

# File format - Update Lab results

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

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

- For the CSV Import/Update file the column name *sample\_specific\_gravity\_CP* 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 field *sample\_specific\_gravity\_CP* is different from and functionally NOT related to the existing field *confirmed\_specific\_gravity* that is exclusively associated with the Steroid Profile.

## 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 four values Negative / PAAF / ATF / blank. It is not mandatory to include neither the column name nor any value
- *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)

## 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.

## ADAMS Release 4.1.1 - 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; Confirmation will be required
- 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)

### Important rules for the Update:

- if the initial value for a Confounding factor is set to "yes", then for the Batch Update it will be enforced to provide a confirmed value
- if the *date\_received* of the sample is on or after 16 March, the GC/C/IRMS conclusion (column *irms\_consistent*) no longer applies
- if results with a *date\_received* before 1 Jan 2016 are updated with new IRMS details (target compounds, endogenous reference compounds, confounding factors etc), the system will require complete relevant details

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

The following will be effective as of the start date of the TD2016EAAS & TD2016IRMS Reporting in 2016.

- **Sample collection date is mandatory** if the sample is received after the start date of the TD2016EAAS & TD2016IRMS Reporting in 2016

[Click here for a sample CSV file for ADAMS v4.0](#)

Each sample record in the CSV/XML file should contain at least the mandatory fields. Once the update is triggered for the sample record in the input file, ADAMS will look for the corresponding result record in the database, based on the unique identification of 5 fields: *sample code, sample type, sample AB, Lab name, date received*.

As a general rule, each time an update is proposed for a result record in the database, ADAMS will validate on mandatory fields and business rules as they are prevalent on the Lab results page. ADAMS will apply the validity-check on the resultant of the value in the database and the value in the input file.

Below are comments on updatable fields (for the CSV file the sequence of the columns is not relevant).

Field	Column header	Comments	Example(s)
Sample Code	sample_code <b>MANDATORY</b>	No update allowed. The sample code must be unique in combination with the sample type, sampleAB, the Lab name and the Date received by the Lab.	"1479265"
Sample Type	sample_type <b>MANDATORY</b>	No update allowed.	"URINE" "BLOOD"
Sample A or B	sampleAB <b>MANDATORY</b>	No update allowed. <b>It is possible to have the values "B1" and "B2" for samples reported after January 1st 2015. (ADAMS Release 4.0)</b>	"A" "B", "B1", "B2"
Date Received by Lab	date_received <b>MANDATORY</b>	No update allowed (yyyy-MM-dd)	"2012-01-12" "2012-11-28"
Date of Sample Collection	sample_collection_date	There are business rules, such as date_received can not be earlier than sample_collection date etc.  <b>This field is mandatory for samples with a date received after 1 Jan 2016</b>	"2012-01-28"
Date results reported	analysis_report_date	There are business rules, such as analysis_report_date can not be earlier than sample_collection date etc.	"2012-04-13"
Analysis date	Analysis_date	There are business rules, such as analysis_date can not be earlier than sample_collection date etc.	"2012-04-13"
Analysis time	Analysis_time		"9:10"
Country	country		"US or "USA"
Region	region		"US-KY"
City	city		"Montreal"
lin	lin		"A127692"
Mission Order #	mo_number		"M-127698"
Screen T/E Ratio	te_ratio	<b>Only relevant for results received before January 1st 2014.</b>	"2.4"
pH	ph		"5"
Specific gravity	specific_gravity	On the UI this corresponds with the field <i>Sample Specific Gravity (Initial Testing Procedure)</i> .  Becomes mandatory if a Steroid profile variable is entered. <b>This field is mandatory for results received after January 1st 2014</b>	"1.003" "2.3612"
Sample Specific Gravity (Confirmation Procedure)	sample_specific_gravity_CP	<b>Introduced in ADAMS Release 7 May 2019</b>  A value indicating the <i>Sample Specific Gravity (Confirmation Procedure)</i> for Urine sample.  value (eg. 1.025) with 3 digits after comma  Min - Max: [1.001 - 1.050]  For samples with a date_received that is equal to or later than <b>1 March 2019</b> AND with a Test result = <b>AAF/ATF</b> , it is <b>mandatory</b> to provide a value for the Sample Specific Gravity (Confirmation Procedure). This is for Urine A/B/B1/B2 samples.	"1.003" "2.3612"

Validity	valid	urine sample validity. <b>This field is mandatory for results received after January 1st 2014</b>  <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 column 'valid' will be disregarded). For samples with a date_received before 16 March 2016 the validity column remains mandatory</b>	"Yes" or "No"
Send notification of results to	send_result_to	The new value overwrites the old value. Even if the old value has multiple organization names e.g. FINA CCES and the new value is NADA, the entire FINA CCES will be replaced by NADA	"UCI" "CCES"
Test Authority	ta	<b>This is a mandatory field for samples reported after January 1st 2015. (ADAMS Release 4.0)</b>	"ITTF"
Sample Collection Authority	sca	If the mandatory SCA is missing in the database and in the file, AND the status of the record is (partially) submitted, then an error is given.	"AIBA"
Results Management Authority	rma	<b>This is an optional field for samples reported after January 1st 2015. (ADAMS Release 4.0)</b>	
Test Type	test_type		"IC" "OOC"
Name of the competition	competition_name		"2011 Worldcup"
Sport	sport_code	The combination of sport and discipline is validated.	"SK" "AQ"
Sport discipline	discipline_code	One may indicate only the discipline in the file (sport in the database is taken)	"SK" "AQ"
Athlete Gender	gender		"M", "F", "X"
Test result	test_result	If an invalid Test result transition is proposed, then the record is rejected.	"Negative" "NotAnalyzed" "AAF", "ATF"
Test Result reason	test_result_reason		"text"
Special type of analysis	analysis_attribute	The new value overwrites the old value, even if the old value has multiple attributes.  • For Urine:  ESAs (incl. recombinant EPOs and analogues) [internal code EPO]; GC/C/IRMS [code IRMS]; Insulins [code Insulin]; <b>GHRF (GHRH/GHS/GHRP) [code GH] see below</b> ; GnRH [code GnRH]; IGF-1 analogues (code IGF1); Other (code Other)  <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>  • For Blood:  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]  ** ADAMS 3.5 ** in case a hGH or hGH Markers substance is included in the Update file or present in the database, then the resultant of the update makes it necessary to have the hGH or hGH Markers attribute included for the resultant Lab result as well	"EPO", "hGH" "GC/C/IRMS" "Other", "hGH Markers" "EPO Other"
GC/C/IRMS conclusion	irms_consistent	When a value is specified, the analysis_attribute is the file should be 'IRMS'  <b>This will no longer be effective when the new IRMS functionality will be implemented as of 16 March 2016.</b>	"yes" "no"
Analysis Details / Explanation	analysis_details	Free text (in case of a partially submitted ATF, this text can also be updated when the record is 'locked')	

LH-Analysis	lh_analysis lh_concentration lh_lod	Applicable to Urine samples A, B, B1, B2. The new <b>non-blank</b> value in the file overwrites the old value in the database.  <ul style="list-style-type: none"> <li>• <i>lh_analysis</i> : value in the file can be either Negative, PAAF, ATF or blank. A blank value does NOT overwrite a value in the database</li> <li>• <i>lh_concentration</i>: value in the file can be a positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7</li> <li>• <i>lh_lod</i>: value in the file can be a positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7</li> </ul>	"Negative" "PAAF" "ATF" "" "0.2" "1.9" "2" "0" "8"
Prohibited substance	prohibited_substance[index]	The index is a number ranging from 1 to 10. If the record is not 'locked', the values from the file supersede the values in the database, otherwise any new substances will be added to the database. If a metabolite is included in the file, the substance becomes mandatory.	"danazol"
Prohibited substance value	prohibited_substance_value[index]		"2.3"
Prohibited substance unit	prohibited_substance_unit[index]		"IU/L"
Prohibited substance details	prohibited_substance_details[index]	Free text (in case of a partially submitted ATF, this text can also be updated when the record is 'locked')	"free text"
Metabolite-only indicator	prohibited_substance_metabolite_only[index]		"Y" "N"
Metabolite	prohibited_substance_metabolite[index]	Free text for the metabolite. If the record is not 'locked', the values from the file supersede the values in the database, otherwise any new metabolites are added to the database.	"text"
Prohibited substance value	prohibited_substance_metabolite_value[index]		"4.15"
Prohibited substance unit	prohibited_substance_metabolite_unit[index]		"IU/L"
Confirmed value of the steroid profile variable with the same index	steroid_profile_variable_confirmed[index]	Confirmed valued for steroid profile variable	
Uncertainty of the steroid profile variable with the same index	steroid_profile_variable_uc[index]	No - If steroid_profile_variable_confirmed value is added then this value should be added - Added Since V3.4	
Steroid profile variables	Steroid_profile_variable_code[index]	The index is from 1 to 6. <b>This field is mandatory for results received after January 1st 2014</b>  SP variables can always be added (even if the result is 'locked'). The Specific Gravity is mandatory when an SP variable assumes a value.	Current codes are: androsterone, epitestosterone, 5b-androstanediol, 5a-androstanediol, testosterone, etiocholanolone, T/E.
Steroid profile variables value	Steroid_profile_variable_value[index]	<b>For samples with a received date after 1 Jan 2016, a value of '-2' will be allowed for Epitestosterone</b>	"12"
Threshold substance – mean value	prohibited_substance_mean[index]		"2.1234"
Threshold substance – mean unit	prohibited_substance_mean_unit[index]		"IU/L"
Threshold substance – uncertainty	prohibited_substance_uncertainty[index]		"3.1234"
Threshold substance – uncertainty unit	prohibited_substance_uncertainty_unit[index]		"IU/L"
Indicator Monitoring	monitoring	It is possible to indicate 'y'(es) for monitoring while leaving the monitored_substance data blank. If you however provide values for monitored_substance, then the 'y' should be on for 'monitoring' ('n' and empty are then not allowed).	"y", "n", ""
Comments Monitored	comments_monitored		"comments"

Monitored substance	monitored_substance[index]	The specific substance code has to be used. For the codes see the download centre on our website. The index is a number ranging from 1 to 15.	"caffeine"
Monitored substance value	monitored_substance_value[index]		"2.3"
Monitored substance unit	monitored_substance_unit[index]		"IU/L"
<b>Microbial contamination parameters, and confirmation</b>	ratio_5aand_a ratio_5band_etio ratio_freet_totalt ratio_5aand_a_confirmed ratio_5band_etio_confirmed	<b>These fields become effective for Urine samples (type 'A') with a date received after 16 March 2016.</b>  ratio_5aand_a and ratio_5band_etio refer to 5aAND/A or 5AND/Etio and are both mandatory for the screening procedure.  ratio_freet_totalt refers to "Free T/total T", which is not-mandatory.  All are decimal values  Similar for the confirmed values:  ratio_5aand_a_confirmed, ratio_5band_etio_confirmed (ratio_freet_totalt doesn't require confirmation)	
<b>Confirmed specific gravity</b>	confirmed_specific_gravity	<b>This field is mandatory for Urine samples with a date received after 1 Jan 2016</b>  When the user is confirming the result, the Specific Gravity must be confirmed. This is mandatory.	
<b>Suspicious SP confirmation request status</b>	confirmation_request_status samplea_inadequate_volume normal_athlete_profile valid_teratio_firsstest irms_method_unavailable other_reason	<b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b>  The confirmation request status is mandatory for a Suspicious Steroidal Passport under certain conditions.  The selection options are boolean values (true/false)	
<b>Presence of confounding factors</b>	CF_code[index] CF_presence[index] CF_conc[index] CF_unit[index]	<b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b>  <b>CF_code[index]:</b> 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'. The index number ranges from 1 to 6.  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 CF_codes for index 1 to 6 should be present in the Import file.  <b>CF_presence[index]:</b> Boolean with values True (yes-confounding factor is present) or False (no - confounding factor is not present). Mandatory for all indices from 1 to 6.  <b>CF_conc[index]:</b> decimal value for the estimated concentration of the confounding factor. This is currently only applicable to <i>Ethyl Glucuronide</i> : it is an optional field, yet the Lab should enter a value if concentration is above 5 ug/mL.  <b>CF_unit[index]:</b> unit for the estimated concentration of the confounding factor. This is currently only applicable to <i>Ethyl Glucuronide</i> , and defaults to ug/mL (optional field).	
<b>Confirmation of the presence of confounding factors</b>	CF_presence_confirmed[index] CF_conc_confirmed[index]	<b>These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.</b>  The CF_code[index] will be used.  <b>CF_presence_confirmed[index]:</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  <b>CF_conc_confirmed[index]:</b> decimal value for the <i>Confirmed</i> estimated concentration of the confounding factor. This is currently only applicable to <i>Ethyl Glucuronide</i> . It is mandatory if for any index (CF_code_confirmed[index] = 'ethylglucuronide' AND CF_presence_confirmed[index] = 'True').	

<b>IRMS Target Compounds</b>	TC_variable_code[index] TC_variable_d_value[index] TC_variable_u_value[index]	<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>TC_variable_code[index]:</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. Index should not have a limit. 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>TC_variable_d_value[index]:</b> (0/00) decimal value or integer as per ADM2 settings for each variable. Mandatory if a TC_code is included for the same index.</p> <p><b>TC_variable_u_value[index]:</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 index.</p>	
<b>Endogenous Reference Compounds</b>	ERC_variable_code ERC_variable_d_value ERC_variable_u_value	<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>ERC_variable_code:</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. Possible values: Pregnenediol (PD), 5-androst-16-en-3-ol (16-en), 11-hydroxyandrosterone (11-OHA), 11-ketoetiocholanolone (11-O-Etio)</p> <p><b>ERC_variable_d_value:</b> (0/00) decimal value or integer as per ADM2 settings for the variable. Mandatory if the analysis_attribute = IRMS is included. If there is no ERC-code then it is assumed that it is for PD.</p> <p><b>ERC_variable_u_value:</b> uc (0/00) decimal value or integer as per ADM2 settings for the variable. Mandatory if the analysis_attribute = IRMS is included. If there is no ERC-code then it is assumed that it is for PD.</p>	
<b>Comments for the IRMS reporting</b>	IRMS_comments	free text comments to the IRMS analysis for the sample (optional)  <p><b>This field becomes effective as per 16 March 2016 and applies to Urine samples with a date received after 1 Jan 2016.</b></p>	
<b>Overall IRMS conclusion</b>	irms_conclusion	<p><b>This variable becomes effective as per release 4.7.0</b></p> <p>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>	