CSV file

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 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.

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 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). A value entered for the LOD implies that the "concentration of LH was less than this specified LOD'.

CSV template: Example CSV Import - 5 June 2018.csv

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; Confirmation will be required

- Labs will have to indicate whether the TA approved or not the *suspicious confirmation procedure request*: this information is <u>mandatory</u> under certain conditions
- *Presence/Absence of Confounding factors, as per ITP*: this information is <u>mandatory</u>
- *Confirmation of the presence of confounding factors*: this information is <u>mandatory</u>

- *values of IRMS Target Compounds, and associated uc*: at least one is <u>mandatory</u>
- *values of Endogenous Reference Compounds, and associated uc*: one is <u>mandatory</u> (preferentially PDiol)
- *IRMS Comments*: free text (optional)

****** **NEW**: Click here for a **sample CSV file** for release 4.1.1 in March   **********NEW:** containing *confirmed* values for Microbial contamination markers

<u>Important rules for the Import:</u>

- if the date_received of the sample is <u>on or after 16 March</u>, the microbial confirmation markers are required (not needed if *before 16 March*)
- if a Confirmed value is provided in the CSV 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 <u>on or after 16 March</u> , the GC/C/IRMS conclusion (column irms_consistent) no longer applies

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ADAMS 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 **<u>1 January 2016</u>**.

- The existing field *Sample collection date* is <u>mandatory</u> if the date received of the Urine/Blood sample is after 1 January 2016
- Additional field in CSV/XML: *Confirmed specific gravity* is <u>mandatory</u> 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

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1 January 2016: Analysis attribute for Urine

As of <u>1 January 2016</u> 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]*

This file specifies the CSV file import format for lab analysis results. It has been designed to be as simple as possible, with only one line per sample and a minimum set of mandatory data per sample. The sequence of the columns is not relevant.
The mandatory fields per sample match the fields required in the ADAMS application. The status of each result record is determined by the user action (e.g. POST) taken immediately following import.

MANDATORY FIELDS

Field	Column header	Description	Example(s)
Sample Code	sample_code	This is the identifying number on the sample collection kit. The sample code must be unique in combination with the sample type, the Lab name and the Date received by the Lab.	"1479265"
Sample Type	sample_type	This specifies the type of sample analyzed.	"URINE" "BLOOD"
Date Received by Lab	date_received	This specifies the date that the sample was received by the laboratory (yyyy-MM-dd)	"2006-01-12" "2006-11-28"

Sample Collection Authority	sca	Short name of the ADO organization in charge of the Sample Collection. For the codes see the download centre on our website.	"AIBA"
Testing Authority	ta	This field contains the short-name identifier of the Testing Agency, which is generally the laboratory's customer. This is a mandatory field for samples reported after January 1st 2015. (ADAMS Release 4.0)	"ITTF"
Test Type	test_type	This field is used to indicate whether the sample was collected in- or out-of-competition	"IC" "OOC"
Sport	sport_code	This field is used to report the sport of the athlete who contributed the sample. The WADA sport identifier code must be used in this field, not the sport's name. For the codes see the download centre on our website.	"SK" "AQ"
Sport discipline	discipline_code	This sport discipline's specific code. For the codes see the download centre on our website.	"SK" "AQ"
Test result	test_result	Negative, NotAnalyzed, ATF, AAF	"Negative" "NotAnalyzed" "AAF" , "ATF"
Specific Gravity	specific_gravity	On the UI this corresponds with the field *Sample Specific Gravity (Initial Testing Procedure)*. value (eg. 1.025) with 3 digits after comma Min - Max: [1.001 - 1.050]	1.025
Sample Specific Gravity (Confirmation Procedure)	sample_specific_gravity_CP	**Introduced in ADAMS Release 7 May 2019** A value indicating the *Sample Specific Gravity (Confirmation Procedure)* 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 **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.	1.025
Validity	valid	urine sample validity. **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**	"Yes" or "No"
Steroid profile variables	Steroid_profile_variable_code[index]	Specific code of the steroid profile variable.This field is mandatory for results received after January 1st 2014	Current codes are: androsterone, epitestosterone, 5b-androstanediol, 5a-androstanediol, testosterone, etiocholanolone, T/E.
Steroid profile variables	Steroid_profile_variable_value[index]	Decimal value or integer as per ADM2 settings for each variable. **For samples with a received date after 1 Jan 2016, a value of '-2' will be allowed for Epitestosterone.**	"12"
Specific gravity	specific_gravity	This field specifies the specific gravity analyzed in the sample. Decimal value with max. 4 digits after the decimal point. Any extra digits will be discarded when saving the results. With the introduction of the Steroid Profile it becomes mandatory with range [1.001 - 1.050] set by Adm2. This field is mandatory for results received after January 1st 2014	"1.003" "1.050"

Date of Sample Collection	sample_collection_date	This field contains the sample collection date (yyyy-MM-dd) **This field is mandatory for samples with a date received after 1 Jan 2016**	"2006-01-28"
Microbial contamination parameters, and confirmation	ratio_5aand_a ratio_5band_etio ratio_freet_totalt ratio_5aand_a_confirmed ratio_5band_etio_confirmed	**These fields become effective for Urine samples (type 'A') with a date received after 16 March 2016.** 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) For samples other than type 'A' the microbial contamination parameters details are optional.	ratio_5aand_a: "0.10234" ratio_5band_etio: "010246" ratio_freet_totalt: "0.0203" ratio_5aand_a_confirmed: 0.10235 ratio_5band_etio_confirmed: 0.10234
Confirmed specific gravity	confirmed_specific_gravity	**This field is mandatory for Urine 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.	"1.003"
Suspicious SP confirmation request status	confirmation_request_status samplea_inadequate_volume normal_athlete_profile valid_teratio_firsttest irms_method_unavailable other_reason	**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 (true/false)	
Presence of confounding factors	CF_code[index] CF_presence[index] CF_conc[index] CF_unit[index]	**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.** **CF_code[index]:** 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'** . The index number ranges from 1 to 8. 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. **CF_presence[index]:** Boolean with values True (yes-confounding factor is present) or False (no - confounding factor is not present). Mandatory for all indices from 1 to 8. **CF_conc[index]:** decimal value for the estimated concentration of the confounding factor. This is currently only applicable to *Ethyl Glucuronide'* : it is an optional field, yet the Lab should enter a value if concentration is above 5 ug/mL. **CF_unit[index]:** unit for the estimated concentration of the confounding factor. This is currently only applicable to *Ethyl Glucuronide'* , and defaults to ug/mL (optional field).	CF_code[1]=ethylglucuronide CF_presence[1]=True CF_conc[1]=7 CF_unit[1]=ug/mL

Confirmation of the presence of confounding factors	CF_presence_confirmed[index] CF_conc_confirmed[index]	**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.** The CF_code[index] will be used. **CF_presence_confirmed[index]:** Boolean with values True (yes-*Confirmed* confounding factor is present) or False (no- *Confirmed* 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 **CF_conc_confirmed[index]:** decimal value for the *Confirmed* estimated concentration of the confounding factor. This is currently only applicable to *Ethyl Glucuronide'*. It is mandatory if for any index (CF_code_confirmed[index] = 'ethylglucuronide' AND CF_presence_confirmed[index] = 'True').	CF_presence_confirmed[1]=True CF_conc_confirmed[1]=7
IRMS Target Compounds	TC_variable_code[index] TC_variable_d_value[index] TC_variable_u_value[index]	**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.** **TC_variable_code[index]:** specific code of the IRMS Target_Compound variable. If Lab results are entered after the start date of the TD2016EAAS & 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). **TC_variable_d_value[index]: (0/00)** decimal value or integer as per ADM2 settings for each variable. Mandatory if a TC_code is included for the same index. **TC_variable_u_value[index]:** 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.	TC_variable_code[1]=boldenone
Endogenous Reference Compounds	ERC_variable_code ERC_variable_d_value ERC_variable_u_value	**These fields become effective as per 16 March 2016 and apply to Urine samples with a date received after 1 Jan 2016.** **ERC_variable_code:** 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: Pregnanediol (PD), 5-androst-16-en-3-ol (16-en), 11-hydroxyandrosterone (11-OHA), 11-ketoetiocholanolone (11-O-Etio), Androsterone (Androsterone) **ERC_variable_d_value:** (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. **ERC_variable_u_value:** 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.	ERC_variable_code=16-en
Overall IRMS conclusion	irms_conclusion	**This variable becomes effective as per release 4.7.0** The possible values: • Negative • AAF • ATF • ATF_technical • ATF_opinion This field is **mandatory** 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).	irms_conclusion = AAF irms_conclusion = ATF_technical

OPTIONAL FIELDS

Field	Column header	Description	Example(s)
Results Management Authority	rma	This field contains the short-name identifier of the Results Management Authority, which will follow up on the result with the Results Management. This is an *optional* field for samples reported after January 1st 2015. (ADAMS Release 4.0)	"ITTF"
Sample A or B	sampleAB	Allowable values: A, B, B1, B2 . If left blank, then sample A will be assumed. It is possible to specify the values "B1" and "B2" for samples reported after January 1st 2015. (ADAMS Release 4.0)	"A" "B" , "B1", "B2" " "
Test Result reason	test_result_reason	The reason substantiating the result selected. (This text will be added to the activity generated at creation)	"text"
Analysis Details / Explanation	analysis_details	This field is used to provide any relevant information concerning the analyses performed by the laboratory or specific observations made.	"The samples were analyzed for anabolic and masking agents, diuretics, and hCG using methods 1001, 2001, and 6001."
Lab Internal Reference Number	lin	This field is used to record the internal sample code assigned to the sample upon receipt by the laboratory.	"A127692" "A127693"
Mission Order Number	mo_number	This field is used to record the mission order/ sample collection order number (if available).	"M-127698"
Date of Analysis Report	analysis_report_date	This field contains the date that the sample analysis results were reported to the TA. (yyyy-MM-dd)	"2006-04-13"
Country (of Sample Collection)	country	This field contains the country code of where the sample was collected. It can be provided in either 2-character ISO format or 3-character Olympic format. For the codes see the download centre on our website.	"EE" or "EST" "US" or "USA"
Region (of Sample Collection)	region	This field contains an ISO code identifying the region within the country of sample collection. For the codes see the download centre on our website.	"CA-AB" "US-KY"
City (of Sample Collection)	city	This field contains the city where the sample was collected.	"Montreal" "Warsaw"
Athlete Gender	gender	This field specifies the gender of the athlete who provided the sample. Empty means 'X'	"M" "F" "X"
Screen T/E Ratio	te_ratio	This field specifies the T/E ratio analyzed in the sample. Decimal value with max. 2 digits after the decimal point. Any extra digits will be discarded when saving the results (do not include any other modifier such as ":1"). Only for the import of results received before January 1st 2014.	"2.4" "4.62"
pH	ph	This field specifies the pH analyzed in the sample. Decimal value with max. 2 digits after the decimal point. Any extra digits will be discarded when saving the results.	"5" "2.4"

Special type of analysis	analysis_attribute	Default is blank. Multiple types are allowed but need to be separated by a '|'. ▪ For Urine: ESAs (incl. recombinant EPOs and analogues) [internal code EPO]; GC/C/IRMS [code IRMS] ; Insulins [code Insulin] ; GHR F (GHRH/GHS/GHRP) [code GH] see below; GnRH [code GnRH] ; IGF-1 analogues (code IGF1); Other (code Other) **As of <u>January 2016</u> 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]* ● 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 [code IGF1b] ; Insulins [code Insulinsb] ; Other [code Other] ** ADAMS 3.5 ** in case a hGH or hGH Markers substance is included in the import file, then the hGH or hGH Markers attribute becomes mandatory.	"EPO" "IRMS" "Other" "EPO|IRMS", as of Jan 2016: GHRH "hGH|Other" "hGH Markers" "hGH|EPOb|hGH Markers"
GC/C/IRMS conclusion	irms_consistent	This field is relevant in case the analysis attribute contains the value GC/C/IRMS . When left empty AND the Sample type is Urine AND the analysis attribute contains the value GC/C/IRMS, then: ● If the result is AAF, then irms_consistent is set to 'yes' ● If the result is Negative or ATF, the irms_consistent is set to 'no' **This will no longer be effective when the new IRMS functionality will be implemented as of 16 March 2016.**	"yes" "no" empty
Comments for the IRMS reporting	IRMS_comments	free text comments to the IRMS analysis for the sample (optional) **This field becomes effective as per 16 March 2016 and applies to Urine samples with a date received after 1 Jan 2016.**	
Send notification of results to	send_result_to	This field specifies the short name of the organization(s) to be notified of the result. For the codes see the download centre on our website.	"UCI" "CCES"
Name of the competition	competition_name	In case the test_type is 'IC' (in-competition): free text	"2011 Worldcup"
LH-Analysis	lh_analysis lh_concentration lh_lod	For Urine samples A, B, B1, B2 it is *optional* to provide the LH-Analysis details: ● *lh_analysis* : value can be either Negative, PAAF, ATF or blank. Blank value implies that No LH-Analysis was performed. ● *lh_concentration*: a numeric value - positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7 ● *lh_lod*: a numeric value - positive integer or a decimal with 1 digit after decimal point, e.g. 3 or 2.7	"Negative" "PAAF" "ATF" " " "0.2" "1.9" "2" "0" "8"
Prohibited substance	prohibited_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 10. *A maximum number of 10 prohibited substance columns (and associated prohibited substance value and prohibited substance unit columns) may be included in a file*. If a metabolite is included in the file the substance becomes mandatory.	"danazol"
Prohibited substance value	prohibited_substance_value[index]	The decimal value of the prohibited substance [index]	"2.3"

Prohibited substance unit	prohibited_substance_unit[index]	The specific code of the unit of measure for analysis related to the prohibited substance[index]	"IU/L"
Prohibited substance details	prohibited_substance_details[index]	Free text for the details concerning finding.	"free text"
Metabolite-only indicator	prohibited_substance_metabolite_only[index]	Indicator that signifies whether metabolite(s) only were detected. Default is 'N'. If 'Y' then the substance becomes mandatory.	"Y" "N"
Metabolite	prohibited_substance_metabolite[index]	Free text for the metabolite. The index is a number ranging from 1 to 10. *A maximum number of 10 metabolite columns (and associated metabolite value and metabolite unit columns) may be included in a file.*	"text"
Prohibited substance value	prohibited_substance_metabolite_value[index]	The decimal value of the metabolite [index]	"4.15"
Prohibited substance unit	prohibited_substance_metabolite_unit[index]	The specific code of the unit of measure for analysis related to the metabolite[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	
Threshold substance – mean value	prohibited_substance_mean[index]	Decimal value of the Mean when a special threshold substance is concerned (max. 5 digits apart from the decimal point)	"2.1234"
Threshold substance – mean unit	prohibited_substance_mean_unit[index]	Specific code of the unit of measure	"IU/L"
Threshold substance – uncertainty	prohibited_substance_uncertainty[index]	Decimal value of the Uncertainty when a special threshold substance is concerned (max. 5 digits apart from the decimal point)	"3.1234"
Threshold substance – uncertainty unit	prohibited_substance_uncertainty_unit[index]	Specific code of the unit of measure	"IU/L"
Indicator Monitoring	monitoring	To indicate whether the sample was analysed for the Monitoring program or not. Possible values : 'y', 'n', or empty. Default is No. 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 to the monitored sample (per sample and not per substance)	"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]	The decimal value of the monitored substance [index]	"2.3"
Monitored substance unit	monitored_substance_unit[index]	The specific code of the unit of measure for analysis related to the monitored substance[index]	"IU/L"
Test method code	test_method_code[index]	This code has to be a valid code as has been pre-defined by the Lab-administrator. The index is a number ranging from 1 to 15.	"ISO906"

| Test method comments	methods_comments	A free text field to detail the test method codes utilized in the analysis and which will appear on the ADAMS test report.	"We used various methods for analysing this sample: N2, N78, ISO9067."

Date Format

Please note that if you are using an older version of Excel, the date format may not be shown as yyyy-MM-dd but as dd/MM/yyyy. You can find out the actual values however by opening your CSV-file in Wordpad. So don't be misled by how it is displayed in Excel.

Where do I find the codes to be used in my import-file for the SportDiscipline, Country, Region, Substance and short names of the TA?

The codes to use for sport, discipline, country and region are listed in the following file, available on the WADA Web site: http://www.wada-ama.org/Documents/ADAMS/Training_User_Guides/ ADAMS_Codes_for_Sport_Discipline_Country_Region.pdf
The code list for substances can also be found in the download centre: http://www.wada-ama.org/en/ADAMS/ADAMS-Training-and-User-guides
If you do not have the organization short name for the TA, you may click the "contact" link in the taskbar in ADAMS, and perform a search. The short name is shown before the hyphen and the long organization name, as in the following example for FEI:
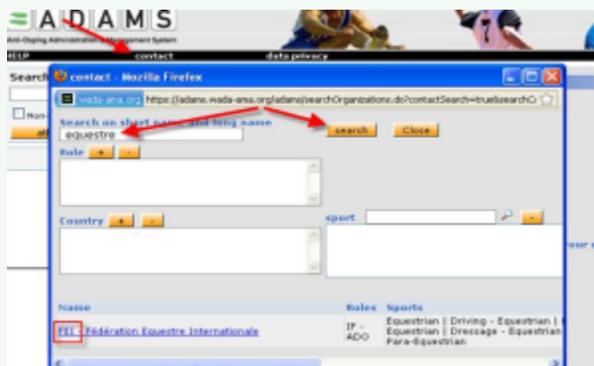
If I have commas within my comments text for the samples that I would like to upload, how do I deal with that?

When you use Excel to enter your text with commas in the special input-field and save your file as a CSV-file, the system will automatically store it with commas between the columns and there should not be a problem.However, if you are creating your CSV-file off-hand (e.g. from WordPad) it is better to make sure that the entire text is included within double quotes. Otherwise, the file to be imported will not be valid since the data will not match up with the column.
For example, for the free-text field Analysis Details/Explanation:

"The samples were analyzed for anabolic and masking agents, diuretics, and hCG using methods 1001, 2001, and 6001."