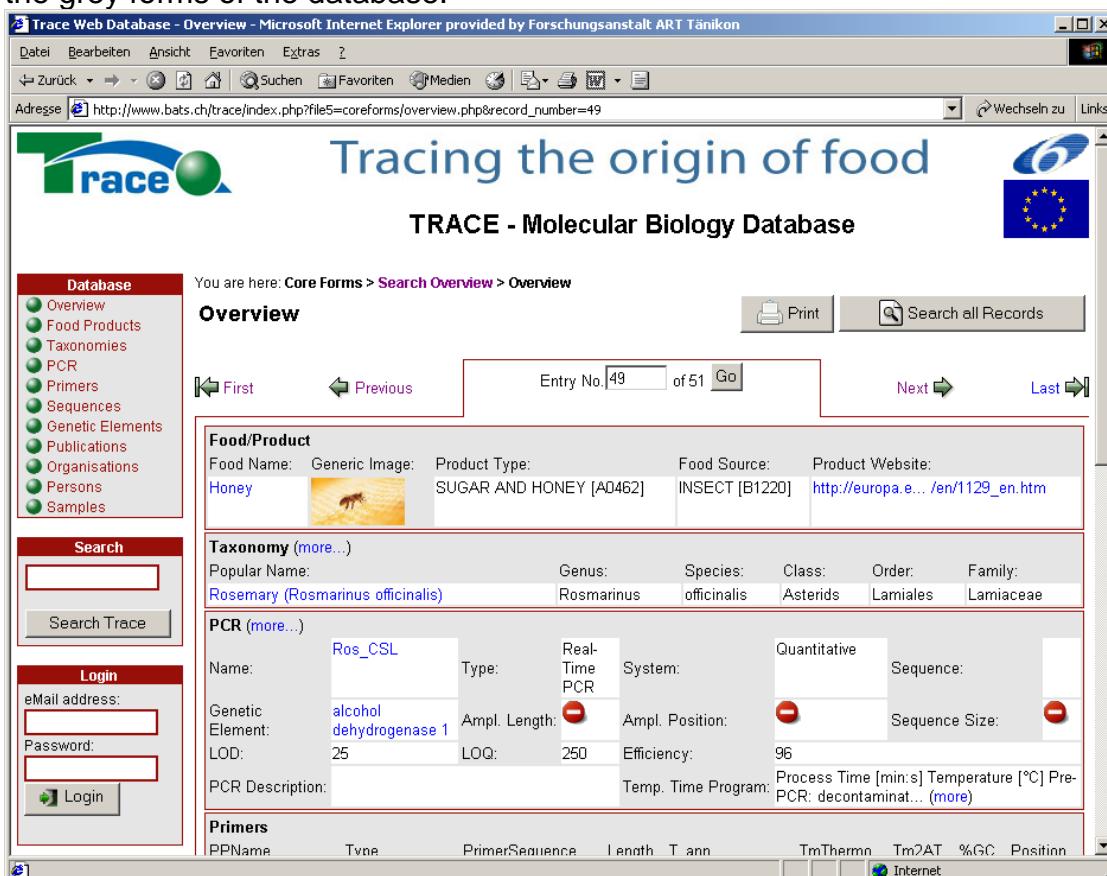
At the top left of the dataset, a bread-crumb-trail always shows the database-user his current position in the website by saying: You are here: followed by a hierarchical path of the websites document structure.



**Figure 2:** The bread-crumb-trail shows the database-user his current position in the website by saying.

### 3 Functional boxes

A further helpful usability-improvement for the database-user is the separation of the TRACE-information into functional and logical boxes, divided by red lines, e.g. for taxonomic information, molecular information, information on foods, information about the institution and contacts, information about publications. In addition, we marked the separation of the descriptive surrounding information (title of the box, name of the attributes, navigation) in dark grey from the data itself in white boxes. This helps the user to see, which data (white fields) has been filled in by the TRACE-partners into the grey forms of the database.

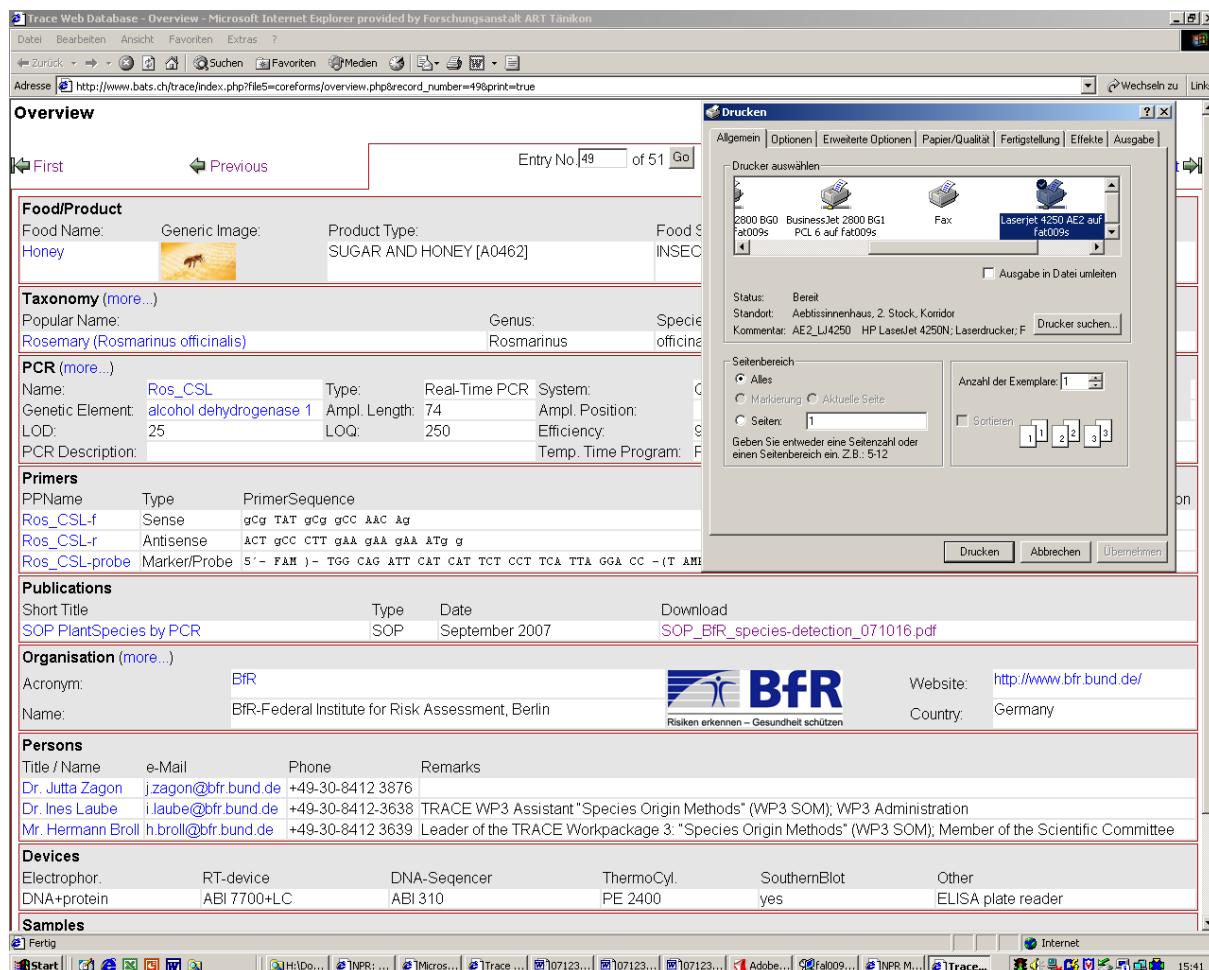


The screenshot displays the TRACE - Molecular Biology Database interface. At the top, there is a header with the TRACE logo, the title "Tracing the origin of food", and the European Union flag. Below the header, the page title is "TRACE - Molecular Biology Database". On the left side, there is a vertical sidebar with a "Database" section containing links for Overview, Food Products, Taxonomies, PCR, Primers, Sequences, Genetic Elements, Publications, Organisations, Persons, and Samples. There is also a "Search" section with a search bar and a "Login" section with fields for eMail address and Password, and a "Login" button. The main content area has a breadcrumb trail: "You are here: Core Forms > Search Overview > Overview". The main content is titled "Overview". It includes a search bar with "Entry No. 49 of 51 Go" and navigation buttons for First, Previous, Next, and Last. Below this, there are several functional boxes separated by red lines. The first box is "Food/Product" with fields for Food Name (Honey), Generic Image (bee), Product Type (SUGAR AND HONEY [A0462]), Food Source (INSECT [B1220]), and Product Website ([http://europa.e.../en/1129\\_en.htm](http://europa.e.../en/1129_en.htm)). The second box is "Taxonomy (more...)" with fields for Popular Name (Rosemary (Rosmarinus officinalis)), Genus (Rosmarinus), Species (officinalis), Class (Asterids), Order (Lamiales), and Family (Lamiaceae). The third box is "PCR (more...)" with fields for Name (Ros\_CS1), Type (Real-Time PCR), System (Quantitative), Sequence, and various parameters like Ampl. Length, Ampl. Position, Efficiency, and Sequence Size. The fourth box is "Primers" with columns for PPName, Type, PrimerSequence, Length, T\_m, TmThermo, Tm2AT, %GC, and Position.

**Figure 3:** Separation of the TRACE-information into functional and logical boxes.

## 4 Easy-to-print function

Many database-users still want to print out important data. Therefore we implemented an easy-to-print function for single records and for the whole database itself. After choosing the PRINT-button, the user gets a new webpage showing the chosen record in a print-optimised design, without any navigation and with an activated printer-dialogue.

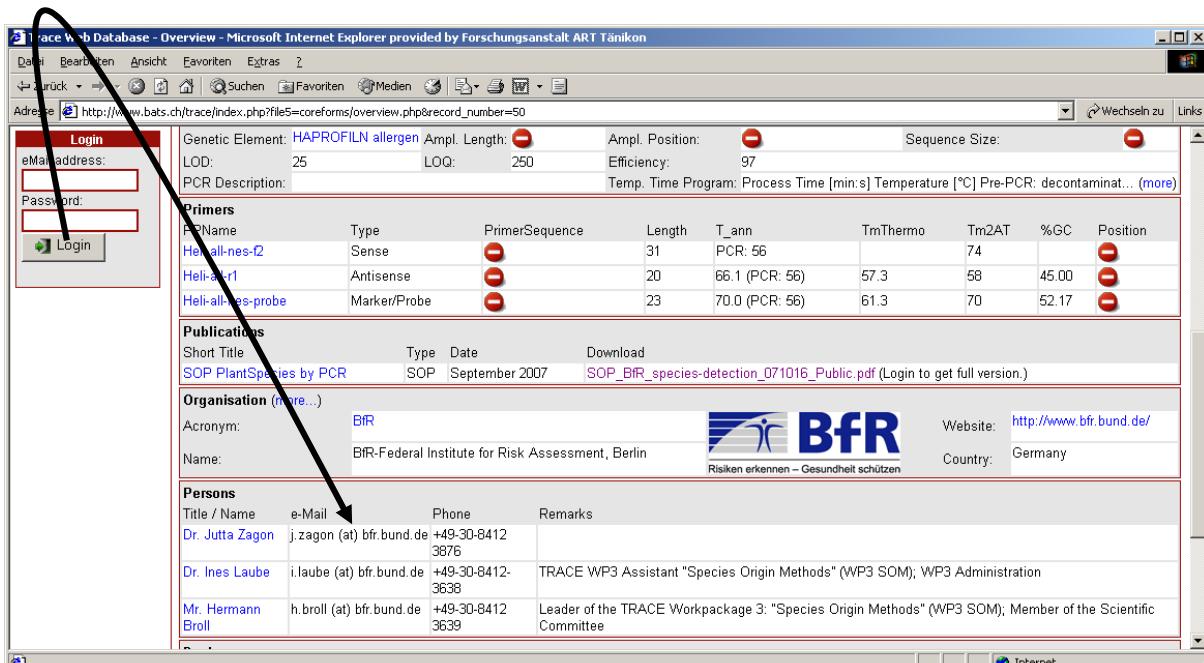


**Figure 4: Printer-optimised webpage** showing the chosen record in a printer-optimised design, without any navigation and with an activated printer-dialogue.

## 5 Privacy - Protection against abuse by spammers

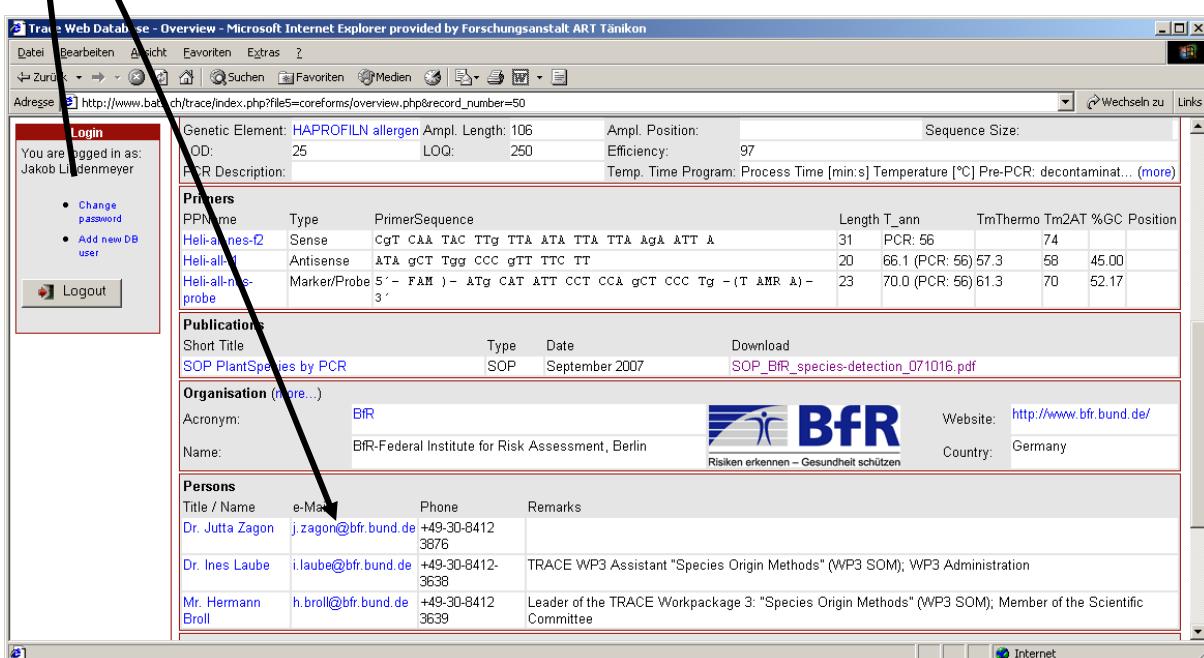
In the overview-records, the contact-table, the organisation-data-set and in the data-set of the persons, all the e-mail addresses of the TRACE-members are secured against possible indexing by spam-bots:

The "@"-sign has been replaced by the two letters " (at) " and the mailto-link has been removed (top figure). Spambots should have troubles, trying to catch these addresses for possible spamming. If the database-user logs into the WP3-database, the full e-mail-address with the mailto-link is displayed (figure at the bottom).



Title / Name	e-Mail	Phone	Remarks
Dr. Jutta Zagon	j.zagon (at) bfr.bund.de 3876	+49-30-8412	
Dr. Ines Laube	i.laube (at) bfr.bund.de 3638	+49-30-8412-	TRACE WP3 Assistant "Species Origin Methods" (WP3 SOM); WP3 Administration
Mr. Hermann Broll	h.broll (at) bfr.bund.de 3639	+49-30-8412	Leader of the TRACE Workpackage 3: "Species Origin Methods" (WP3 SOM); Member of the Scientific Committee

**Figure 5: e-mail addresses of the TRACE-members** without login (top figure) having the "@"-sign been replaced by the two letters " (at) " and the mailto-link has been removed. After login: the full e-mail-address with the mailto-link is displayed (bottom figure).



Title / Name	e-Mail	Phone	Remarks
Dr. Jutta Zagon	j.zagon@bfr.bund.de 3876	+49-30-8412	
Dr. Ines Laube	i.laube@bfr.bund.de 3638	+49-30-8412-	TRACE WP3 Assistant "Species Origin Methods" (WP3 SOM); WP3 Administration
Mr. Hermann Broll	h.broll@bfr.bund.de 3639	+49-30-8412	Leader of the TRACE Workpackage 3: "Species Origin Methods" (WP3 SOM); Member of the Scientific Committee

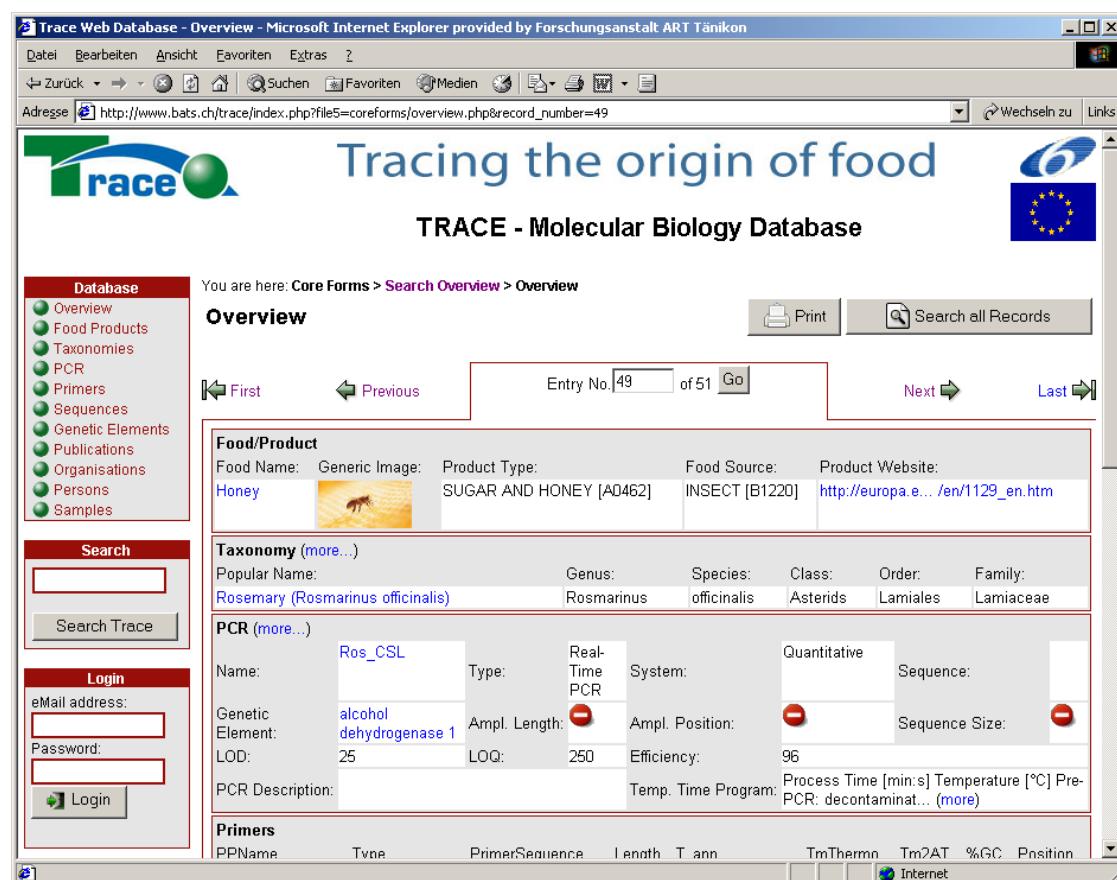
## 6 Accessibility

Except from the logos, all the rest of the design of the TRACE molecular biology database is done by using only text elements and style sheets, but without any pictures. This supports a slim and therefore fast design of the front-end of the database, which also supports many accessibility needs such as mobile devices.

## 7 Final critic

A negative point is the white background of the new design of the database front-end, because the background-colour white is already used for the fields of the inserted data. But white as background colour was set as default by the new design of the whole TRACE website, and the molecular biology database has to be compatible to the general TRACE website-design.

We tried to correct the disadvantages of the white background in the new design by implementing grey backgrounds in the functional and logical boxes. Like this, the white data-fields are highlighted from the grey background of its box.



The screenshot shows a Microsoft Internet Explorer window displaying the TRACE Molecular Biology Database. The title bar reads "Trace Web Database - Overview - Microsoft Internet Explorer provided by Forschungsanstalt ART Tänikon". The main content area is titled "Tracing the origin of food" and "TRACE - Molecular Biology Database". A sidebar on the left contains links for "Database" (Overview, Food Products, Taxonomies, PCR, Primers, Sequences, Genetic Elements, Publications, Organisations, Persons, Samples), "Search" (Search Trace), and "Login" (eMail address, Password, Login button). The main content area shows a search result for "Honey". The search results are presented in several logical boxes with different backgrounds:

- Food/Product:** Shows "Food Name: Generic Image: Product Type: Food Source: Product Website:". The "Food Name" field "Honey" and its image are highlighted in white against a grey background.
- Taxonomy (more...):** Shows "Popular Name: Rosmarinus officinalis" and "Genus: Rosmarinus Species: officinalis Class: Asterids Order: Lamiales Family: Lamiaceae". The "Popular Name" field is highlighted in white.
- PCR (more...):** Shows "Name: Ros\_CS1 Type: Real-Time PCR System: Quantitative Sequence:". The "Name" field "Ros\_CS1" is highlighted in white.
- Primers:** Shows columns for PPName, Type, PrimerSequence, Length, T\_m, TmThermo, Tm2AT, %GC, Position, and Internet. The first row's "PPName" column is highlighted in white.

**Figure 6: Grey backgrounds in the functional and logical boxes** highlight the white data-fields from the grey background of its box.

# User-questionnaire

For the TRACE Molecular Biology Database  
Version 0.4, 31.12.2007

Authors: Jakob Lindenmeyer, Tobias Krais

## 1 Time and type of the questionnaire

It is planned to distribute the user-questionnaire among the WP3-members in March 2008 1 month before the 4<sup>th</sup> TRACE annual conference. Like this, the results can be presented at the annual conference. The distribution will be done either by a web-form or by e-mail. The details will be discussed with the coordinator of TRACE work package 3.

## 2 Information about the database-user

### 2.1 Short version

1. Your TRACE-partner-number
2. Your name

### 2.2 Long version

1. Your First name
2. Your Family name
3. Name of your institution
4. Your TRACE-partner-number
5. Do you attend the 4<sup>th</sup> TRACE conference in Terremolinas?

## 3 Database usage

1. Did you already use the TRACE molecular biology database?
2. Why not?  
(No time | Not relevant for my work | I'll wait for the final version | No Internet)
3. How many times did you use the WP3-database?
4. When was the last time you used it?
5. For how long?
6. Did you have problems using the database?
7. Did you login into the confidential part for WP3-members?
8. Did you have problems during the login-procedure?
9. How do you rate the speed of the database: fast – OK – or too slow?
10. Your general feedback on the usage of the database:

## 4 Relevance of the data

1. Regarding your work: Which part of the WP3-database is the most interesting?
  - Overview
  - PCR
  - Primer
  - Taxonomy
  - Organisations

### 4.1 Importance of the data

1. Which attributes / data-fields of this part are most important for your work?
2. Which data are you missing?
3. Which data is not necessary?
4. Your general feedback on the current data in the database:

### 4.2 Confidentiality of the data

1. In your opinion: Are there too many data marked as confidential?
2. In your opinion: Which data should be confidential until the projects end?

## 5 Special database features and functionality

1. Which additional functionality would you need for your work with the WP3-database?  
e.g.
2. Do you want to print a single records you are interested in?
3. Do you want to print the whole database?
4. Do you want to print just all the records or also the structure of the database?
5. How do you like the new design of the database?
6. What do you think of the navigation? Too many menus or to little menus?
7. Which similar online-databases do you see as good examples for the WP3-database?