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| from: | German delegation |
| to: | Working Group on Information Exchange and Data Protection (DAPIX / DNA experts) |
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| Subject: | Implementation of Council Decisions 2008/615/JHA and 2008/616/JHA ("Prüm Decisions") - *Implementation guide - DNA Data Exchange* |

Delegations will find in annex an updated version of the draft implementation guide concerning DNA data exchange Prüm provisions based on knowledge and experience of and prepared by experts of the German Bundeskriminalamt (BKA). This draft implementation guide should be considered a living document subject to further modification in line with discussions about implementation issues within the DAPIX / DNA subgroup.

The draft implementation guide contains a number of recommendations from a technical and forensic point of view. It serves the purpose of guiding in detailed and concrete terms the IT implementation of the Prüm requirements. The main objective is to provide Member States with more insights into the implementation of software components and with an insider view of implementation details.

This version of the implementation guide takes account of comments made by DNA data exchange IT experts on the previous version. The changes made to the former version are set out in **bold** in order to improve the readability and follow-up discussion of the document.

DAPIX DNA experts are invited to comment the suggested recommendations in annex and exchange views on the content of the document for its further improvement at the meeting on 27 February 2013.

Bundeskriminalamt

IT05 Biometrics

# Implementation Guide – DNA Data Exchange
# Council Decision 2008/616/JHA

February 21, 2013

(Draft)


Bundeskriminalamt

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## Executive Summary

This Implementation Guide has been written especially from a technical and forensic point of view. As a supplement to Council Decision 2008/616/JHA, it explains and describes in more details and in concrete terms the requirements contained in the official documents. This guide tackles especially the issues having an impact on common communication and application interfaces. In regard to ever more Member States entering daily police operations on DNA data exchange, it proves advantageous to agree upon a common set of specifications and standards which reflect the needs of all Member States. The implementation of the specified items, objects and mechanisms in conformity to the commonly defined specifications and standards may be taken by each country itself.

The main objective of this supplementary document is to provide all Member States with more insights into the implementation of the software components. What is not very technically defined and/or described in the official legal documents has been explained and annotated in this guide. The Member States , especially those which intend to develop and maintain software components by themselves, could gain an insider view of the implementation details.

**During the further development of this living document, it is necessary always to keep the XML Schema file in accordance with the rules set by the "Prüm Decisions", e.g. including the new additional ESS loci. Moreover, construction of a suitable DNA test set, harmonisation of a viable test plan with all Member States, and further development of a binding software implementation and a migration plan at the EU level play an important rule in EU DNA data exchange.**

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# 1 BACKGROUND

## 1.1 Foreword

Since the integration of the Treaty of Prüm into the EU legal framework in June 2008, DNA data exchange in daily police operations has been regulated by Council Decision 2008/615/JHA and 2008/616/JHA respectively (referred to hereinafter as "Council Decisions", "Prüm Decisions" or "Decision"). The technical and forensic requirements are described in Chapter 1 of the Annex of Decision 2008/616/JHA. However, there are places in the official document, which need clearer descriptions and exacter specifications to avoid ambiguity in the implementations.

This implementation guide is aimed at providing Member States with tangible benefits in their own implementations of the software components for DNA data exchange, and can be thus served as a supplement to the related parts of the Council Decisions.

## 1.2 Introduction

The main objective of this DNA Implementation Guide is to give more explanation and more accurate description to the Chapter 1 of the Annex in conformity with the content of the official document. This document tackles both issues about IT and forensic matters which are not exactly defined, not clearly stated and still left open to interpretations. So far as it is possible, best viable options have been suggested for choice by Member States.

## 1.3 Scope

This document has been written especially for the Chapter 1 of the Annex of Council Decision 2008/616/JHA, Exchange of DNA Data, mainly covering the following aspects:

- Interface Control Document
- XML Schema
- Inclusion and matching rules
- Application architecture
- Network infrastructure
- Testing methodology
- Further steps

## 1.4 Normative References

- Council Decision 2008/615/JHA
- Council Decision 2008/616/JHA
- W3C XML Schema Part 1: Structures Second Edition (28 October 2004)
- W3C Namespaces in XML 1.0 (Third Edition), 8 December 2009

# 2 CONSIDERATION ON FORENSIC ISSUES

The content of the Chapter 1.1 and 1.2 of the Annex of Council Decision 2008/616/JHA is explained and annotated in this part from a detailed technical point of view, especially of the implementation aspects. These issues, which have not been explicitly specified in Chapter 1.1 and 1.2, are treated in more detail by providing possible options to solve the still open issues.

## 2.1 General Description of the Properties of DNA profiles

- Range of ESS loci

The table in the Chapter 1.1 contains 24 loci including the 7 ESS ones. Upon the new decision made by the ENFSI group, 5 more new loci (D1S1656, D2S441, D10S1248, D12S391 and D22S1045) have been adopted as more promising candidates for DNA identification and verification procedures. The range of ESS loci for identification and verification purposes has to be expanded to include these 5 new loci according to the last sentence of the 1st paragraph of the "Inclusion Rules". From a technical point of view, the following measures in the implementation note should be accomplished.

Implementation note:

- o Customize the XML-based communication components deployed at the sites of Member States
- o Modify EU/Prüm indexed DNA data structure of each Member State for DNA data exchange
- o Modify national DNA data pool in conformity with respective national policies

## 2.2 Inclusion Rules

The inclusion rules for reference profiles are differentiated from those for stain profiles. There should be at least six full designated of the 12 ESS loci (Council Resolution of 30 November 2009 on the exchange of DNA analysis results 2009/C 296/01) for a reference profile to be qualified for the inclusion. However, stain profiles have to contain at least six full designated loci and may contain any additional loci or blank depending on their availability. The following issues should be tackled and clarified for the specified inclusion rules of the Decision:

- Full designated loci and rare valued locus

  The footnote on page 20 of the annex to Decision 2008/616/JHA states that "Full designated" means the handling of rare allele values is included. Actually, a locus fully assigned with numerical values and/or a wild card (*) will be considered as full designated. Practically in the forensic labs in the Member States, the treatment of a rare valued locus in its presentation form in one country could be differentiated from the others. As having described in this paragraph relating wild cards, the following issues should be considered:

- An array of letters is currently in use in Member States with the possible indications of a rare valued locus or a locus with no value at all or something else. According to the rule defined in the Decision, any of these letters should be substituted by a wild card (*). The ambiguity of this rule leads to a mixture of different kinds of substituted information in lieu of real allele values of a locus. The match engine can not be therefore in the situation to differentiate “rare value” case from “no information” and/or other cases.
- The cases for a rare valued locus are not clearly defined in the Decision. There is no mention of the relationship of a wildcard substitution of the numerical values “0”, “1” or “99” and tri allelic values to the rare value treatment. A complete list of rare value cases should be included in a revised Decision **later.**

Implementation note

- Do not substitute any “blank” and/or “no value available” spaces with a wild card
- Only substitute a rare valued locus with a wild card**.** The substitute of rare values by a wildcard has already been used in police daily operations among all connected Member States. The Member States, which have not yet participated in daily operations, should pay attention to this technical note so that an automated identification procedure may be carried out more effectively in terms of the least inclusion rule defined in the Decision (see footnote on page 20 as mentioned above).

- Order of allele values of a locus

  This issue is not regulated in the Decision. In practice, a lower valued allele should be put at the first position and the higher one at the second position.

  Implementation note:
  - Match Engine should be implemented, so that the both positions of the numerical values will be checked, i.e. to allow permutation check.
- Delimiter of micro variant allele values

  It is not clearly stated for the delimiter in the Decision. It should use a dot instead of a comma for this case. The definition of a delimiter has the impact on the structural format of a data pool.
- Wild cards

  In order to differentiate a locus with rare values from those with other cases, a wild card (*) should be used only to substitute a rare valued allele. More than one wild card can be used to store a DNA profile in indexed DNA databases. The Decision has not specified this issue very clearly.

Implementation note:

- Insert a common note as attachment to the Decision stating that a wild card (*) shall be used only for the substitution of a rare valued allele.
- On the understanding that a wildcard will be used only for substitution of rare allele values, there **exist** the following **cases** of "full designated loci" as specified in the Decision**:**
    - 5 full numerically valued loci plus a wildcard indicating rare allele value ("5+1" inclusion rule)
    - 6 full numerically valued loci without wildcards ("6" inclusion rule)
    - 6 full numerically valued loci plus a wildcard or more ("6+1" inclusion rule)
    - more than 6 full numerically valued loci without wildcards ("7up" inclusion rule)
    - more than 6 full numerically valued loci plus a wildcard or more ("7up+1" inclusion rule)

  All these cases fulfill the inclusion rules defined by the Decision. From a biological viewpoint, a wildcard representing a numerical rare allele value, which is not comparable to each other among different DNA databases, makes a 6-loci **profile** satisfying the above "5+1" inclusion rule more significant than any regular numerical value. The least inclusion rule ("5+1") could lead further to the positive result of an identification procedure.

- Any other substitution rules for a blank, "unknown", "no value available" or "drop outs" provide no functional add-on values for an automated identification procedure. These would-be substitutes will be ignored by match engines. Therefore there is no need to describe this issue in detail for the time being. (…)

- Blank spaces

  This issue is not regulated in the current version of the Decision. At the current stage the following implementation options could be considered.

  Implementation notes:

  - Do not store any blanks in DNA indexed databases

- Tri-allelic values

  A tri-allelic valued locus, especially of a reference profile, mostly indicates a case of rare value. The tri-allelic loci of a stain profile may contradict this assertion. Upon the Decision, the first allele will be accepted and other two alleles shall be converted to a wild card (*) for searches. Applications at national sites should do this conversion before a tri-allelic locus will be included into the indexed DNA database.

- Homozygosis

  In the case of homozygosis a blank allele space has to be substituted by the same value of the other allele of the locus. In consideration of the CODIS system, a locus, e.g., with a value pair of “a”,“ “ shall be transformed into the value pair of “a”,”a” before being put into the DNA indexed database for search and comparison by other Member States.

  Implementation note:

  Match engines shall only consider the value pair of the form “a”,”a” an occurrence of the homozygosis.
- No mixed profiles are allowed to be included in indexed DNA databases

## 2.3 Matching Rules

The matching rules are described as follows (see 1st paragraph on page 21 of the Annex to Decision 2008/616/JHA):

1. The loci to be matched and/or compared should be contained in both of DNA profiles
2. A hit is defined as one that at least six full designated loci exclusive of amelogenin match between both DNA profiles.
3. A near match is only accepted, if there are at least six full designated matched loci in both DNA profiles (see the foot note on “full designated” on page 20 as mentioned above)
4. A near match is defined as one, when the value of only one of all compared alleles is different in both DNA profiles.
5. The first wildcard encountered is considered a difference. The other wild card/s should be considered only in the case that the corresponding loci containing the further wildcard/s are not present in the profile to be compared
6. A near match can come from three categories: matches involving wildcards, micro-variants and mismatches
7. There are four hit quality levels defined (see §4.2.2.3 Interface Control Document on the page 25 of the Annex to satisfy the rules as defined above:
   - Hit Quality 1 (exact match)
     a match of at least 6 full designated loci with all the same numerical allele values compared in both DNA profiles
   - Hit Quality 2 (near match/wild card)
     a match including a wild card for the substitution of a rare allele value which is allowed in terms of “six full designated loci” according to the Decision (see footnote on page 20 as mentioned above)
   - Hit Quality 3 (near match/micro variant)
     a match accepting one difference in the case of micro variant which is allowed in addition to the six full designated loci

- Hit Quality 4 (near match/mismatch)
  a match with other kind of a difference which is allowed in addition to the six full designated loci

The Matching Rules could be described by the following axioms:

- Axiom 1
  A full match (Q1) is given when at least 6 numerical loci are found equal and there is neither a near match nor any other loci that do not match.
- Axiom 2
  A near match (Q2, Q3 and Q4) allows only one difference in comparison
- Axiom 3
  A “no hit” message should be given out by a match engine, if there exist more than one difference

## 2.4 Using anonymous DNA test set over test environments

In order to meet the requirement of the EU legal constraints, test environments and anonymous DNA profiles should be used for qualitative and quantitative tests over the deployed communication network sTESTA. From the operational point of view, the separation of a test environment from the operational one can mitigate the potential negative influences on daily police operations caused by unpredictable testing behaviors. If a physical separated testing environment could not be established due to technical, financial or organizational reasons, it proves advantageous to configure a logical or virtual separation of test and production data.

A test set of pseudo DNA profiles consists of three major components: 1) a data pool containing a substantial amount of pseudo DNA profiles covering most possible cases for correctness check and error verification, 2) a pool of requests with properly selected DNA profiles to be sent to other EU countries for matching; 3) a pool of SHOULD-BE answers to the corresponding requests. This **set of** pseudo DNA profiles should cover possible correct and incorrect cases to verify the conformity to the Decision.

Implementation note:

- Set up a physically separated testing environment if possible, or
- Separate test and productive data logically and virtually
- Install the DAPIX test set of pseudo DNA profiles at both sides of the involved testing parties
- Use also anonymous DNA stain profiles in a mass comparison **tests**

## 2.5 Reporting Rules

All four hit quality categories and "not hit" will be generated by the systems and forwarded back to the requesting countries in an automated procedure. The follow-up requests concerning the details of hits, especially person related information, shall be conducted in accordance with the Article 5 (and 10 for dactyloscopic data) of Council Decision 2008/615/JHA.

# 3 FUNCTIONAL ANALYSIS

The following measures in the implementation note should be fulfilled in accordance with section 3.1 of the Annex of the Council Decision 2008/616/JHA.

Implementation note:

- In mint condition, the response to an incoming request will be generated by the match engine within a few seconds, then processed and forwarded to the requesting party by the communication center through the sTESTA.
- Due to the underlying transport protocol SMTP via different email server nodes between two parties involved in the communication, there is no way to guarantee a certain amount of delivery time of the response to reach the requesting party.

Each MS shall implement a monitoring functionality to recognize unresolved search requests

# 4 DNA INTERFACE CONTROL DOCUMENT (ICD)

Section 4 of the Annex contains a general description of data items and structures to be used for implementation by XML mechanism. The items contained in the tables of the ICD are described in an informal language. The formal definitions of XML elements are included in the Appendices of this implementation guide.

Currently, all countries use the XML Schema Version 1.0 in accordance with the Treaty of Prüm but this needs an update with regard to the Prüm Decisions. Before any final agreement about this ICD is reached, it is necessary **to keep the XML Schema Version in conformity with the decisions such as including the five new ESS loci and to develop a binding software implementation and a migration plan at the EU level. Germany has released its Communication Center (DE-CC V.1.1) in the 3Q12 with the new features of interoperability to interact with foreign systems, which have been developed in conformity with the EU Prüm Decision, e.g. CODIS 7 and backward compatibility with older version of XML Schema V.1.0 of the German DE-CC. These new features of the DE-CC have successfully been verified in the test rounds with many EU countries in daily operations.**

## 4.1 General Guidance and Standards

On account of EU legal constraints on police operations, a set of ICD (Interface Control Document) items with their SHOULD-BE characteristics have been adopted for the implementation of DNA data exchange among Member States. The procedure is based on a set of identification characteristics of the non-coding part of an analyzed human DNA sample, i.e. the particular molecular structure at the various DNA locations (loci). The established technology STRs (Short Tandem Repeats) has been deployed in analyzing human DNA samples. After a few modifications to the standard originally set up within the framework of the Treaty of Prüm, these items contained in the ICD have been widely used by all Member States.

## 4.2 XML structure and principles

For the communication among the parties involved, there is one root XML element named "PRUEMDNA" defined in the XML Schema file and visibly contained in a XML instance document for requests and responses. For the purposes of technical processes, e.g. databases, in the background, other necessary items and fields are implemented invisibly to end users in the outside world.

All tables in the section 4.2 of the Annex of Council Decision 2008/616/JHA containing the items implemented are annotated in this section with the corresponding section numbers and the correction of typographical errors. All annotated tables listed below take a same table structure.

**Table 1: Section 4.2.1 "XML Schema Element PRUEMDNA"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| Header | **PRUEM_header** | Complex | 1 | Containing info about a general description of DNA data exchange |
| Datas | **PRUEM_datas** | Complex | 1-500 | Containing DNA samples for exchange as many as to 500 profiles |

**Table 2: Section 4.2.2.1 "Complex Type PRUEM_header"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| Type | PRUEM_header_type | Simple | 1 | M := Multiple Profiles upon Article 4<br>S := Single Profile upon Article 3<br>(Included in the XSD V.1.0, but not yet implemented in V.1.0) |
| Direction | PRUEM_header_dir | Simple | 1 | Indicating the message flow: request or answer |
| Ref | string | Primitive build-in | 1 | Referencing XML instance document |
| generator | string | Primitive build-in | 1 | Indicating generator of XML instance document |
| schema_version | string | Primitive build-in | 1 | Containing version number of XML Schema |
| requesting | **PRUEM_header_info** | Complex | 1 | Containing info of a requesting country |
| requested | **PRUEM_header_info** | Complex | 1 | Containing info of a requested or country |

**Table 3: Section 4.2.2.2 "Simple type PRUEM_header_dir"**

| Value | Description |
|---|---|
| R | R stands for Requests |
| A | A stands for Answer |

**Table 4: Section 4.2.2.3 "Complex type PRUEM_header_info"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| source_isocode | string | Primitive build-in | 1 | ISO 3166-2 code of the requesting member state |
| destination_isocode | string | Primitive build-in | 1 | ISO 3166-2 code of the requested member state |
| request_id | string | Primitive build-in | 1 | Unique identifier of a request |
| Date | date | Primitive build-in | 1 | Date of message creation |
| Time | time | Primitive build-in | 1 | Time of message creation |

**Table 5: Section 4.2.3.1 "Complex type PRUEM_datas"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| Reqtype | PRUEM_request_type | Simple | N.A. | Denoting the type of requests (Article 3 or 4); It has not been implemented in the XML Schema version 1.0, but will be done in the version 1.1 |
| Date | date | Primitive build-in | 0-1 | Indicating the date of data file to be stored |
| Type | PRUEM_data_type | Simple | 0-1 | DNA profile category: stain or person (reference) profiles |
| Result | PRUEM_data_result | Simple | 1 | Matching result category |
| Agency | string | Primitive build-in | 1 | Agency name in the requesting and requested country |
| profile_ident | string | Primitive build-in | 1 | Unique profile ID in the EU member state |
| Message | string | Primitive build-in | 0-1 | Error messages in the case of the returned value "E" of result |
| Profile | **IPSG_DNA_profile** | Complex | 0-1 | The data of profile will be contained in a response XML instance document if "direction" = "A" and "result" = "H" |
| match_id | string | Primitive build-in | 0-1 | Profile ID of the requesting profile in the case of a Hit |
| Quality | PRUEM_hitquality_type | Simple | 0-1 | Indicating 4 Hit quality levels |
| Hitcount | integer | Derived build-in | 0-1 | Number of counts of matched alleles |
| Rescount | integer | Derived build-in | N.A. | Number of counts of matched profiles in the answer.<br>If "direction" = R(equest) then "rescount" is empty<br>If "quality" = "0" then "rescount" is empty<br>(It has not been implemented in the XML Schema version 1.0, but will be done in the version 1.1) |

**Table 6: Section 4.2.3.2 "Simple type PRUEM_request_type"**

| Value | Description |
|---|---|
| 3 | Requests pursuant to Article 3 of EU Council Decision 2008/615/JHA |
| 4 | Requests pursuant to Article 4 of EU Council Decision 2008/615/JHA |

Note:

This simple type "PRUEM_request_type" has not yet been implemented in the XML Schema version 1.0. However, this feature is included in the XML Schema version 1.1 further developed by Germany. The tests of the version 1.1.7 have successfully been carried out between Austria and Germany. It is envisaged that version 1.1 will be released for the Member States carrying out DNA data exchange in police daily operations after the finalization of the tests among all Member States connected over the productive environments.

**Table 7: Section 4.2.3.3 "Simple type PRUEM_hitquality_type"**

| Value | Description |
|---|---|
| 0 | Referring original requesting profile:<br>If "No Hit" then original requesting profile to be sent back only |
| 1 | Exact match:<br>All available (numerical) allele values without wildcards in the compared profiles are identical. |
| 2 | Near Match (wildcard):<br>Only one value of all compared alleles containing wildcards is different in the two DNA profiles. |
| 3 | Near Match (microvariant):<br>Only one value of all compared alleles containing deviation (mirovariant) is different in the two profiles. |
| 4 | Near Match (mismatch):<br>Only one value of all compared alleles is different in the two profiles in addition to six full designated matched loci. |

Note:

A near match is only accepted if there are at least six full designated matched loci in the two compared DNA profiles.

**Table 8: Section 4.2.3.4 "Simple type PRUEM_data_tape"**

| Value | Description |
|---|---|
| P | Person profile |
| S | Stain profile |

**Table 9: Section 4.2.3.5 "Simple type PRUEM_data_result"**

| Value | Description |
|---|---|
| U | Undefined, if direction = R(equest) |
| H | Hit |
| N | No Hit |
| E | Error |

Note:

- Error codes have been specified as follows:
- Format error of a locus
- Not enough number of ESS loci
- Not enough number of loci
- Invalid locus ordering
- Invalid locus value
- (can be extended)

A detailed error code catalogue has not yet been implemented in the XML Schema version 1.0, but will be implemented in the **further versions of XML Schema**.

**Table 10: Section 4.2.3.6 "Complex type IPSG_DNA_profile"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| ess_issol | IPSG_DNA_ISSOL | Complex | 0-1 | group of loci corresponding to the ESS |
| additional_loci | IPSG_DNA_additional_loci | Complex | 0-1 | other additional loci |
| Marker | string | Primitive build-in | 0-1 | (Genetic) marker |
| profile_id | string | Primitive build-in | 0-1 | unique identifier of a DNA profile |

Note:

- From historical reasons, the term "issol" has been used as field names in the specification. In the future versions of the specification this term will be deleted.
- The term of "IPSG" (Interpol Secretariat General) will be substituted by the "ESS" (European Standard Set of Loci) in the future version of the specification and be implemented in the XML Schema files

**Table 11: Section 4.2.3.7 "Complex type IPSG_DNA_ISSOL"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| Vwa | **IPSG_DNA_locus** | Complex | 0-1 | Locus vwa |
| th01 | **IPSG_DNA_locus** | Complex | 0-1 | Locus th01 |
| d21s11 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d21s11 |
| Fga | **IPSG_DNA_locus** | Complex | 0-1 | Locus fga |
| d8s1179 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d8s1179 |
| d3s1358 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d3s1358 |
| d18s51 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d18s51 |
| Amelogenin | **IPSG_DNA_locus** | Complex | 0-1 | Amelogenin |

Note: see note of the Table 10

Table 12: Section 4.2.3.8: complex type of the new ESS loci

Note: Implementation XML Name Tag must be harmonised in DAPIX.

| | | | | |
|---|---|---|---|---|
| d1S1656 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d1S1656 |
| d2S441 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d2S441 |
| d10S1248 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d10S1248 |
| d12S391 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d12S391 |
| d22S1045 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d22S1045 |

**Table 13: Section 4.2.3.8 "Complex type IPSG_DNA_additional_loci"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| Tpox | **IPSG_DNA_locus** | Complex | 0-1 | Locus tpox |
| csf1po | **IPSG_DNA_locus** | Complex | 0-1 | Locus csf1po |
| d13s317 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d13s317 |
| d7s820 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d7s820 |
| d5s818 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d5s818 |
| d16s539 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d16s539 |
| d2s1338 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d2s1338 |
| d19s433 | **IPSG_DNA_locus** | Complex | 0-1 | Locus d19s433 |
| penta_d | **IPSG_DNA_locus** | Complex | 0-1 | Locus penta_d |
| penta_e | **IPSG_DNA_locus** | Complex | 0-1 | Locus penta_e |
| Fes | **IPSG_DNA_locus** | Complex | 0-1 | Locus fes |
| f13a1 | **IPSG_DNA_locus** | Complex | 0-1 | Locus f13a1 |
| f13b | **IPSG_DNA_locus** | Complex | 0-1 | Locus f13b |
| se33 | **IPSG_DNA_locus** | Complex | 0-1 | Locus se33 |
| cd4 | **IPSG_DNA_locus** | Complex | 0-1 | Locus cd4 |
| Gaba | **IPSG_DNA_locus** | Complex | 0-1 | Locus gaba |

Note: see note of the Table 10

**Table 14: Section 4.2.3.9 "Complex type IPSG_DNA_locus"**

| Fields | Type Name | Type Category | Occ | Description |
|---|---|---|---|---|
| low_allele | string | Primitive build-in | 1 | Allele with smaller value |
| high_allele | string | Primitive build-in | 1 | Allele with larger value |

## 4.3 XML Message between Member States

### 4.3.1 Request Message

The following message describes the structure of a request for the DNA Data Exchange among Member States.

**Table 15: Logical structure of a request message**

| Item | Occ. | Item Type | Remarks |
|---|---|---|---|
| PRUEMDNA | 1 | XML element | root element |
| *Header* | | | logical structure indicator |
| Header | 1 | PRUEM_header (XML Complex Type) | See Table 2 |
| *Body* | | | logical structure indicator |
| *Request* | | | logical structure indicator |
| $Datas_1$ | 1-500 | PRUEM_datas (XML Complex Type) | See Table 5 |
| …….. | | | |
| $Datas_N$ | | | |

### 4.3.2 Response Message

The following message describes the structure of a response (answer) for the DNA Data Exchange among Member States.

**Table 16: Logical structure of a response message**

| Item | Occ. | Item Type | Remarks/Example |
|---|---|---|---|
| PRUEMDNA | 1 | XML element | root element |
| *Header* | | | logical structure indicator |
| Header | 1 | PRUEM_header (XML Complex Type) | See table 2 |
| type | 1 | PRUEM_hearder_type | “M” |
| direction | 1 | PRUEM_header_dir | “A” |
| ref | 1 | string | “PRUEM_DNA_Response.xml” |
| generator | 1 | string | “PRUEM DNA Communication Center” |
| schema_version | 1 | string | “1.0” |
| requesting | 1 | PRUEM_header_info | See table 4 |
| source_isocode | 1 | string | “AT” |
| destination_isocode | 1 | string | “DE” |
| request_id | 1 | string | “1281431941845” |
| date | 1 | date | “2010-08-10” |
| time | 1 | time | “22:10:20” |
| requested | 1 | PRUEM_header_info | See table 4 |
| source_isocode | 1 | string | “DE” |
| destination_isocode | 1 | string | “AT” |
| request_id | 1 | string | “1281431941845” |
| date | 1 | date | “2010-08-10” |
| time | 1 | time | “22:10:25” |
| *Body* | | | logical structure indicator |
| *Answer* | | | logical structure indicator |
| datas | 1-500 | PRUEM_datas | See table 5 |
| type | 1 | PRUEM_data_type | “S” |
| result | 1 | PRUEM_data_result | “H” |
| agency | 1 | string | “BKA ZD22” |
| profile_ident | 1 | string | “K012345678900” |
| Match_id | 1 | string | “30000000_1/1” |
| quality | 1 | PRUEM_hitquality_type | “1” |
| hitcount | 1 | integer | “6” |
| profile | 1 | IPSG_DNA_profile | See table 10 (matched profile sent back) |
| datas | | | |
| type | 1 | PRUEM_data_type | “S” |
| result | 1 | PRUEM_data_result | “N” |
| agency | 1 | string | “BK II.6.1.3” |
| profile_ident | 1 | string | “30000000_3/1 |
| quality | 1 | PRUEM_hitquality_type | “0” |
| hitcount | 1 | integer | “0” |
| profile | 1 | IPSG_DNA_profile | See table 10 (original profile sent back) |
| datas | | | |
| …… | | | |

## 4.4 Backward compatibility and interoperability of XML Schemas

Under the regulations of the Treaty of Prüm, the communication software components using the XML Schema version 1.0 have been deployed in almost all Member States in the production environments. During the progress of the DNA data exchange in the context of the Council Decisions, a few countries have developed and improved the match engine and communication software components by their own technical forces. Three kinds of communication software components will be deployed in the near future over the production environments:

- Communication Center developed by Germany
- Communication software components developed by other Member States **themselves**
- Message Center integrated in the CODIS 7 to be provided by FBI/UNISYS

In order to keep pace with the changing IT landscape and make different kinds of communication software components to be able to talk with each other, the backward compatibility and interoperability of **the communication software play a vital role in the DNA data exchange**. One night switch to a single new version of communication interface at the sites of all productive Member States may be theoretically appropriate for a smooth and seamless transit, but in practice infeasible from the organisational point of view. **A complex migration scenario of a diversified IT landscape at EU level may be facilitated by a communication software with components having the features of interoperability and backward compatibility.**

Implementation note:

- Description and specification in this guide can be served as guidelines on the implementation of interoperable communication components in Member States by themselves.
- Existing communication components of different sources should keep backward compatibility of the new version with the old one and the interoperability with those deployed by other countries.
- The mechanism of XSLT (XSL Transformations) is considered one of the state-of-the-art technologies to implement the requirements mentioned above in this section.

## 4.5 DNA XML Namespaces

Since the implementation according to the Treaty of Prüm, the generic W3C XML Namespace has been adopted in the communication interfaces. There are no other notions of XML Namespace having been created and used in the context of EU **Prüm** DNA data exchange yet. Due to the diversification of the software development domains and involvement of multiple countries further to develop communication interfaces, the items and objects defined in a certain application domain have to be effectively differentiated from the other items and objects with same names.

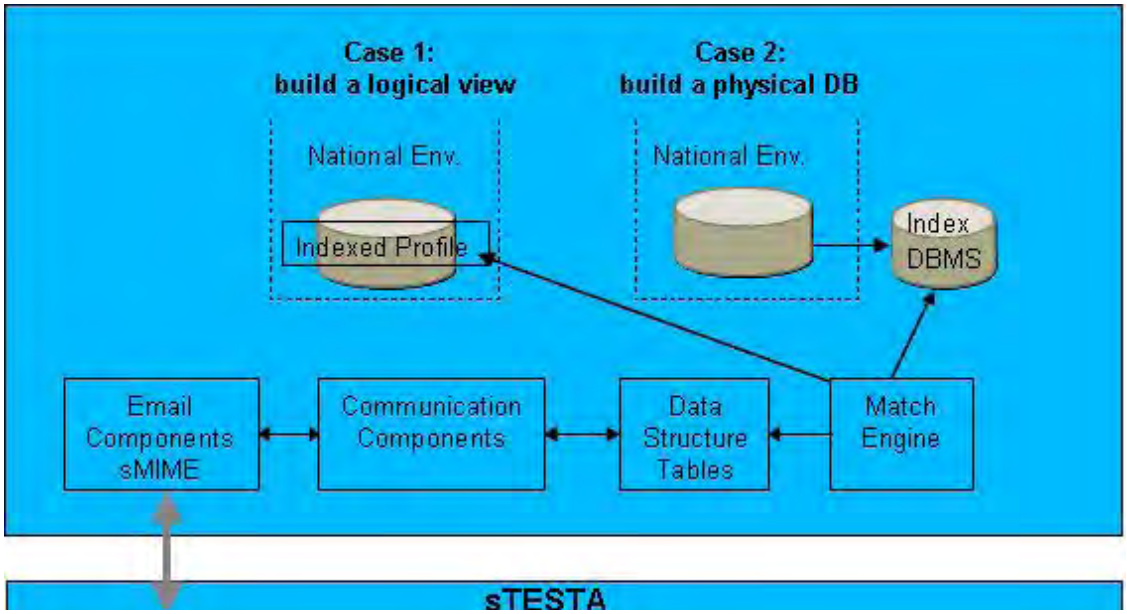
It is predicted the construction and using of XML Namespace in new versions of communication interface would become ever more important and significant.

# 5 APPLICATION AND COMMUNICATION ARCHITECTURE

## 5.1 Description of the General Topology

The system of EU DNA Data Exchange has been designed decentralized, that means there are no substantial functional components realized and deployed in a central site. All databases, applications and email components, with the exception of **an EU** central email relay server, are located at the local sites of respective Member States. The requesting country will get answers/responses from the requested country in an automated procedure within a defined time frame. From experience in police daily operations this time frame varies from seconds to at most 15 minutes **as defined in the Prüm Decision.**

**Figure 1: General Topology of Application and Communication Architecture**



## 5.2 Security Standards and Data Protection

The design of the security architecture in three levels fulfils the legal and data protection requirements.

At the data level a HIT notification does not contain any personal information. The further investigation after a HIT notification will be carried out merely by means of an identification number with a view to exchanging more detailed information with the parties involved by specially authorized officers.

The encryption protocol sMIME is deployed to process email messages embodying requests and answers in XML format. By using this technology, the integrity of data coming across the country boundaries has been guaranteed.

All users of the Members States are connected through the logically closed EU-wide sTESTA network, where there is no trivial and direct connection to the Internet. The active access devices to the sTESTA at the national sites do use standard encryption mechanisms at the layer 2 and/or 3 in conformity with the 7-layered ISO/OSI Model.

## 5.3 Implementation Considerations

Member States have worked out a common set of definitions, standards and specifications, which reflects requirements of IT, forensic and police functional areas as contained in Council Decisions 2008/615/JHA and 2008/616/JHA. So far as it is possible, the open source software packages have been used in order to maintain the interoperability and at the same time to reduce the costs of the products.

The explanation and more detailed description in this implementation guide could support Member States in developing the product components by themselves.

### 5.3.1 Match Engine

During the development period of the software components, two kinds of match engines have been implemented for common use of DNA Data Exchange in compliance with the matching rules defined by the Council Decisions (see section 2.3 of this document). Microsoft SQL and Oracle based match engines work together by providing HIT and/or No-HIT results over the sTESTA network to the parties involved. Up to now there are no other kinds of match engines to be involved in the processing. It is predicted that some other kinds of match engines would be brought into play in the near future. If new kinds of match engines would be developed by Member States, the rules described in the section 2.3 of this document should be taken into account.

Functional Description of the Match Engine:

```
Begin
    allocate sufficient table space in the deployed DBMS
      (It depends upon the amount of requests of DNA profiles; As a rule of thumb, 100 MB
      is generally appropriate.)
    check periodically incoming requests in an interface table by a DB polling mechanism;
    ifthere are some incoming requests
    then
      {
      fetch them sequentially;
      parallelize the processing, if possible (German Oracle Match Engine does);
      compare them with entries in the indexed DB upon the matching rules set in
      the section 2.3;
          write results with different processing flags into another interface table;
          }
    else
      wait for another polling period;
End
```

Two interface tables are used for the processing by the match engine. One table serves as a place to store the values of DNA loci to be searched by other parties; the other holds administrative information such as profile identification, profile category, etc. It is not forcibly to put information into two interface tables. A single interface table holding all necessary information could also be used for this purpose.

Typically, a match engine should be implemented so that its behavior can be controlled by configuration parameters. For instance, there are a bunch of global control parameters of a typical match engine, which can be adjusted to suit different purposes of the operations. All the global control parameters of a match engine can be grouped in two categories: one consisting of parameters for dealing with the national specialties such as agency name, own ISO country code, setting of rare value, email address, etc and another category comprising parameters for handling information relating communication with other Member States countries such as status of the Member States (active in the test/production or not, what kind of DNA profiles to be sent, holding back or not of responses upon Art. 3, etc.).

### 5.3.2 Communication Center

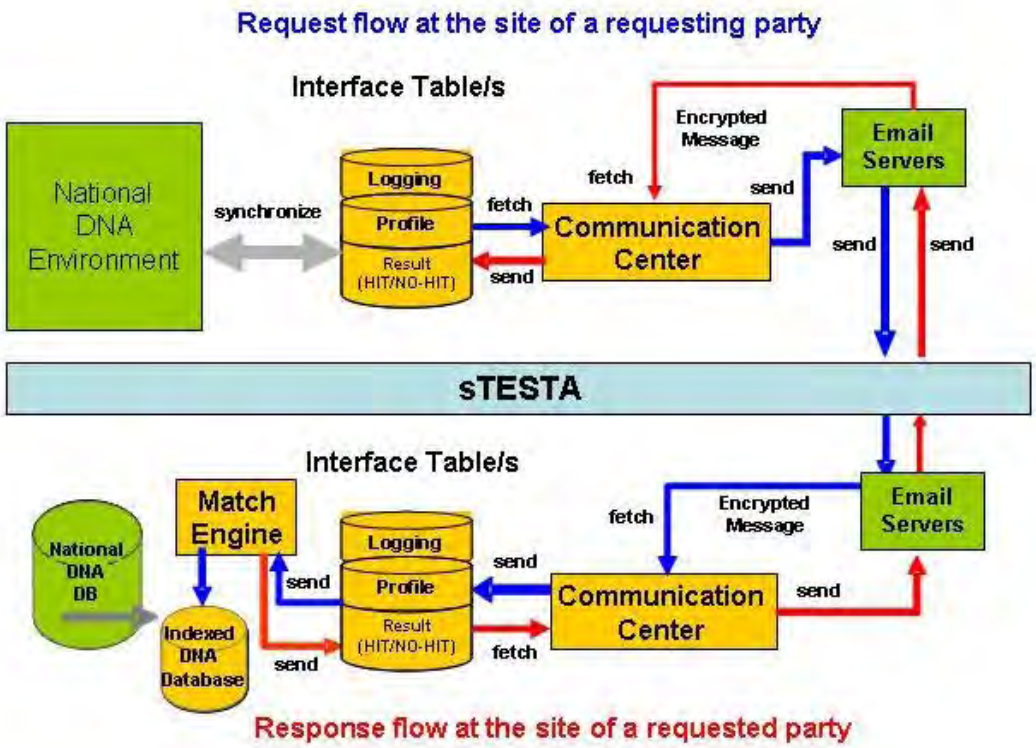
The DNA Communication Center provides the interface for the exchange of DNA requests and results among Member States to generate and handling XML based messages. Before messages with DNA requests in XML format will be sent to other parties, Communication Center encrypts messages via sMIME. This piece of software has to be installed at the testing and production sites of each EU Member State.

DNA profile data in requests and responses are exchanged among participating countries in XML format wrapped in an encrypted message. The data are sent as file attachments. The following requirements must be met for the communication:

- SMTP and POP3 email components must be set up in the involved member state site
- The corresponding email addresses for tests and production have to be established upon the specification contained in the paragraph 5.7.4 (Network Address Assignment) of the Chapter 1 of the Annex of Council Decision 2008/616/JHA. With regard to the change of sTESTA domain, this set of parameters should be kept up-to-date.
- The subject field of a message containing DNA request/s should be filled out with the string “PRUEM DNA Request”
- The request file attached must have the name “PRUEM_DNA_Request.xml”
- The subject field of a message containing DNA answer/response should be filled out with the string “PRUEM DNA Response”
- The response file attached must have the name “PRUEM_DNA_Response.xml”
- XML instance documents to be exchanged must comply with the EU DNA Data Exchange XML Schema definition in the file “PRUEMDNA.xsd”

The workflow of the Communication Center is shown in the following diagram:

**Figure 2: Workflow of the Communication Center**




The German Communication Center has been implemented as a set of Java applications. It can run in any standard J2EE Servlet container. The Servlets manage four individual independent threads, which maintain incoming and outgoing messages with Member States. The servlet containers and threads implemented in the German Communication Center can be started, stopped and status-checked by the routines at the level of the operating system. With the help of several property files the behavior of the Communication Center can be configured. JDBC is used to establish the connection to and the interaction with databases. However any kind of other *x*DBC, e.g. ODBC, can be deployed to fulfill these functions. Error messages will be written into a log file.

The four property files contain the configurable information as shown in the following tables:

**Table 17: Configuring the thread "RequestInThread"**

| Name | Description |
|---|---|
| Pop3Server | IP address or host name of the POP3 server from which incoming DNA requests can be collected |
| Pop3User | User/mailbox for incoming DNA requests |
| Pop3Passwd | Password for the mailbox |
| Interval | Time interval in milliseconds how often the mailbox should be searched for incoming requests |
| HomeIsoCode | ISO code of the own Member State |

**Table 18: Configuring the thread "RequestOutThread"**

| Name | Description |
|---|---|
| SMTPServer | IP address or host name of the local SMTP mail server through which requests are sent |
| SMTPUser | User name for the authentication on the SMTP server. If no authentication is required, " " can be entered. |
| SMTPPasswd | Password for the authentication on the SMTP server. If no authentication is required, " " can be entered. |
| Interval | Time interval in milliseconds how often checks should be made in the table PROFILE as to whether there are any new search requests. |
| HomeIsoCode | ISO code of the own Member State |
| HomeMailAddress | Sender e-mail address of the respective Member State |

**Table 19: Configuring the thread "ResponseInThread"**

| Name | Description |
|---|---|
| Pop3Server | IP address or host name of the POP3 server from which incoming DNA responses can be collected |
| Pop3User | User/mailbox for incoming DNA responses |
| Pop3Passwd | Password for the mailbox |
| Interval | Time interval in milliseconds how often the mailbox should be searched for incoming responses |
| HomeIsoCode | ISO code of the own Member State |

**Table 20: Configuring the thread "ResponseOutThread"**

| Name | Description |
|---|---|
| SMTPServer | IP address or host name of the local SMTP mail server through which responses are sent |
| SMTPUser | User name for the authentication on the SMTP server. If no authentication is required, " " can be entered. |
| SMTPPasswd | Password for the authentication on the SMTP server. If no authentication is required, " " can be entered. |
| Interval | Time interval in milliseconds how often checks should be made in the table RESULT if there are any new results. |
| HomeIsoCode | ISO code of the own Member State |
| HomeMailAddress | Sender e-mail address of the respective Member State |

An open source based key management package has been embedded in the communication among Member States. Because of the restrictions of the Java-SDK imposed by the US export regulations, the asymmetrical encryption mechanism with a key length of 64 bit is used for encryption and decryption of messages.

In the following table, the main functions of the JavaMail-Crypto-API have been summarized.

**Table 21: Main Functions of JavaMail Crypto API**

| **Name** | **Description** |
|---|---|
| HomeIsoCode | ISO code of the own Member State |
| KeyStore | KeyStore file which contains the private key of the Member State |
| KeyStorePublic | KeyStore file which contains the public keys of the other Member States |
| KeyStorePass | Password for accessing the keystores (the same password is valid for both) |
| CertDir | Directory where the public keys of the other Member States can be found. This directory is not required during run-time because the public keys are in the corresponding keystore. |
| MAIL_xx | Mail addresses of the other Member States to which the requests and responses are sent (xx -> ISO code of the respective Member State) |
| IN<br>OUT<br>ERR | Directories where incoming and outgoing e-mails are logged. In case of an error, the logging is done in the ERR directory. |

It is not restricted to use this Java package only. So long as there is none of the general PKI infrastructure facilities existing, the following options can be deployed for DNA data exchange:

- Option: DC-certificates

  **D**ecentralized generation and **C**entralized deposition of certificates

  This option DC has currently been deployed for DNA Data exchange. Each Member State generates a key pair by itself and sends the generated the certificate with the corresponding public key to the party and/or parties to be involved in the communication. A central **Prüm Helpdesk server at Europol** manages a deposit site for all valid certificates to being provided by Member States.
- Option: CC-certificates

  **C**entralized generation and **C**entralized deposition of certificates

  A central place should function as the Certificate Authority (CA), where public certificates will be signed and administered. After receipt of signed public certificates by this central CA, a pair of keys (public and private) will be generated locally at the site of a Member State. The generated public key will be further administered by the CA. The end-to-end communication via sMIME or alike suffices to key exchange among Member States.

  This option is favored from technical and administrative point of view. **However, there is no such a common CA having been chosen by Member States yet.**

### 5.3.3 Network Connections

The EU wide logically closed Network sTESTA is deployed for DNA Data Exchange among Member States. Each member state has to establish a direct national access point to the sTESTA or an indirect secure link between the site, where DNA software components are installed and administered, and the site with the deployed national access point to the sTESTA.

Email messages carrying DNA requests and answers go through the sTESTA cloud and administered by an EU Email Relay Server.

Upon the current specification (paragraph 5.7.5, Chapter 1 of the Annex of the Council Decision 2008/616/JHA), the syntax of the defined email domain assumes the form as follows:

"*application-type*.pruem.*ms-iso-code*.**eu-admin.net**"

The syntax of the italics part of the domain (sub domain) is described in the Council Decision. Since the transition of TESTA II to sTESTA the generic part of the email domain "eu-admin.net" has been changed to sTESTA related format by the provider of the network. In order to avoid interruption of the network services, the historically implemented email domain is still maintained by the network service provider. However, it is strongly recommended that the currently deployed email domain should be customized to the sTESTA conform format as soon as possible.

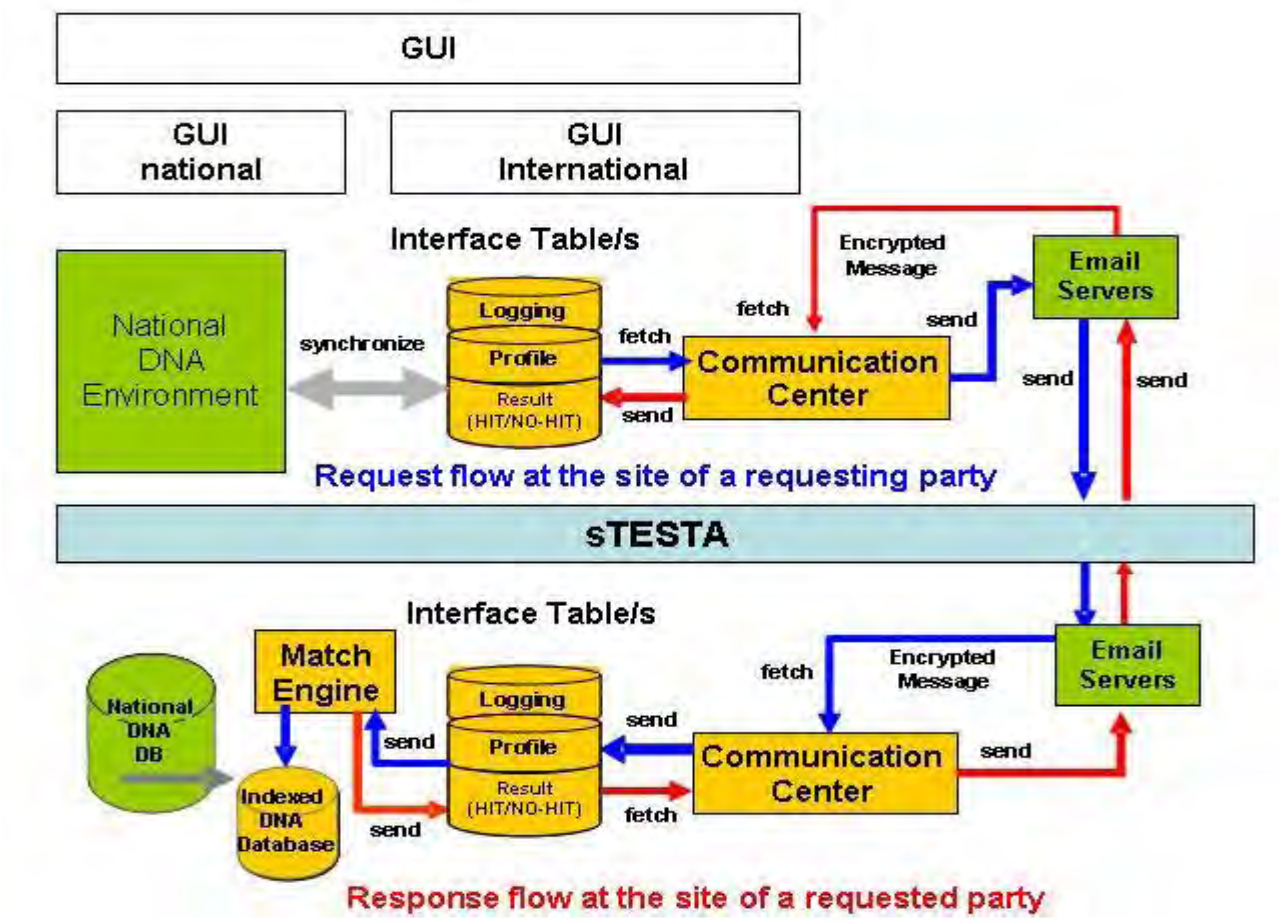
### 5.3.4 Other applications

Besides the match engines, communication centers and email components, other kinds of applications are deployed at national sites. In view of the diversified national regulations, there are no specific requirements for the additional applications. The general aspects of some of these applications are described in the following sections.

#### 5.3.4.1 Graphical User Interface

Typically two kind of GUI: national and international can be implemented by presenting data flow in the sections as indicated in the following diagram. The major parts of the information contained in the databases can thus be rendered to users by GUI applications. With no strict national regulations imposed on demarcation of functional duties, these two GUI applications may be integrated into one.

**Figure 3: Place where to set a Graphical User Interface**




### 5.3.4.2 Workflow components at national levels

After a hit notification is received in an automated procedure at the first step, the further verification and investigation of this hit depend very much on the workflow at the national level known as the second step. As the Council Decisions do not regulate the step 2, there is no common components rendered to Member States.

### 5.3.4.3 Making IT based statistics

We differentiate two kinds of statistics: one based on IT operational information, which may be obtained in the automated procedure and another based on police functional requirements. The former can be constructed by evaluating the parameters in the logging databases according to the Council Decisions. The logging databases have been implemented at the sites of Member States in daily operations. A statistics meeting the functional needs could be compiled only after a harmonisation at EU level.

# 6 CONFORMANCE TESTING METHODOLOGY

## 6.1 Using a defined DNA test set

As mentioned in the section 2.4, a test set of pseudo and/or anonymous DNA profiles should be used for test purposes. It is critical that a DNA system claimed to conform to a reference system in operations is actually conformant. Thus there is a need for a standardized conformance testing methodology to be developed for evaluation and acceptance purposes.

With regards to conformance testing of included data content and format, a conformance testing framework with appropriate testing methods and procedures, a common set of pseudo/anonymous DNA profiles, testing and reporting requirements and test assertions has been developed and is available for MS starting DNA data exchange.

## 6.2 Three levels of conformance testing

A conformance testing round comprises three levels of tests.

**Level 1**: Data Format Conformance

In Level 1 testing, a set of data records in the indexed Database shall be checked for field-by-field and byte-by-byte conformance with the inclusion rules defined by the Council Decision. The potential data format errors can be found this way.

**Level 2**: Internal Consistency Checking

In Level 2 testing, a set of data records shall be checked to determine if they are internally consistent. For this purpose, the well-defined test assertions should be applied.

**Level 3**: Content Checking

Level 3 conformance testing is defined as a conformance testing methodology that checks if the generated request containing a DNA profile by an implementation unit is a faithful representation regulated by the inclusion rules. The well-defined DAPIX DNA test set can be used for this purpose.

This conformance testing methodology should be designed and implemented during the further development and deployment of DNA data exchange at the EU level.

## 6.3 Definition of the test procedure

Since the start of DNA daily operations in 2006, three kinds of acceptance tests have been carried out among the parties involved. They are

- Connection Tests over the sTESTA
- DNA data exchange upon Article 3 (reference and stain profiles)
- DNA data exchange upon Article 4 (stain profiles only)

The conformance testing methodology as described above has been applied empirically, but has not taken shape fully in the context of a standardised conformance testing. Once the framework of conformance testing methodology will be laid down, all these acceptance tests should be embedded into the defined testing framework

# 7 CURRENT STATUS AND FURTHER DEVELOPMENT

## 7.1 Standards versus products

For the time being, a variety of the software components of match engines and communication center has been deployed at the sites of Member States in police daily operations and/or closely before entering operations. It is very difficult to keep all the components at the EU level always up-to-date from technical, organisational and financial aspects.

A more effective way to maintain and further develop an interoperable array of software components at the EU level is to work on a set of common standards and specifications. Each country could implement the products of its own at the national level in conformity with the common standards and specifications. The rules and requirements defined in the Council Decisions provide Member States with a good start of the work on standards.

## 7.2 A general procedure

After integration of the Treaty of Prüm into the legal framework of EU, the number of the countries, which should participate in DNA data exchange, has increased to 27. Therefore, a general procedure for further development of the standards and specifications and deployment of DNA data exchange components has to be defined at the EU level.

## 7.3 DNA XML Schema V.1.0

This version of XML Schema file has been developed by Germany and served as standardized interface for the communication among all members of the Treaty of Prüm, which has been signed on 27 May 2005 by seven EU countries and officially acknowledged by a few other EU countries later on. The additional EU countries have filed their intentions and willingness to join the operations according to the Treaty of Prüm.

This version of XML Schema file has been deployed between Austria and Germany right at the very beginning of the operation on 5 December 2006 and successively used at the sites of other Member States joining the daily operations.
For historical reasons, this version of XML Schema file contains some elements using the names which are historically correct but no more up to date in the context of the Council Decisions of 2008, such as “IPSG”. These XML tag names should be customized in the future versions (V. 2.x).

By exploiting the defined features upon the ATIA (Administrative and Technical Implementation Agreement) of the Treaty of Prüm, this version of XML Schema provides a common communication interface for the connected countries. Germany implemented the Prüm communication components by means of a bunch of open source products and primarily JAVA-based programming codes, which have been made available free of charge to the Prüm Treaty Member States according to the decision made by the Prüm JWG (Joint Working Group) with the members from the ministerial level of all Prüm countries. The organisational regulations under the legal framework of the Council Decisions may vary.

The type and element definitions for the ICD implementation are listed in the following tables and diagrams.

In addition to the standard build-in types defined by the W3C, the Simple and Complex Types used in the XML Schema for EU DNA Data Exchange are summarized in the following table.

**Table 22: XML Type Definitions used in EU DNA Data Exchange**

| | Name | Facets | | | Type Definition | Comment |
|---|---|---|---|---|---|---|
| | | minLen | enumeration | maxLen | | |
| Simple Type | PRUEM_data_type | 1 | P/S | 1 | string | Type name |
| | PRUEM_data_result | 1 | U/H/N/E | 1 | string | Type name |
| | PRUEM_header_dir | 1 | A/R | 1 | string | Type name |
| | PRUEM_header_type | | (M/S) | | string | Not implemented in the version 1.0 |
| | PRUEM_request_type | | (3/4) | | string | Not implemented in the version 1.0 |
| | PRUEM_hitquality_type | 1 | 0/1/2/3/4 | 1 | string | Type name |
| | source_isocode | 1 | | 4 | string | Element name |
| | destination_isocode | 1 | | 4 | string | Element name |
| | Agency | 1 | | 127 | string | Element name |
| | profile_ident | 1 | | 127 | string | Element name |
| | match_ident | 0 | | 127 | string | Element name |
| | Message | 1 | | 127 | string | Element name |
| Complex Type | PRUEM_header | N.A | | | See table 2 | Type name |
| | PRUEM_header_info | N.A. | | | See table 4 | Type name |
| | PRUEM_datas | N.A | | | See table 5 | Type name |
| | IPSG_DNA_profile | N.A. | | | See table 10 | Type name |
| | IPSG_DNA_ISSOL | N.A. | | | See table 11 | Type name |
| | IPSG_DNA_additional_loci | N.A. | | | See table 12 | Type name |
| | IPSG_DNA_locus | N.A. | | | See table 13 | Type name |

Elements defined in the XML Schema are shown in the following table.

**Table 23: XML Element Definitions used in EU DNA Data Exchange**

| Element Name | Type name | Type Category | Content Model | Referenced in |
|---|---|---|---|---|
| date | Data | Primitive build-in | | PRUEM_header_info and PRUEM_datas |
| PRUEMDNA | | Complex | Sequence | Root element |
| header | PRUEM_header | Complex | Sequence item | PRUEMDNA |
| datas | PRUEM_datas | Complex | Sequence item | PRUEMDNA |
| direction | PRUEM_header_dir | Simple | Sequence item | PRUEM_header |
| ref | String | Primitive build-in | Sequence item | PRUEM_header |
| generator | String | Primitive build-in | Sequence item | PRUEM_header |
| schema_version | String | Primitive build-in | Sequence item | PRUEM_header |
| requesting | PRUEM_header_info | Complex | Sequence item | PRUEM_header |
| requested | PRUEM_header_info | Complex | Sequence item | PRUEM_header |
| source_isocode | String | Primitive build-in | Sequence item | PRUEM_header_info |
| destination_isocode | String | Primitive build-in | Sequence item | PRUEM_header_info |
| Request_id | String | Primitive build-in | Sequence item | PRUEM_header_info |
| time | Time | Primitive build-in | Sequence item | PRUEM_header_info |
| type | PRUEM_data_type | Simple | Sequence item | PRUEM_datas |
| result | PRUEM_data_result | Simple | Sequence item | PRUEM_datas |
| agency | String | Primitive build-in | Sequence item | PRUEM_datas |
| profile_ident | String | Primitive build-in | Sequence item | PRUEM_datas |
| match_ident | String | Primitive build-in | Sequence item | PRUEM_datas |
| quality | PRUEM_hitquality_type | Simple | Sequence item | PRUEM_datas |
| hitcount | Integer | Derived build-in | Sequence item | PRUEM_datas |

| | | | | |
|---|---|---|---|---|
| message | String | Primitive build-in | Sequence item | PRUEM_datas |
| profile | IPSG_DNA_profile | Complex | Sequence item | PRUEM_datas |
| ess_issol | IPSG_DNA_ISSOL | Complex | Sequence item | IPSG_DNA_profile |
| additional_loci | ISPG_DNA_additional_loci | Complex | Sequence item | IPSG_DNA_profile |
| marker | String | Primitive build | Sequence item | IPSG_DNA_profile |
| profile_id | String | Primitive build | Sequence item | IPSG_DNA_profile |
| d3s1358 | IPSG_DNA_locus | Complex | Sequence item | IPSG_DNA_ISSOL |
| d18s51 | IPSG_DNA_locus | Complex | Sequence item | IPSG_DNA_ISSOL |
| amelogenin | IPSG_DNA_locus | Complex | Sequence item | IPSG_DNA_ISSOL |
| tpox | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| csf1po | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d13s317 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d7s820 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d5s818 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d16s539 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d2s1338 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d19s433 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| penta_d | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| penta_e | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| fes | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| f13a1 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| f13b | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| se33 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| cd4 | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |

| | | | | |
|---|---|---|---|---|
| gaba | IPSG_DNA_locus | Complex | Sequence item | ISPG_DNA_additional_loci |
| d1S1656 | IPSG_DNA_locus | Complex | 0-1 | Locus d1S1656 |
| d2S441 | IPSG_DNA_locus | Complex | 0-1 | Locus d2S441 |
| d10S1248 | IPSG_DNA_locus | Complex | 0-1 | Locus d10S1248 |
| d12S391 | IPSG_DNA_locus | Complex | 0-1 | Locus d12S391 |
| d22S1045 | IPSG_DNA_locus | Complex | 0-1 | Locus d22S1045 |
| low_allele | String | Primitive build | Sequence item | IPSG_DNA_locus |
| high_allele | String | Primitive build | Sequence item | IPSG_DNA_locus |

The following set of diagrams[1] illustrates the internal structure of all XML elements with the simple and complex type information in the version 1.0.

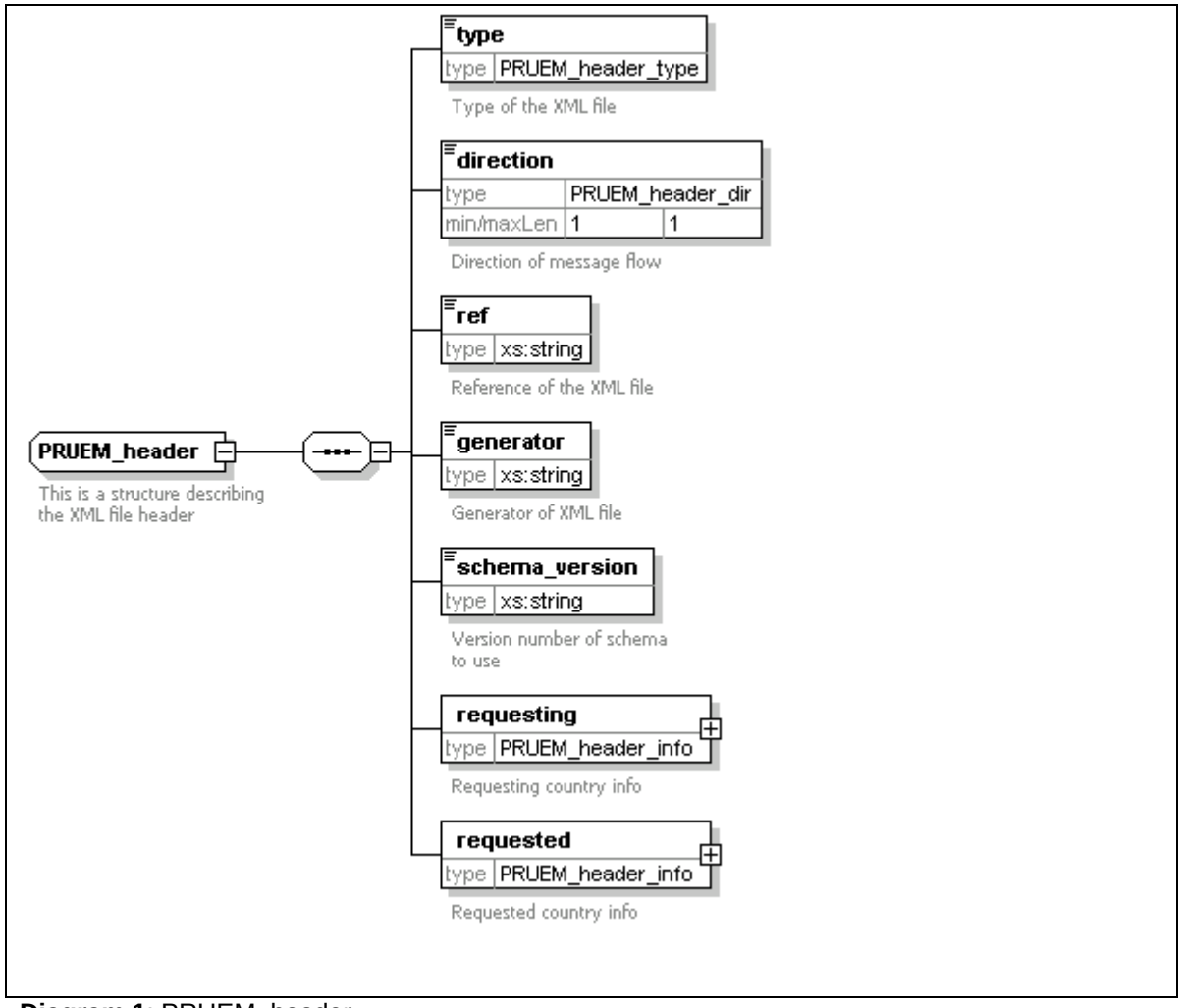



**Diagram 1**: PRUEM_header

[1] The diagrams listed in this section are basically generated by © XMLSpy of the company Altova and customized by the author of this implementation guide

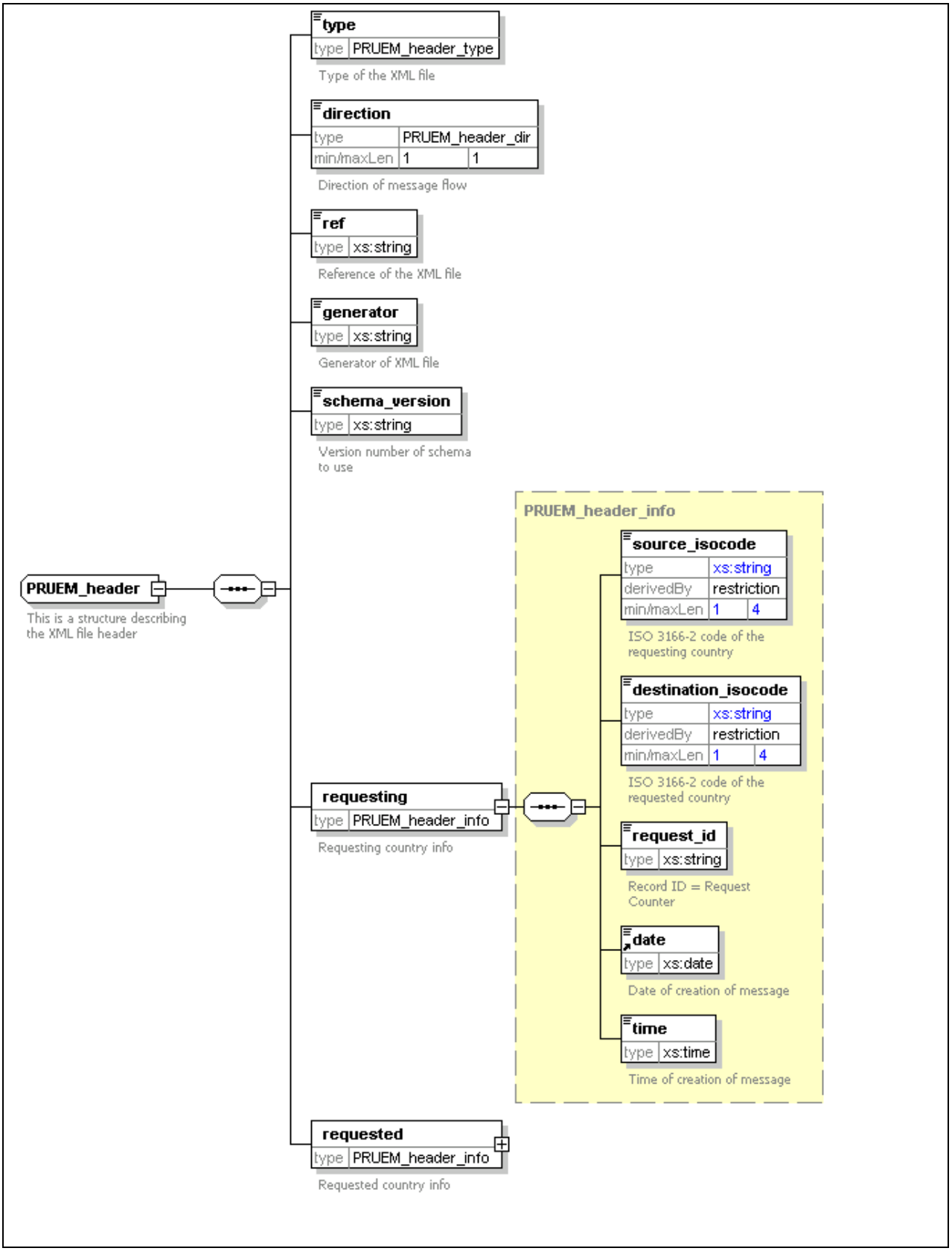



**Diagram 2:** PRUEM_header_requesting

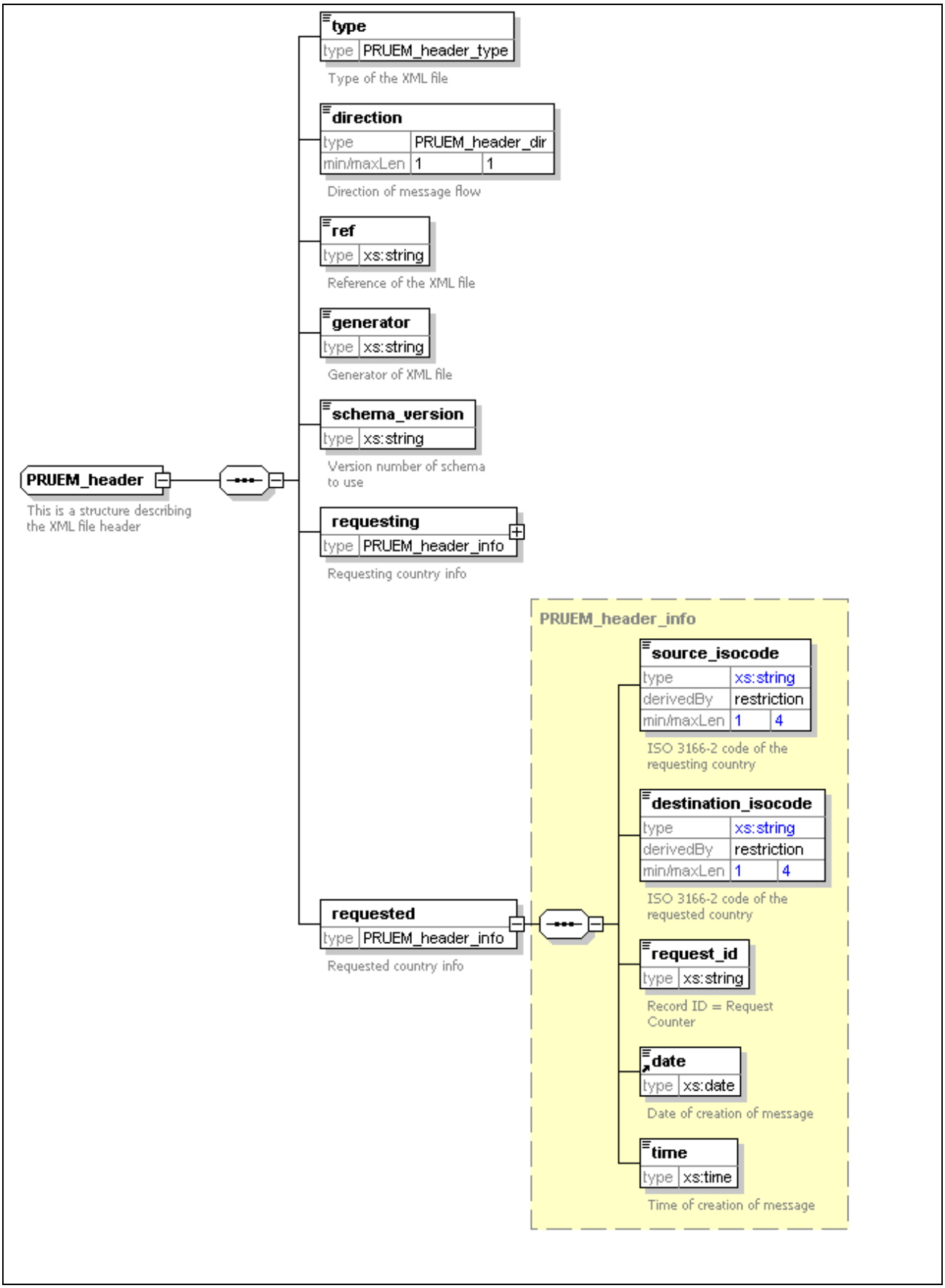



**Diagram 3: PRUEM_header_requested**

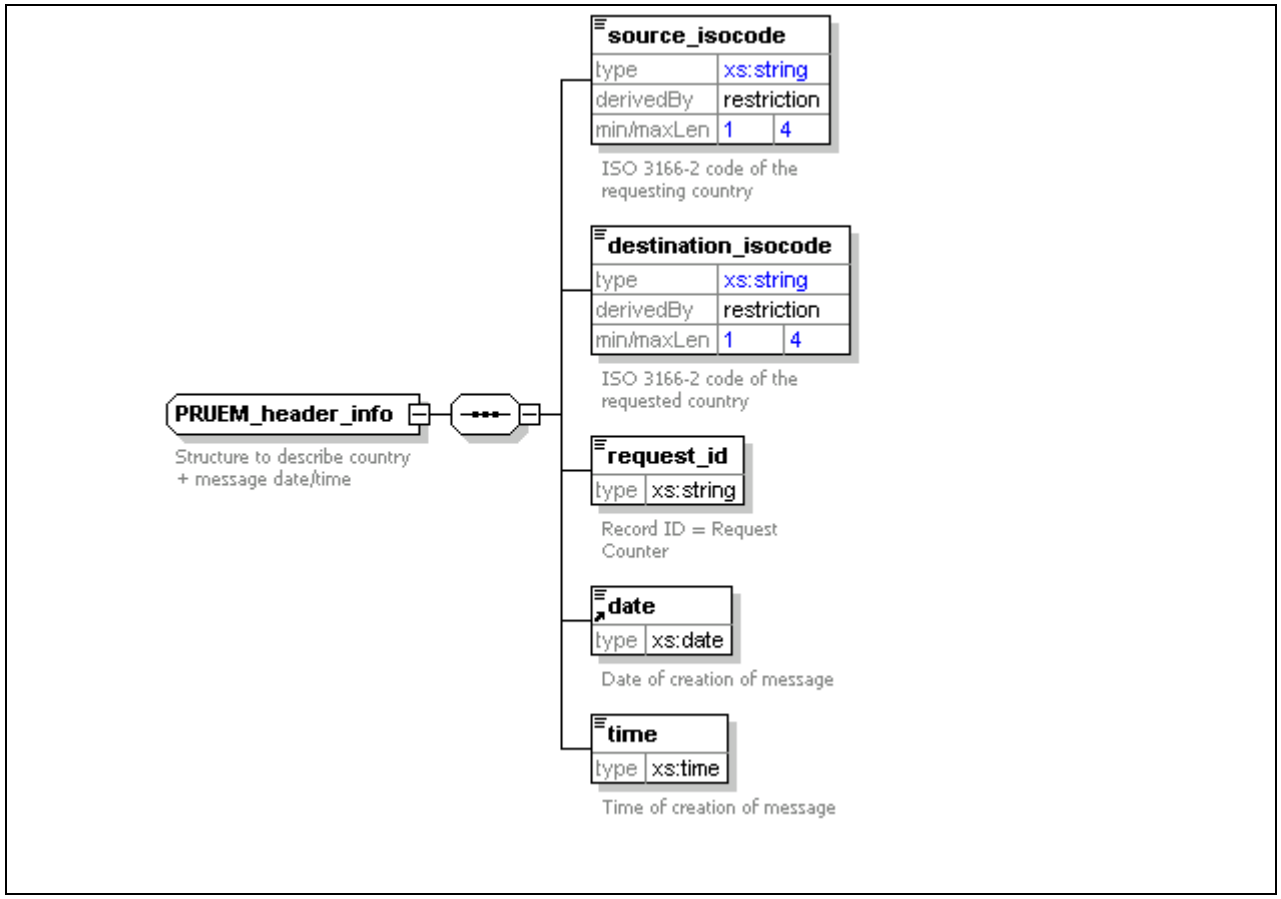



**Diagram 4: PRUEM_header_info**

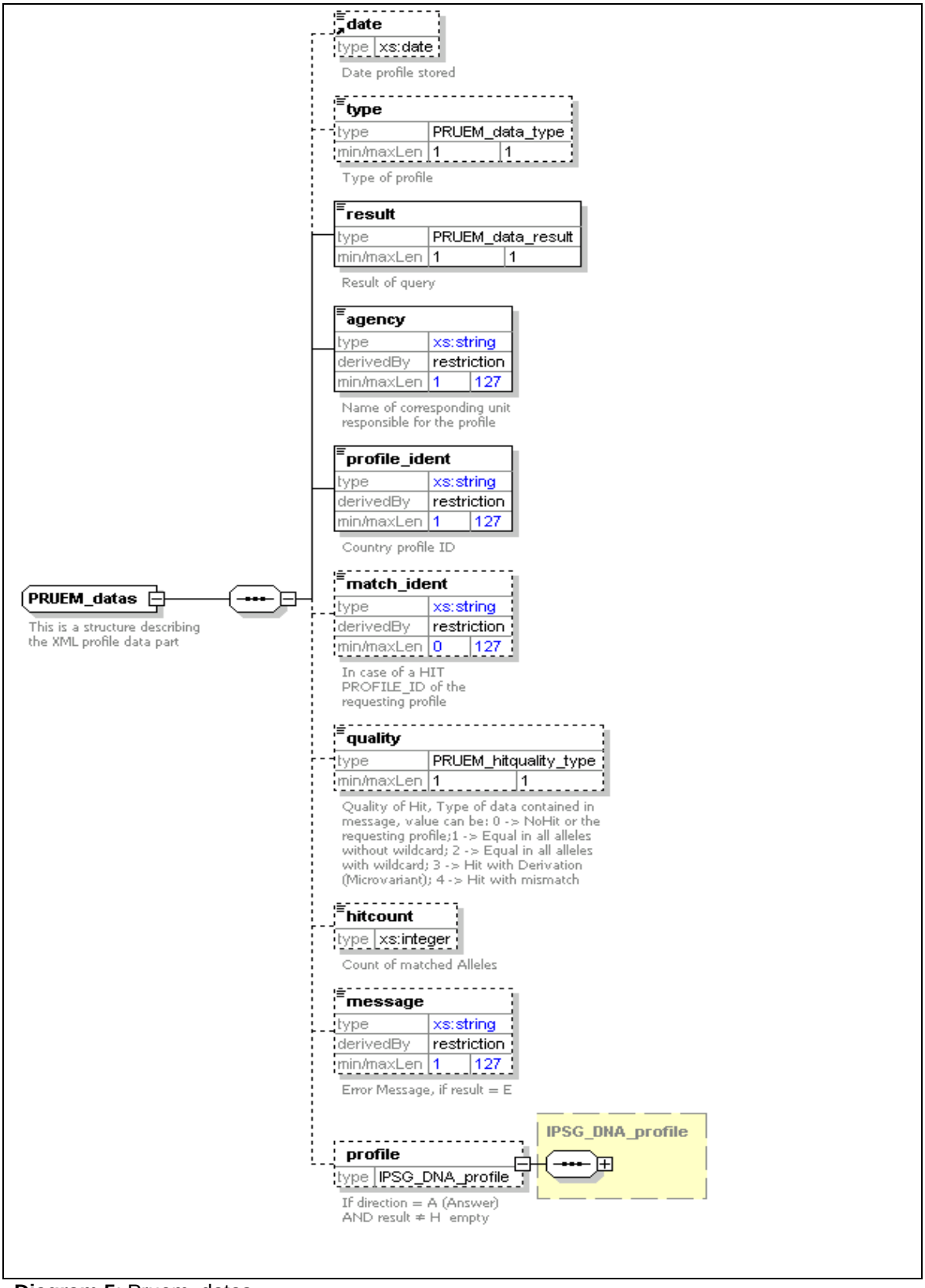



**Diagram 5**: Pruem_datas

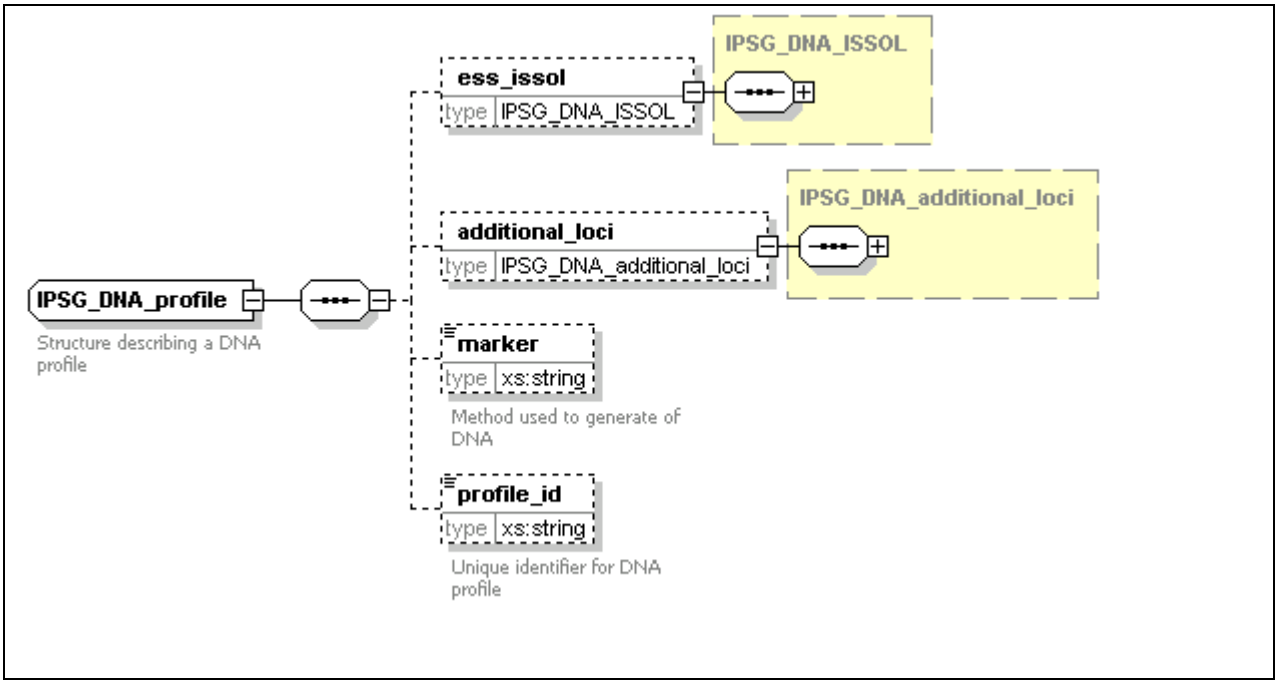



**Diagram 6:** IPSG_DNA_profile

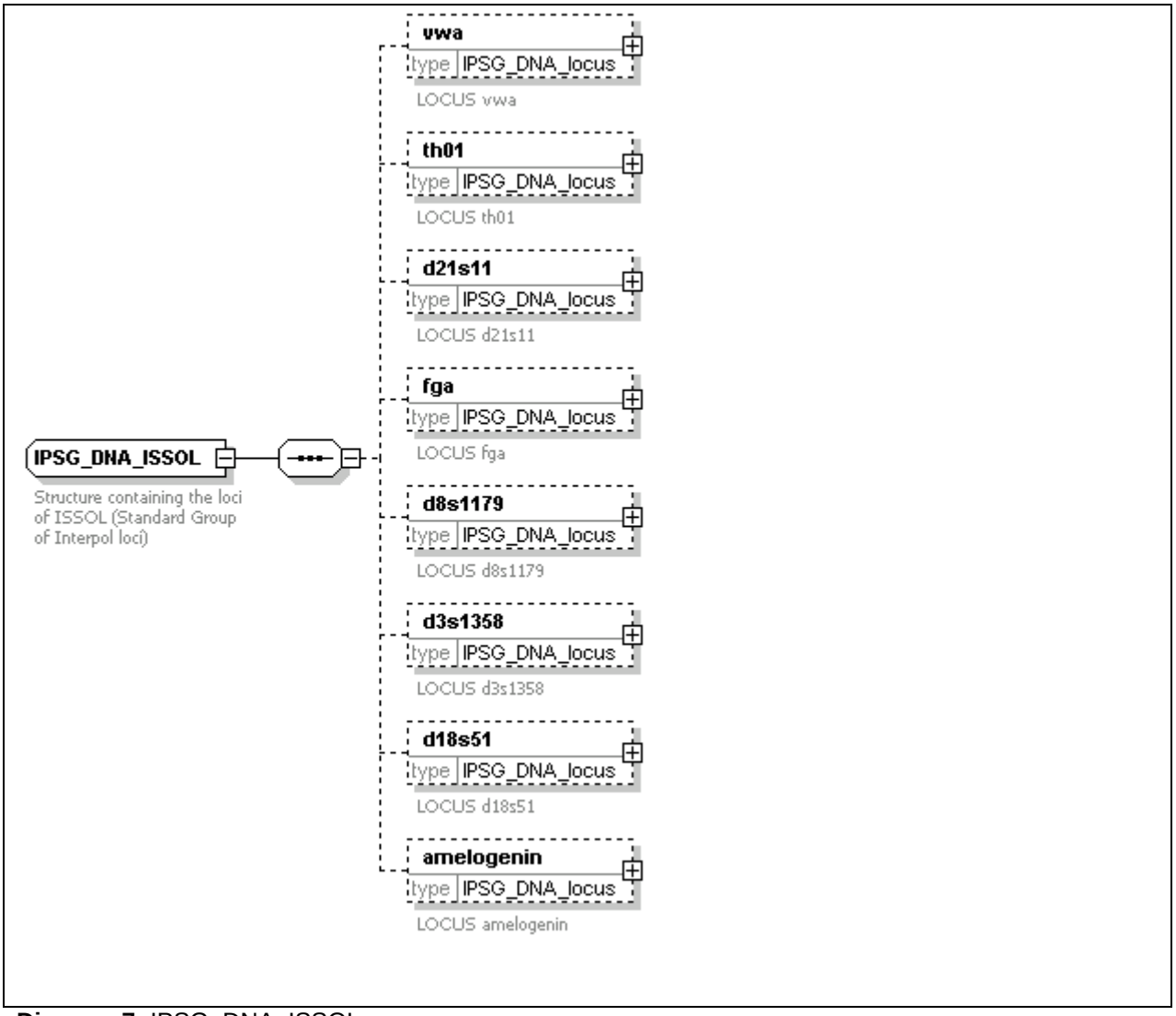



**Diagram 7:** IPSG_DNA_ISSOL

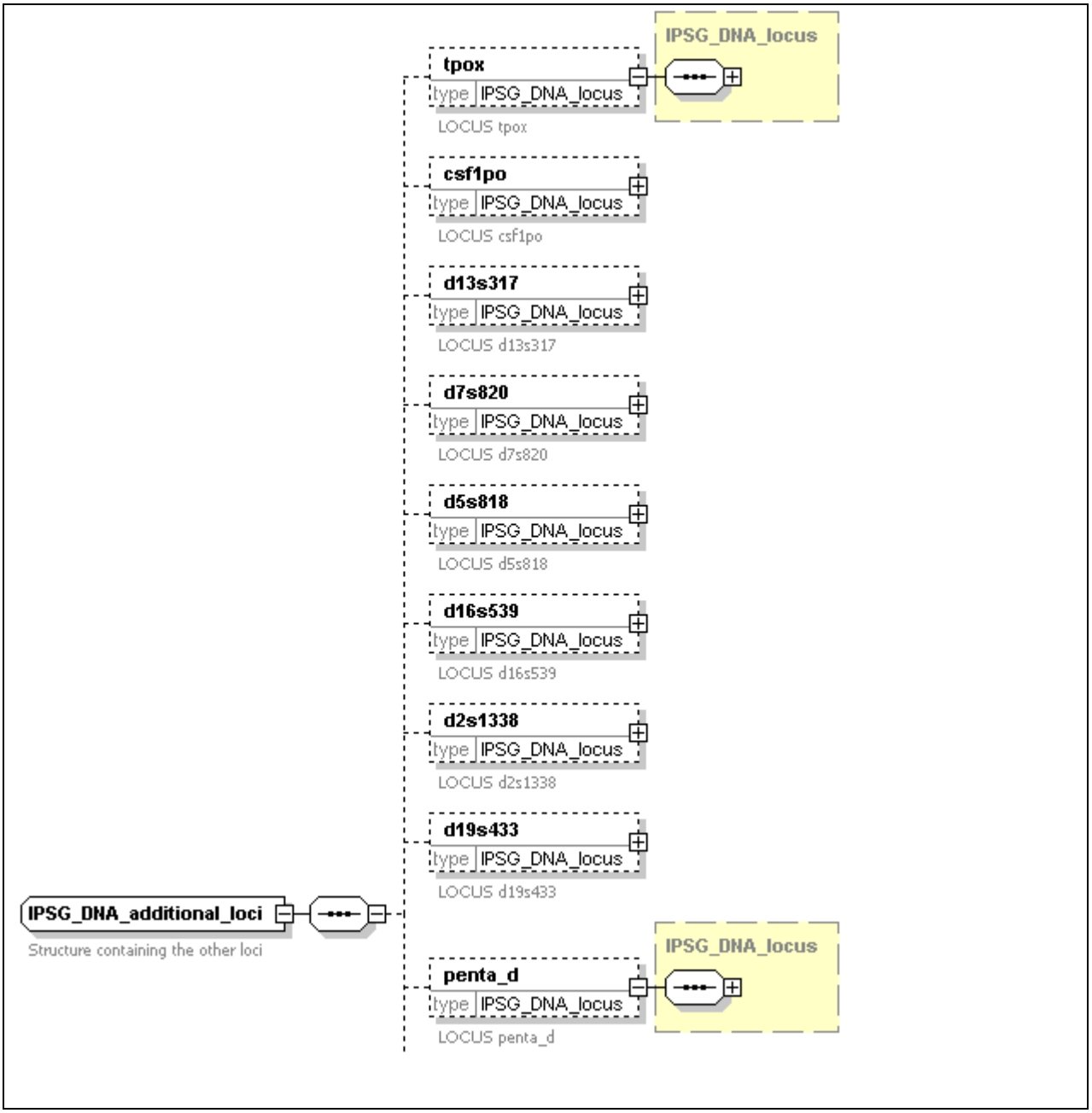



**Diagram 8**: IPSG_DNA_additional_loci (part 1)

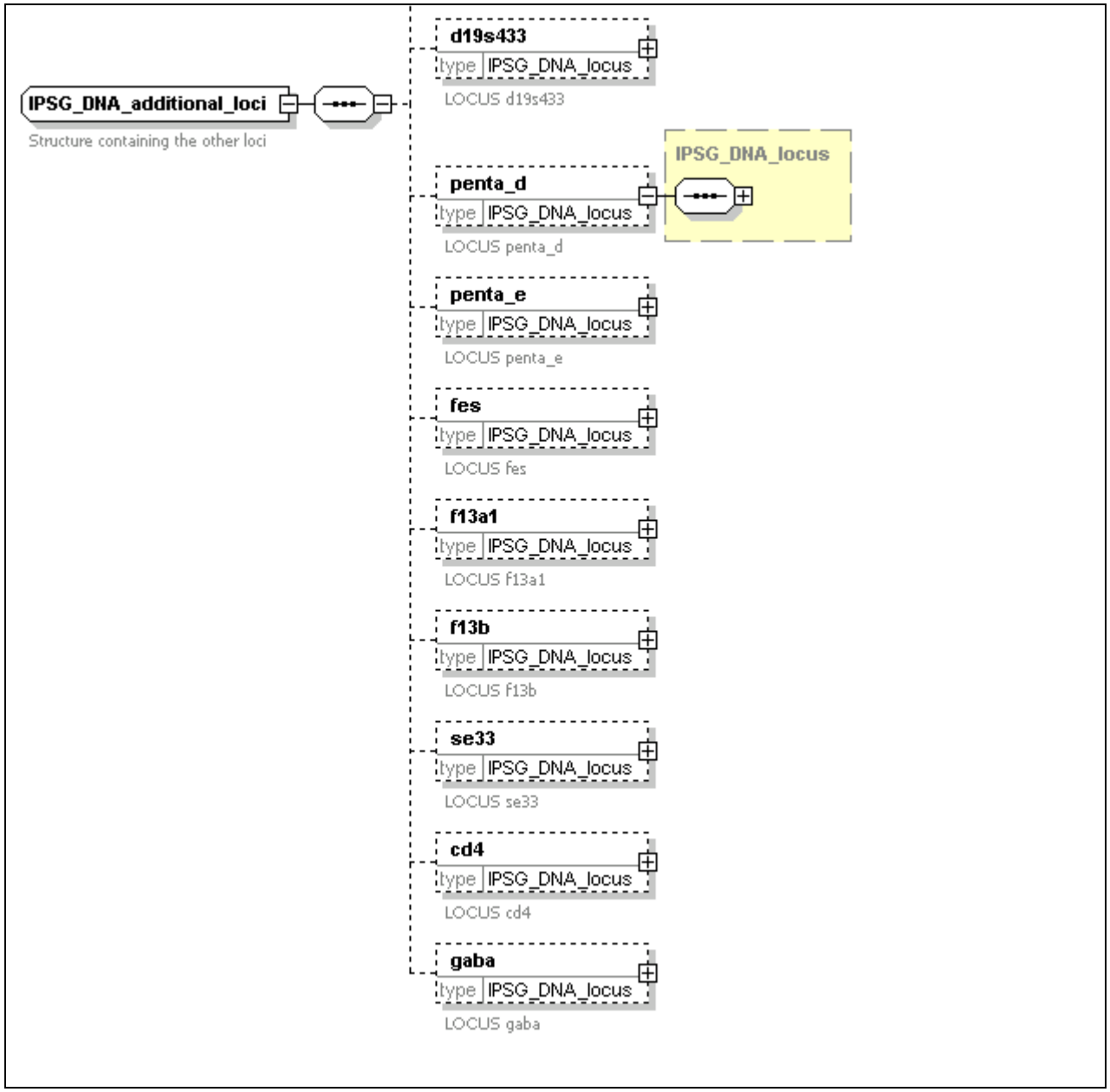



**Diagram 9**: IPSG_DNA_additional_loci (part 2)


**Diagram 10**: IPSG_DNA_locus

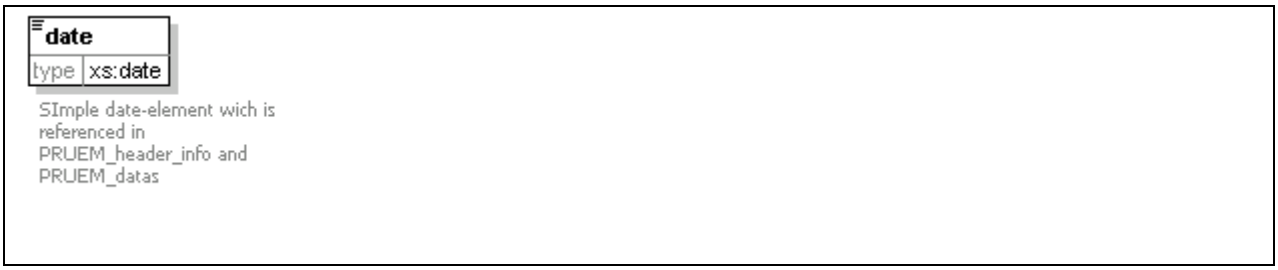



**Diagram 11**: Element „date“

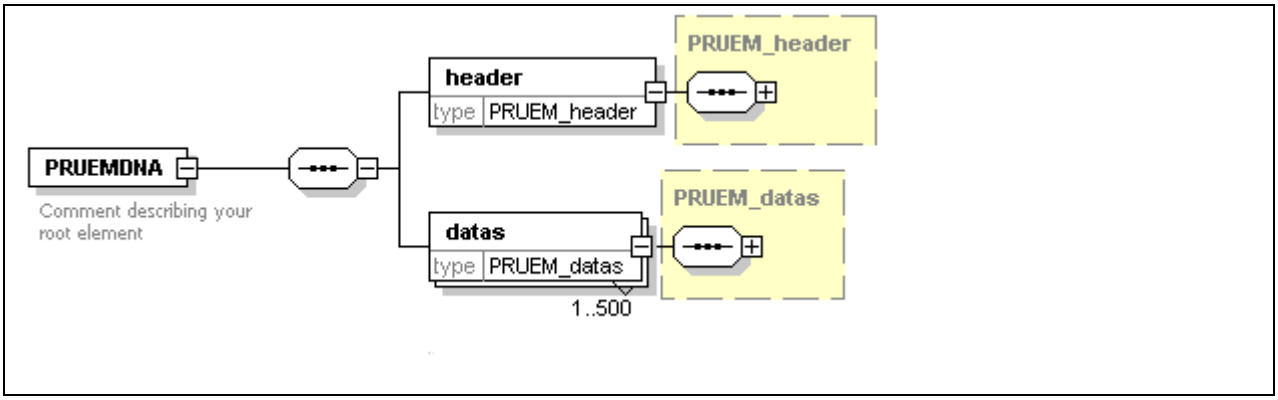



**Diagram 12**: Element „PRUEMDNA“

## 7.4 Further development of the DNA XML Schema files

The further developed DNA XML Schema Version 1.1 contains the following improvements, which are required by the Council Decisions:

- Handling DNA data exchange with the reference to Article 3 or Article 4
- Completing the implementation of some parts in the version 1.0 (e.g. PRUEM_header_type)
- Providing backward compatibility with version 1.0 and interoperability with other versions of XML Schemas
- Including 5 additional ESS loci being accepted by the EU
- Concerning other miscellaneous features

The XML Schema version 1.1 has been released by Germany in 3Q12 and is included in the following section..

## 7.5 DNA XML Schema V.1.1

```
<?xml version="1.0"?>
<!-- edited with XMLSpy v2006 sp2 U (http://www.altova.com) by BKA (BKA) -->
<xs:schema xmlns:pruem-dna="http://europa.eu/2008/pruem/dna/1.1"
xmlns:xs="http://www.w3.org/2001/XMLSchema" targetNamespace="http://europa.eu/2008/pruem/dna/1.1"
elementFormDefault="qualified" attributeFormDefault="unqualified">
	<xs:element name="PRUEMDNA">
		<xs:annotation>
			<xs:documentation>EU Pruem DNA Communication Center is for internal use ONLY. The
distribution of the software package to any third party or parties without the persission of the software owner,
Bundeskriminalamt in Germany (BKA), is strictly prohibited; however, the XML Schema file is served as the common
communication interface among EU member states for DNA Data Exchange in police daily
operations.</xs:documentation>
			<xs:documentation>Schema Version: 1.1</xs:documentation>
			<xs:documentation>Date of the version: September 26, 2012</xs:documentation>
			<xs:documentation>Root element PRUEM DNA</xs:documentation>
		</xs:annotation>
		<xs:complexType>
			<xs:sequence>
				<xs:element name="header" type="pruem-dna:PRUEM_header"/>
				<xs:element name="datas" type="pruem-dna:PRUEM_datas" maxOccurs="500"/>
			</xs:sequence>
		</xs:complexType>
	</xs:element>
	<xs:complexType name="PRUEM_header">
		<xs:annotation>
			<xs:documentation>This is a structure describing the XML file header.</xs:documentation>
		</xs:annotation>
		<xs:sequence>
			<xs:element name="direction" type="pruem-dna:PRUEM_header_dir">
				<xs:annotation>
					<xs:documentation>Direction of message flow</xs:documentation>
				</xs:annotation>
			</xs:element>
			<xs:element name="ref" type="xs:string">
				<xs:annotation>
					<xs:documentation>Reference of the XML file</xs:documentation>
```

```
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="generator" type="xs:string">
                        <xs:annotation>
                            <xs:documentation>Generator of XML file</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="schema_version" type="xs:string">
                        <xs:annotation>
                            <xs:documentation>Version number of schema to
use</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="requesting" type="pruem-dna:PRUEM_header_info">
                        <xs:annotation>
                            <xs:documentation>Requesting Member State info</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="requested" type="pruem-dna:PRUEM_header_info">
                        <xs:annotation>
                            <xs:documentation>Requested Member State  info</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                </xs:sequence>
            </xs:complexType>
            <xs:simpleType name="PRUEM_header_dir">
                <xs:annotation>
                    <xs:documentation>
                    of data contained in message, value can be:

                    -> Request



                    -> Answer

                        </xs:documentation>
                </xs:annotation>
                <xs:restriction base="xs:string">
                    <xs:minLength value="1"/>
                    <xs:maxLength value="1"/>
                    <xs:enumeration value="R"/>
                    <xs:enumeration value="A"/>
                    <!-- Request -->
                    <!-- Answer  -->
                </xs:restriction>
            </xs:simpleType>
            <xs:complexType name="PRUEM_header_info">
                <xs:annotation>
                    <xs:documentation>Structure to describe country + message
date/time</xs:documentation>
                </xs:annotation>
                <xs:sequence>
                    <xs:element name="source_isocode">
                        <xs:annotation>
                            <xs:documentation>ISO 3166-2 code of the requesting Member
State</xs:documentation>
                        </xs:annotation>
                        <xs:simpleType>
                            <xs:restriction base="xs:string">
                                <xs:minLength value="1"/>
                                <xs:maxLength value="4"/>
                            </xs:restriction>
                        </xs:simpleType>
                    </xs:element>
```

```
                        <xs:element name="destination_isocode">
                                <xs:annotation>
                                        <xs:documentation>ISO 3166-2 code of the requested Member
State</xs:documentation>
                                </xs:annotation>
                                <xs:simpleType>
                                        <xs:restriction base="xs:string">
                                                <xs:minLength value="1"/>
                                                <xs:maxLength value="4"/>
                                        </xs:restriction>
                                </xs:simpleType>
                        </xs:element>
                        <xs:element name="request_id" type="xs:string">
                                <xs:annotation>
                                        <xs:documentation>Unique Identifier for a request</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element ref="pruem-dna:date">
                                <xs:annotation>
                                        <xs:documentation>Date of creation of message</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="time" type="xs:time">
                                <xs:annotation>
                                        <xs:documentation>Time of creation of message</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                </xs:sequence>
        </xs:complexType>
        <xs:complexType name="PRUEM_datas">
                <xs:annotation>
                        <xs:documentation>This is a structure describing the XML profile data part
</xs:documentation>
                </xs:annotation>
                <xs:sequence>
                        <xs:element name="reqtype" type="pruem-dna:PRUEM_request_type" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>Type of request (Article 3 or 4)</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element ref="pruem-dna:date" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>Date profile stored </xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="type" type="pruem-dna:PRUEM_data_type" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>Type of profile </xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="result" type="pruem-dna:PRUEM_data_result">
                                <xs:annotation>
                                        <xs:documentation>Result of request</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="agency">
                                <xs:annotation>
                                        <xs:documentation>Name of corresponding unit responsible for the
profile</xs:documentation>
                                </xs:annotation>
                                <xs:simpleType>
                                        <xs:restriction base="xs:string">
                                                <xs:minLength value="1"/>
                                                <xs:maxLength value="127"/>
                                        </xs:restriction>
```

```
                    </xs:simpleType>
                </xs:element>
                <xs:element name="profile_ident">
                    <xs:annotation>
                        <xs:documentation>Unqiue Member State profile ID</xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:string">
                            <xs:minLength value="1"/>
                            <xs:maxLength value="127"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
                <xs:element name="match_id" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>In case of a HIT PROFILE_ID of the requesting
profile</xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:string">
                            <xs:minLength value="0"/>
                            <xs:maxLength value="127"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
                <xs:element name="quality" type="pruem-dna:PRUEM_hitquality_type" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>
                        of Hit:

                            -> NoHit or the requesting profile
                            -> Equal in all alleles without wildcard
                            -> Equal in all alleles with wildcard
                            -> Hit with Derivation (Microvariant)
                            -> Hit with mismatch
                            </xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="hitcount" type="xs:short" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>Count of matched Alleles</xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="rescount" type="xs:short" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>Count of matched profiles. If direction = R (Request),
then empty. If quality != 0 (the original requested profile), then empty.
                        </xs:documentation>
                    </xs:annotation>
                </xs:element>
                <xs:element name="message" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>Error Message, if result = E </xs:documentation>
                    </xs:annotation>
                    <xs:simpleType>
                        <xs:restriction base="xs:string">
                            <xs:minLength value="1"/>
                            <xs:maxLength value="127"/>
                        </xs:restriction>
                    </xs:simpleType>
                </xs:element>
                <xs:element name="profile" type="pruem-dna:IPSG_DNA_profile" minOccurs="0">
                    <xs:annotation>
                        <xs:documentation>If direction = A (Answer) AND result != H (Hit)
empty</xs:documentation>
```

```
                        </xs:annotation>
                    </xs:element>
                </xs:sequence>
            </xs:complexType>
            <xs:simpleType name="PRUEM_request_type">
                <xs:annotation>
                    <xs:documentation>Type of request (Article 3 or 4)</xs:documentation>
                </xs:annotation>
                <xs:restriction base="xs:string">
                    <xs:minLength value="1"/>
                    <xs:maxLength value="1"/>
                    <xs:enumeration value="3"/>
                    <xs:enumeration value="4"/>
                    <!-- Requests pursuant to Article 3 of Decision 2008/.../JHA -->
                    <!-- Requests pursuant to Article 4 of Decision 2008/.../JHA -->
                </xs:restriction>
            </xs:simpleType>
            <xs:simpleType name="PRUEM_hitquality_type">
                <xs:annotation>
                    <xs:documentation>Quality of Hit, Type of data contained in message, value can be: 0 -> NoHit or the requesting profile;1 -> Equal in all alleles without wildcard; 2 -> Equal in all alleles with wildcard; 3 -> Hit with Derivation (Microvariant); 4 -> Hit with mismatch
                    </xs:documentation>
                </xs:annotation>
                <xs:restriction base="xs:string">
                    <xs:minLength value="1"/>
                    <xs:maxLength value="1"/>
                    <xs:enumeration value="0"/>
                    <xs:enumeration value="1"/>
                    <xs:enumeration value="2"/>
                    <xs:enumeration value="3"/>
                    <xs:enumeration value="4"/>
                    <!--
                    original requesting profile:

                    "Not Hit": original requesting profile sent back only;
                    "Hit": original requesting profile and matched profiles sent back.

                    -->
                    <!--
                    in all available alleles without wildcards.
                    -->
                    <!--
                    in all available alleles with wildcards
                    -->
                    <!--
                    with Deviation (Microvariants)
                    -->
                    <!--
                    with mismatch
                    -->
                </xs:restriction>
            </xs:simpleType>
            <xs:simpleType name="PRUEM_data_type">
                <xs:annotation>
                    <xs:documentation>Type of data contained in message, value can be: P -> Person profile; S -> Stain</xs:documentation>
                </xs:annotation>
                <xs:restriction base="xs:string">
                    <xs:minLength value="1"/>
                    <xs:maxLength value="1"/>
                    <xs:enumeration value="P"/>
                    <xs:enumeration value="S"/>
                    <!-- Person profile -->
                    <!-- Stain profile  -->
```

```
                </xs:restriction>
        </xs:simpleType>
        <xs:simpleType name="PRUEM_data_result">
                <xs:annotation>
                        <xs:documentation>Type of data contained in message, value can be: U ->  Undefined, If direction = R (request); H -> Hit; N -> No hit; E -> Error</xs:documentation>
                </xs:annotation>
                <xs:restriction base="xs:string">
                        <xs:minLength value="1"/>
                        <xs:maxLength value="1"/>
                        <xs:enumeration value="U"/>
                        <xs:enumeration value="H"/>
                        <xs:enumeration value="N"/>
                        <xs:enumeration value="E"/>
                        <!-- Undefined; if direction = R (request) -->
                        <!-- Hit    -->
                        <!-- No Hit -->
                        <!-- Error  -->
                </xs:restriction>
        </xs:simpleType>
        <xs:complexType name="IPSG_DNA_profile">
                <xs:annotation>
                        <xs:documentation>Structure describing a DNA profile</xs:documentation>
                </xs:annotation>
                <xs:sequence>
                        <xs:element name="ess_issol" type="pruem-dna:IPSG_DNA_ISSOL" minOccurs="0"/>
                        <xs:element name="additional_loci" type="pruem-dna:IPSG_DNA_additional_loci" minOccurs="0"/>
                        <xs:element name="marker" type="xs:string" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>Method used to generate of DNA</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="profile_id" type="xs:string" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>Unique identifier for DNA profile</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                </xs:sequence>
        </xs:complexType>
        <xs:complexType name="IPSG_DNA_ISSOL">
                <xs:annotation>
                        <xs:documentation>Structure containing the loci of ISSOL (Standard Group of Interpol loci)</xs:documentation>
                </xs:annotation>
                <xs:sequence>
                        <xs:element name="vwa" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>LOCUS vwa</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="th01" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>LOCUS th01</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="d21s11" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>LOCUS d21s11</xs:documentation>
                                </xs:annotation>
                        </xs:element>
                        <xs:element name="fga" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                                <xs:annotation>
                                        <xs:documentation>LOCUS fga</xs:documentation>
```

```
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d8s1179" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d8s1179</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d3s1358" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d3s1358</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d18s51" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d18s51</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d1s1656" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d1s1656</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d2s441" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d2s441</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d10s1248" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d10s1248</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d12s391" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d12s391</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d22s1045" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS d22s1045</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="amelogenin" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS amelogenin</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                </xs:sequence>
            </xs:complexType>
            <xs:complexType name="IPSG_DNA_additional_loci">
                <xs:annotation>
                    <xs:documentation>Structure containing the other loci</xs:documentation>
                </xs:annotation>
                <xs:sequence>
                    <xs:element name="tpox" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS tpox</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="csf1po" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
                        <xs:annotation>
                            <xs:documentation>LOCUS csf1po</xs:documentation>
                        </xs:annotation>
                    </xs:element>
                    <xs:element name="d13s317" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
```

```
            <xs:annotation>
                <xs:documentation>LOCUS d13s317</xs:documentation>
            </xs:annotation>
</xs:element>
<xs:element name="d7s820" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
            <xs:annotation>
                <xs:documentation>LOCUS d7s820</xs:documentation>
            </xs:annotation>
</xs:element>
<xs:element name="d5s818" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
            <xs:annotation>
                <xs:documentation>LOCUS d5s818</xs:documentation>
            </xs:annotation>
</xs:element>
<xs:element name="d16s539" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
            <xs:annotation>
                <xs:documentation>LOCUS d16s539</xs:documentation>
            </xs:annotation>
</xs:element>
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            </xs:annotation>
</xs:element>
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                <xs:documentation>LOCUS d19s433</xs:documentation>
            </xs:annotation>
</xs:element>
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                <xs:documentation>LOCUS penta_d</xs:documentation>
            </xs:annotation>
</xs:element>
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            </xs:annotation>
</xs:element>
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            </xs:annotation>
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            </xs:annotation>
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            </xs:annotation>
</xs:element>
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            </xs:annotation>
</xs:element>
<xs:element name="gaba" type="pruem-dna:IPSG_DNA_locus" minOccurs="0">
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                                                <xs:documentation>LOCUS gaba</xs:documentation>
                                        </xs:annotation>
                                </xs:element>
                        </xs:sequence>
                </xs:complexType>
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                                <xs:documentation>Structure describing a locus</xs:documentation>
                        </xs:annotation>
                        <xs:sequence>
                                <xs:element name="low_allele" type="xs:string"/>
                                <xs:element name="high_allele" type="xs:string"/>
                        </xs:sequence>
                </xs:complexType>
                <xs:element name="date" type="xs:date">
                        <xs:annotation>
                                <xs:documentation>Simple date-element wich is referenced in PRUEM_header_info and
PRUEM_datas</xs:documentation>
                        </xs:annotation>
                </xs:element>
</xs:schema>
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