

# XML Schema

For the latest files see [File Format](#)

## Future ADAMS Release - Sample Specific Gravity (Confirmation Procedure)

Release 7 May 2019: In conformance with the **TD2019DL** it will be possible to specify the *Sample Specific Gravity (Confirmation Procedure)* for Urine samples.

- For the XML Import/Update file a new tag *sampleSpecificGravityCP* is added: when a Urine Lab result is imported/updated with a *date\_received* that is equal to or later than 1 March 2019 with a Test result = AAF/ATF, it is mandatory to provide a value for the Sample Specific Gravity (Confirmation Procedure).
- Note: the new tag *sampleSpecificGravityCP* different from and functionally NOT related to the existing tag *confirmedSpecificGravity* which is exclusively associated with the Steroid Profile.

The associated XSD schema is [here](#).

## New Confounding Factors as per 1 September 2018

In conformance with **TD2018EAAS** two new Confounding Factors related to the categories of aromatase inhibitors and anti-estrogens will be in force as of 1 September 2018.

The specific codes are:

- 'aromatase' for 'aromatase inhibitors'
- 'anti\_estrogens' for 'anti-estrogens'

## ADAMS Release June 2018

In conformance with **TD2018CG/LH** it will be possible to specify the details regarding the LH-analysis. Three **optional** fields will facilitate this:

- *lh\_analysis* : which may assume one of the 3 values Negative / PAAF / ATF . It is not mandatory to include the tag.
- *lh\_concentration*: is a numeric value (positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7)
- *lh\_lod*: is a numeric value (positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7). A value entered for the LOD implies that the "concentration of LH was less than this specified LOD"

Click here for the corresponding XSD schema that will take effect in June 2018: [labresults.xsd](#) and example XML [XML Import with LH parameters v1.xml](#)

```
<xsd:simpleType name="LHAnalysisResultCodeXSD">
<xsd:restriction base="xsd:string">
<xsd:enumeration value="Negative"/>
<xsd:enumeration value="PAAF"/>
<xsd:enumeration value="ATF"/>
</xsd:restriction>
</xsd:simpleType>
```

```
<xsd:element name="lh_analysis" type="LHAnalysisResultCodeXSD" minOccurs="0"/>
<xsd:element name="lh_concentration" type="xsd:decimal" minOccurs="0"/>
<xsd:element name="lh_lod" type="xsd:decimal" minOccurs="0"/>
```

## ADAMS 4.7.0

For IRMS performed on Urine samples: labs are able to indicate a dedicated **Overall IRMS conclusion** irrespective and independent from the overall Lab test result.

## Note on the ADAMS 4.1.1 release date change from 1 March to 16 March 2016

You may have prepared Import files *before* 16 March 2016 with Lab results containing the new information as stated in the next info bulletin below. When these Lab results are imported *after* 16 March, the system will not reject the new information: the new

columns/tags and their values will be allowed if the date\_received is before 16 March 2016 (and after 1 Jan 2016).

In general, updates made *after 16 March 2016* on older Lab results will allow for providing the new information (depending on the date\_received it will be optional or mandatory).

#### ADAMS Release 4.1.1 - the changes as of 16 March 2016

For samples reported as of **16 March 2016** the following becomes effective, if the date received of the sample is after 1 January 2016:

- Urine lab results validity is calculated based on *microbial contamination markers*: these fields are **mandatory** if the date received is after 16 March 2016
- Labs will have to indicate whether the TA approved or not the *suspicious confirmation procedure request*: this information is **mandatory** under certain conditions
- *Presence/Absence of Confounding factors, as per ITP*: this information is **mandatory**
- *Confirmation of the presence of confounding factors*: this information is **mandatory**
- *values of IRMS Target Compounds, and associated uc*: at least one is **mandatory**
- *values of Endogenous Reference Compounds, and associated uc*: one is **mandatory** (preferentially PDiol)
- *IRMS Comments*: free text (optional)

\*\*\*\*\*NEW An **XSD-schema** is available (also in PDF), and a **sample XML-file** . \*\*\*\*\*NEW: containing *confirmed* values for **Microbi al contamination markers**

#### Important rules for the Import:

- if the date\_received of the sample is on or after 16 March, the microbial confirmation markers are required (not needed if *before 16 March*)
- if a Confirmed value is provided in the XML file for one of the relevant entities to be confirmed (Steroid Profile variable (at least one), confirmed specific gravity, confounding factor, microbial contamination), then the values should be provided for *all* entities
- if the initial value for a Confounding factor is set to "yes", then no confirmed value will be enforced for the Import (unless the previous bullet point applies); for the Batch Update however it will be enforced
- if the date\_received of the sample is on or after 16 March, the GC/C/IRMS conclusion (analysisAttributes consistent) no longer applies

#### ADAMS Release 4.1 - the changes as of 1 January 2016:

The following will be effective as of the start date of the TD2016EAAS & TD2016IRMS Reporting in 2016, which is set to **1 January 2016**.

The existing field *Sample collection date* is **mandatory** if the date received of the Urine/Blood sample is after 1 January 2016

Additional field in CSV/XML: *Confirmed specific gravity* is **mandatory** for the SP confirmation procedure if the date received of the sample is after 1 January 2016

Allowing the value '-2' for the steroid variable *epitestosterone*, if the date received of the sample is after 1 January 2016

#### 1 January 2016: Analysis attribute for Urine

As of **1 January 2016** the name will change for *GHRF (GHRH/GHS/GHRP) [ code GH ]* into *GHRF (GHS/GHRP) [ internal code remains GH ]*; also we will add a new attribute *GHRF (GHRH) [ internal code GHRH ]*

#### BATCH HEADER INFORMATION

Each file must contain one batch header containing the following information:

| Data Element       | Description   |
|--------------------|---|
| File Creation Date | An ISO representation of the date that the data file was created by the laboratory (e.g. 2005-02-15). This date will be stored in ADAMS as the result posting date. |

|                          |   |
|--------------------------|---|
| Transmission Source Name | The name of the organization, department, or possibly individual that is the source of the data transmission. This field is optional, but if provided, it will be stored in the "Observations and Details" area of the result record.   |
| Batch ID or Number       | An internal lab number to identify the batch of results contained within the transmission. This identifier will be stored with each result record in ADAMS.   |
| Lab                      | An identification code indicating the Lab name that is to send the result records.  |
| Testing Type             | A code indicating whether the samples were collected in-competition ("IC") or out-of-competition ("OOC"). This tag is mandatory for the <i>Import</i> operation, whereas it is optional for the <i>Update</i> operation. If mentioned in the header, the suggested value will apply to all results in the body. |
| Comments                 | If desired, comments can be provided. This field is not mandatory.  |

### SAMPLE DETAIL RECORDS

One sample detail record, containing the following information, must be provided for each sample analyzed:

\* Identifies mandatory fields

| Data Element                 | Description  |
|------------------------------|--|
| Sample Code*                 | The unique sample code (e.g. test kit identifier). This will be used to match the result record to the test record.  |
| Lab ID Number (LIN)          | An internal number or code assigned to each sample by the lab. This field is not mandatory, but will be stored in ADAMS if provided.   |
| Sample Type*                 | A code used to identify the type of sample provided (e.g. Blood, Urine)...   |
| Sample A/B*                  | Code to indicate whether the result record relates to the analysis of the "A", the "B", "B1" or "B2" Sample. It is possible to specify the values "B1" and "B2" for samples reported after January 1st 2015. (ADAMS Release 4.0) |
| Date Sample Collected*       | The sample collection date as recorded on the doping control form. (e.g. 2005-02-12)<br><b>This field is mandatory for samples with a date received after 1 Jan 2016</b>   |
| Date Sample Received by Lab* | The date that the lab received the sample (e.g. 2005-02-12)  |
| Gender of Athlete*           | A code (M, F, or X) indicating the gender of the athlete as provided on the doping control form. This field is not mandatory.  |
| Sport & Discipline*          | The sport and discipline in which the athlete competes (e.g. AQ ). ADAMS will record the lab entry even though it may not exactly match the sport and discipline recorded on the sample collection order.                        |
| Event                        | The name of the event (e.g. Men's 100m finals) in which the athlete was competing, as provided on the doping control form.   |
| Sample Collection Authority* | A code indicating the short name of the Sample Collection Authority.   |
| Country of Sample Collection | A code indicating the country in which the sample was collected.   |

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| Region of Sample Collection                      | A code indicating the region in which the sample was collected.   |
| City of Sample Collection                        | The city where the sample was collected. This is not a mandatory field but may be used to verify a match if provided.   |
| Testing Authority*                               | A code indicating the short name of the Testing Authority. This is a mandatory field for samples reported after January 1st 2015. (ADAMS Release 4.0)   |
| Results Management Authority                     | A code indicating the short name of the Results Management Authority. <b>This is an optional field for samples reported after January 1st 2015. (ADAMS Release 4.0)</b><br>Example:<br><pre>&lt;rma&gt; &lt;shortName&gt;CCES&lt;/shortName&gt; &lt;/rma&gt;</pre>  |
| Mission order number                             | Optional  |
| Competition name                                 | If applicable, the name of a competition  |
| Validity*  | urine sample validity - tag: valid with the values "true" or "false". <b>For samples with a date_received on or after 16 March 2016 the validity status is calculated automatically based on the provided microbial contamination markers (any values included in the tag 'validity' will be disregarded).</b> For samples with a date_received before 16 March 2016 the validity column remains mandatory  |
| Screen T/E Ratio                                 | A number indicating the T/E ratio of the sample. For example, 2.6 would indicate a T/E ratio of 2.6:1. This field must only be used for samples received prior to January 1st 2014, it is not a mandatory field.  |
| pH   | A value indicating the pH of the sample. This is not a mandatory field; if it is not provided, the implication will be that the pH of the sample is within acceptable limits.   |
| Specific Gravity*                                | A value indicating the Specific Gravity of the sample - on the UI this corresponds with the field <i>Sample Specific Gravity (Initial Testing Procedure)</i> . This is a mandatory field for samples received after January 1st 2014.   |
| Sample Specific Gravity (Confirmation Procedure) | A value indicating the <i>Sample Specific Gravity (Confirmation Procedure)</i> for Urine samples.<br><b>For samples with a date_received that is equal to or later than 1 March 2019 AND with a Test result = AAF/ATF, it is mandatory to provide a value for the Sample Specific Gravity (Confirmation Procedure). This is for Urine A/B/B1/B2 samples.</b><br>Example:<br><pre>&lt;samplesAttributes&gt;   &lt;attribute&gt;     &lt;code&gt;pH&lt;/code&gt;     &lt;value&gt;7&lt;/value&gt;   &lt;/attribute&gt;   &lt;attribute&gt;     &lt;code&gt;specificGravity&lt;/code&gt;     &lt;value&gt;1.050&lt;/value&gt;   &lt;/attribute&gt;   &lt;attribute&gt;     &lt;code&gt;sampleSpecificGravityCP&lt;/code&gt;     &lt;value&gt;1.05&lt;/value&gt;   &lt;/attribute&gt;   &lt;attribute&gt;     &lt;code&gt;confirmedSpecificGravity&lt;/code&gt;     &lt;value&gt;1.02&lt;/value&gt;   &lt;/attribute&gt; &lt;/samplesAttributes&gt;</pre> |

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| Test Result*                             | A code indicating the test result following the sample analysis ("Negative", AAF, ATF, "NotAnalyzed").   |
| Test Result Reason                       | This is not a mandatory field.   |
| Date results reported                    | Date of reporting the results. This is not a mandatory field.  |
| Analysis Type(s) Performed               | <p>A list of analysis types that were performed on the sample. E.g. "EPO", "GC/C/IRMS", "Transfusion", "HBOCS", "hGH", and "Other". Not mandatory.<br/>For "GC/C/IRMS" a conclusion can be provided (consistent or not). <b>This conclusion is no longer effective for samples with a date_received on or after 16 March 2016.</b></p> <p>For Urine:</p> <p>ESAs (incl. recombinant EPOs and analogues) [internal code EPO]; GC/C/IRMS [code IRMS]; Insulins [code Insulin]; GHRF (GHRH/GHS/GHRP) [code GH]; GnRH [code GnRH]; IGF-1 analogues (code IGF1); Other (code Other)</p> <p><b>As of January 2016 the name will change for GHRF (GHRH/GHS/GHRP) [code GH] into GHRF (GHS/GHRP) [internal code remains GH]; also we will add a new attribute GHRF (GHRH) [internal code GHRH]</b></p> <p>For Blood:</p> <p>GH Isoforms [code hGH]; GH Biomarkers [code hGH Markers]; Blood Transfusions [code Transfusion]; HBOCS [code HBOCS]; ESAs (incl. recombinant EPOs and analogues) [code EPOb]; IGF-1 analogues [IGF1b]; Insulins [code Insulinsb]; Other [code Other]</p> |
| Details                                  | A free-text description (Analysis details/Explanation/ Opinion) of any relevant observations or analyses performed on the sample (e.g. sample tampering or received in poor condition, sample decomposition detected, unusual odor or color detected, etc.). This field is not mandatory. Please note that any departure from the International Standard for Laboratories must be reported to the Testing Authority outside of ADAMS, especially if the sample result is an adverse analytical finding.  |
| Send notification of results to          | A code indicating the short name of the organization the results have to be sent to. Multiple organizations are possible.  |
| LH-Analysis                              | <p>For Urine samples A, B, B1, B2 it is <i>optional</i> to provide a tag for:</p> <ul style="list-style-type: none"> <li><i>lh_analysis</i> : code can be either Negative, PAAF or ATF . If no tag is provided, it is assumed that No LH-Analysis was performed.</li> <li><i>lh_concentration</i>: a numeric value - positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7</li> <li><i>lh_lod</i>: a numeric value - positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7</li> </ul>  |
| Steroid profile variable*                | <p>A code and value indicating the name of the variable and the corresponding value. This field is mandatory for samples received as of January 1st 2014.<br/>Current codes are: androsterone, epitestosterone, 5b-androstanediol, 5a-androstanediol, testosterone, etiocholanolone, T/E.</p>  |
| Prohibited substance                     | The code, value and unit of the prohibited substance.  |
| Metabolite only                          | A flag indicating whether merely metabolite(s) are involved  |
| Mean concentration/ standard uncertainty | If a Threshold substance is concerned, the Mean/ Uncertainty values and units can be indicated   |
| Indicator Monitoring                     | To indicate whether the sample was analysed for the Monitoring programme. Tag: monitoring with possible values 'true' or 'false'   |
| Comments monitored                       | Comments on the monitored sample. Tag: commentsMonitored   |

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| <p>Monitored substance details</p>                                  | <pre> &lt;monitoring&gt;true&lt;/monitoring&gt; &lt;commentsMonitored&gt; My comments to the sample re the Monitoring programme&lt;/commentsMonitored&gt; &lt;monitoredSubstances&gt; &lt;substance&gt; &lt;code&gt;bupropion&lt;/code&gt; &lt;value&gt;100000&lt;/value&gt; &lt;unit&gt;IU/L&lt;/unit&gt; &lt;/substance&gt; &lt;/monitoredSubstances&gt; &lt;/result&gt; </pre>  |
| <p>Test method details</p>  | <pre> &lt;labMethodComments&gt;We used various methods for analysing this sample: N2, N78, ISO9007. &lt;/labMethodComments&gt;  &lt;labMethods&gt; &lt;labMethod&gt; &lt;code&gt;NIOC/1&lt;/code&gt; &lt;/labMethod&gt; &lt;labMethod&gt; &lt;code&gt;ISO/1&lt;/code&gt; &lt;/labMethod&gt; &lt;/labMethods&gt; </pre> <p>The comments are free text, whereas the 'code' is an ISO code as has been pre-defined by the Lab administrator.</p>  |
| <p><b>Microbial contamination parameters*, and confirmation</b></p> | <p><b>These fields become effective for Urine samples (type 'A') with a date received after 16 March 2016.</b></p> <p>ratio_5aand_a and ratio_5band_etio refer to 5aAND/A or 5AND/Etio and are both mandatory for the screening procedure.</p> <p>ratio_freet_totalt refers to "Free T/total T", and is not-mandatory.</p> <p>All are decimal values</p> <p>Similar for the confirmed values:</p> <p>ratio_5aand_a_confirmed and ratio_5band_etio_confirmed (ratio_freet_totalt doesn't require confirmation)</p> <pre> &lt;microbialContamination&gt; &lt;ratio_5aand_a&gt;0.0&lt;/ratio_5aand_a&gt; &lt;ratio_5band_etio&gt;0.0&lt;/ratio_5band_etio&gt; &lt;ratio_freet_totalt&gt;0.0&lt;/ratio_freet_totalt&gt; &lt;ratio_5aand_a_confirmed&gt;0.0&lt;/ratio_5aand_a_confirmed&gt; &lt;ratio_5band_etio_confirmed&gt;0.0&lt;/ratio_5band_etio_confirmed&gt; &lt;/microbialContamination&gt; </pre> <p>For samples other than type 'A' the microbial contamination parameters details are optional.</p> |

**Confirmed specific gravity\***

**This field is mandatory for samples with a date received after 1 Jan 2016**

When the user is confirming the result, the Specific Gravity must be confirmed. This is mandatory.

```
<sample code="testcodegv16nov2015A35" sampleAB="A">
  <type code="Urine">
    <analysisAttributes>
      <attribute>EPO</attribute>
      <attribute>OTHER</attribute>
    </analysisAttributes>
    <samplesAttributes>
      <attribute>
        <code>pH</code>
        <value>7</value>
      </attribute>
      <attribute>
        <code>specificGravity</code>
        <value>1.05</value>
      </attribute>
      <attribute>
        <code>confirmedSpecificGravity</code>
        <value>1.025</value>
      </attribute>
    </samplesAttributes>
    <details>details urine sample</details>
  </type>
  <collectionDate>2015-10-20</collectionDate>
  <receptionDate>2015-10-20</receptionDate>
</sample>
```

**Suspicious SP confirmation request status\***

**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.**

The confirmation request status is mandatory for a Suspicious Steroidal Passport under certain conditions.

The selection options are boolean values for "approvedByTA" or "notApprovedBy TA":

```
<confirmationRequestStatus>
  <approvedByTA>true</approvedByTA>
</confirmationRequestStatus>

or

<confirmationRequestStatus>
  <notApprovedByTA>true</notApprovedByTA>
  <reasonsForNotConfirming>
    <code>sample_inadequate_volume</code>
    <code>athlete_profile_normal</code>
    <code>teratio_valid_firsttest</code>
    <code>irms_method_unavailable</code>
    <code>other</code>
    <otherReason>otherReason</otherReason>
  </reasonsForNotConfirming>
</confirmationRequestStatus>
```

**Presence of confounding factors\***

**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.**

```
<confoundingFactors>
  <confoundingFactor>
    <code>ethylglucuronide</code>
    <presence>true</presence>
    <presenceConfirmed>true</presenceConfirmed>
    <concentration>5.11</concentration>
    <concentrationConfirmed>5.10</concentrationConfirmed>
  </confoundingFactor>
  <confoundingFactor>
    <code>5areductase</code>
    <presence>true</presence>
    <presenceConfirmed>true</presenceConfirmed>
  </confoundingFactor>
  <confoundingFactor>
    <code>ketoconazole</code>
    <presence>true</presence>
    <presenceConfirmed>true</presenceConfirmed>
  </confoundingFactor>
  <confoundingFactor>
    <code>hCG</code>
    <presence>true</presence>
    <presenceConfirmed>true</presenceConfirmed>
  </confoundingFactor>
  <confoundingFactor>
    <code>steroids</code>
    <presence>false</presence>
    <presenceConfirmed>true</presenceConfirmed>
  </confoundingFactor>
  <confoundingFactor>
    <code>masking</code>
    <presence>true</presence>
    <presenceConfirmed>true</presenceConfirmed>
  </confoundingFactor>
</confoundingFactors>
</result>
```

Specific code of the **Confounding Factor** variable. Possible values: 'ethylglucuronide' for 'Ethyl Glucuronide'; '5areductase' for '5a-reductase inhibitors'; 'ketoconazole' for 'ketoconazole or similar'; 'hCG' for 'Heterodimeric hCG'; 'steroids' for 'Anabolic Steroids'; 'masking' for 'Masking Agents and diuretics'; 'aromatase' for 'aromatase inhibitors' and 'anti\_estrogens' for 'anti-estrogens' .

If Lab results are entered after the start date of the TD2016EAAS & TD2016IRMS Reporting in Jan 2016 AND the sample\_type = Urine in the file, then ALL Confounding factors should be present in the Import file.

An exception: If the gender in a Urine Lab result is Female or X (non-Male), the confounding factor hCG should not be mandatory for A, B, B1 and B2 samples. This holds for both the Initial and Confirmed value. If the hCG initial = yes for the Female athlete, there is no need to provide a confirmed value.

**Presence:** Boolean with values True (yes-confounding factor is present) or False (no - confounding factor is not present). Mandatory for all confounding factors.

Decimal value for the estimated **concentration of the confounding factor** *Ethyl Glucuronide*. Optional, yet the Lab should enter a value if concentration is above 5 ug/mL.

|  |   |
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| <p><b>Confirmation of the presence of confounding factors*</b></p> | <p><b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b></p> <p>Specific code of the <b>Confirmed Confounding Factor</b> variable. It is mandatory for all CFs where CF-presence (initial value) = 'True' – the Lab result should eventually contain a CF_code_confirmed = CF_code</p> <p><b>Presenceconfirmed:</b> Boolean with values True (yes- <i>Confirmed</i> confounding factor is present) or False (no- <i>Confirmed</i> confounding factor is not present). It is mandatory for all CFs where CF-presence (initial value) = 'True' – the file should then contain a CF_code_confirmed = CF_code AND a CF_presence_confirmed</p> <p><b>Concentrationconfirmed:</b> decimal value for the <i>Confirmed</i> estimated concentration of the confounding factor <i>Ethyl Glucuronide</i>. It is mandatory if for any index (CF_code_confirmed[index] = 'ethylglucuronide' AND CF_presence_confirmed[index] = 'True')</p>   |
| <p><b>IRMS Target Compounds*</b></p>                               | <p><b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b></p> <p><b>&lt;code&gt;:</b> specific code of the IRMS Target_Compound variable. If Lab results are entered after the start date of the TD2016EAAS &amp; TD2016IRMS Reporting in Jan 2016 AND the analysis_attribute = IRMS in the file, then at least one TC should be present in the Import file. Current possible values with the specific code between brackets: testosterone (T), epitestosterone (E), androsterone (A), etiocholanolone (Etio), "5-androstane-3,17-diol" (5aAdiol), "5-androstane-3,17-diol" (5bAdiol), 19-NA (19-NA), formestane (formestane), boldenone (boldenone), boldenone metabolites (boldenonemet), other TC (other-TC).</p> <p><b>&lt;value&gt;: (0/00)</b> decimal value or integer as per ADM2 settings for each variable. Mandatory if a TC_code is included for the same code.</p> <p><b>&lt;uc&gt;:</b> uc (0/00) decimal value or integer as per ADM2 settings for each variable. Mandatory if a TC_code is included for the same code.</p> |
| <p><b>Endogenous Reference Compounds*</b></p>                      | <p><b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b></p> <p><b>&lt;code&gt;:</b> specific code of the Endogenous Reference Compound variable for IRMS. Can only be present if the analysis_attribute = IRMS; If nothing is entered, then the default is PD. Only one ERC to be entered per result. Possible values: Pregnanediol (PD), 5-androst-16-en-3-ol (16-en), 11-hydroxyandrosterone (11-OHA), 11-ketoetiocholanolone (11-O-Etio), Androsterone (Androsterone)</p> <p><b>&lt;value&gt;:</b> (0/00) decimal value or integer as per ADM2 settings for the variable. Mandatory if the analysis_attribute = IRMS is included.</p> <p><b>&lt;uc&gt;:</b> uc (0/00) decimal value or integer as per ADM2 settings for the variable. Mandatory if the analysis_attribute = IRMS is included.</p>   |

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| <b>Overall IRMS conclusion*</b>        | <p><b>This variable becomes effective as per release 4.7.0</b></p> <p>Tag irmsConclusion with the possible values:</p> <ul style="list-style-type: none"><li>• Negative</li><li>• AAF</li><li>• ATF</li><li>• ATF_technical</li><li>• ATF_opinion</li></ul> <p>This field is <b>mandatory</b> if analysis_attribute = IRMS and the date_received is after 1 Jan 2016 (TDEAAS date) and creation_date is after 16 March 2016 (IRMS-details tab launch date).</p> <pre>&lt;/header&gt; - &lt;body&gt;   - &lt;result valid="true" lin="labInternNbr123"&gt;     &lt;testResult code="Negative" irmsConclusion="ATF_technical"/&gt;     - &lt;athlete gender="M"&gt;       &lt;sport code="DN"/&gt;       &lt;discipline code="10-dance"/&gt;     &lt;/athlete&gt;   - &lt;sample code="U2014.03.07-0800" sampleAB="A"&gt;     - &lt;type code="Urine"&gt;       - &lt;analysisAttributes&gt;</pre> |
| <b>Comments for the IRMS reporting</b> | <p><b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b></p> <p>free text comments to the IRMS analysis for the sample (optional)</p>  |