Section 6. XML Submission Process

The XML data upload module of the LT2 DCTS was created to assist those laboratories who regularly submit a large volume of sample data. Submitting sample data on an individual basis would be a daunting task. If a laboratory is already tracking their sample data within a database, there is no need to duplicate this data entry within the LT2 DCTS. Instead, the laboratory can generate an XML file, based on their sample data. The Lab User can upload this single file to the LT2 DCTS, replacing the data entry with a few simple clicks.

6.1 Who should consider submitting data using XML?

The LT2 DCTS users that may benefit from using the XML upload function include the following:

- Commercial laboratories that need to submit a high volume of sample results to the LT2 DCTS.
- Laboratories that are already tracking their sample data in an electronic source, such as a laboratory information management system (LIMS) or another database that is maintained by an experienced database administrator.

USEPA assistance for those interested in using XML uploads is available through a USEPA-developed tool that automatically extracts data from the laboratory's relational database and creates an XML file that meets the specified document type definition (DTD) requirements. This tool would require an initial mapping of the laboratory's database to the LT2 database structure. Assistance is available from LT2 Technical Support, at stage2mdbp@epa.gov, or the LT2 Hotline, at 1-888-LT2-0020.

6.2 The XML Process

The Lab Data Upload module allows the Lab User to upload an XML file via a web form. The LT2 DCTS will process the file and populate the database with the data from the XML file. After the file is uploaded, the user will receive a confirmation message. The samples will be available for review through the Search screen.

Only Lab Users have the ability to submit electronic files to the LT2 DCTS. Since files will contain data about the sample and the analytical results, it will replace the need for the laboratory to manually enter sample data.

The laboratory will have the ability to pre-approve samples by populating the status field in the XML file. After the data passes LT2 verification checks, the samples will be sent directly to the PWS for review, eliminating the need for a Lab Approver User to access LT2 and individually verify samples. This will provide labs with greater efficiency than the manual entry process. Only Lab Approver Users will be permitted to upload samples in "lab approved" status.

6.2.1 Timing of Transactions

Regardless of the upload time, each file submitted will generate a confirmation record appearing during the user's upload session. This record will indicate the success or failure of the file and detail the exact data errors if the file failed.

Note: The user must keep the web browser open during the upload validation and should not navigate to any other page.

A limited number of samples can be included in a XML file. Since there are a minimal number of data elements tracked by the LT2 DCTS, the space required for each sample is relatively small. However, the larger the XML file, the longer it will take to process the information. It may be more practical to limit the

size of XML files, which will expedite the upload process. *Cryptosporidium* laboratories may consider uploading by 20-sample quality control (QC) batch.

6.2.2 Document Structure

The LT2 DCTS's XML implementation uses DTDs developed specifically for submitting analytical results for water samples. The DTDs describe the format and the data elements required for submitting valid, formatted monitoring data and analytical results in XML format to the LT2 System. There is one DTD for submitting *Cryptosporidium* sample results, and a separate DTD that includes all four *E. coli* methods. These DTDs are included in Appendix A.

Table 6-1 provides a brief description of the field names, descriptions, and types that will be provided by *Cryptosporidium* laboratories, and indicates whether the element is required or optional.

Table 6-1. Cryptosporidium Data Elements

Data Element Name	Data Element Description	Field Type	Requirement
CRYPTO_SAMPLES Information			
PWS_ID	Public Water System ID number	VARCHAR(9)	Required
FACILITY_ID	Public Water System Facility ID number	VARCHAR(15)	Required
SAMPLE_POINT_ID	Sampling Point ID number	VARCHAR(20)	Required
SAMPLE Information			
ANALYTE	Designates file as *Cryptosporidium* sample	VARCHAR(15)	Required
LAB_SAMPLE_ID	Sample identification number	VARCHAR(20)	Required
SAMPLE_COLLECTION_DATE	Sample collection date (Date format is 'DD/MM/YY'), lower bound of 01/01/99 and upper bound of current date	DATE	Required
DATE_FORMAT	Description of the date format using pre-set symbols	VARCHAR	Required
CRYPTO Information			
SAMPLE_VOL_EXAMINED	Designates whether 100% of the sample volume was filtered	VARCHAR(1)	Required
ANALYSIS_TYPE	Sample analysis type	VARCHAR(10)	Required
SAMPLE_VOLUME_FILTERED	Sample volume filtered (L); may be reported to the nearest hundredth and must be greater than 0	NUMBER(20,8)	Required
NO_OF_CRYPTO	Total number of oocysts from all slides, that meet fluorescence, size, and shape criteria under IFA and cannot be ruled out using DAPI or DIC, must be whole number greater than or equal to 0	NUMBER(7)	Required

Data Element Name	Data Element Description	Field Type	Requirement
RESUSPENDED_CONC_VOL	Volume of resuspended concentrate (mL) generated; must be a whole number	NUMBER(20,8)	Required if SAMPLE_VOL_EXAMINED = N
RESUSPENDED_CONC_VOL_IMS	Volume of resuspended concentrate (mL) transferred to IMS; must be a whole number	NUMBER(20,8)	Required if SAMPLE_VOL_EXAMINED = N
NUM_FILTERS	Number of filters used; must be a whole number greater than or equal to 0	NUMBER	Required if (SAMPLE_VOL_EXAMINED = N) OR (SMAPLE_VOL_FILTERED <10)
PELLET_VOLUME	Pellet volume (mL) generated; may be reported to the nearest hundredth	NUMBER(20,8)	Required if (SAMPLE_VOL_EXAMINED = N) OR (SMAPLE_VOL_FILTERED <10)
SAMPLE_VOLUME_SPIKED	Sample volume spiked (L); may be reported to the nearest hundredth	NUMBER(20,8)	Required if ANALYSIS_TYPE = MS
NO_OF_CRYPTO_SPIKE	Estimated number of oocysts spiked; may be reported to the nearest hundredth	VARCHAR	Optional
VALID_STATUS_CODE	The status of the sample	VARCHAR(20)	Optional
LAB_COMMENT	Comments regarding the sample data	VARCHAR(4000)	Optional
RESAMPLE	Displays whether the sample is a resample	VARCHAR(1)	Required
ORIG_SAMPLE_COLLECTION_DATE	The date the original sample was collected	DATE	Required if RESAMPLE = 1
LAB_RESAMPLE_EXPLANATION	The lab's justification as to why the resample was collected	VARCHAR(4000)	Required if RESAMPLE = 1

Table 6-2 provides a brief description of the field names, descriptions, and types that will be provided by *E. coli* laboratories, and indicates whether the element is required or optional. Shaded rows are elements that may be required, depending on the sample and whether the laboratory enters the final result into the LT2 DCTS or enters primary measurements into the LT2 DCTS for automatic calculation of the final result.

Table 6-2. E. coli Data Elements

Data Element Name	Data Element Description	Field Type	Requirement
ECOLI_SAMPLES Information			
PWS_ID	Public Water System ID number	VARCHAR(9)	Required
FACILITY_ID	Public Water System Facility ID number	VARCHAR(15)	Required
SAMPLE_POINT_ID	Sampling Point ID number	VARCHAR(20)	Required
SAMPLE Information			
ANALYTE	Designates file as *E. coli* sample	VARCHAR(15)	Required
LAB_SAMPLE_ID	Sample identification number	VARCHAR(20)	Required
SAMPLE_COLLECTION_DATE	Sample collection date (Date format is 'DD/MM/YY'); lower bound of 01/01/99 and upper bound of current date	DATE	Required
DATE_FORMAT	Description of the date format using pre-set symbols	VARCHAR	Required
ECOLI Information			
ANALYTICAL_MEHTOD_NUMBER	Analytical method number	VARCHAR(40)	Required
SOURCE_WATER_TYPE	Source water type	VARCHAR(20)	Required
TURBIDITY_VALUE	Turbidity result - must be greater than or equal to 0 and may be reported to the hundredth	NUMBER(5)	Required for filtered systems with a population greater than 10,000
SAMPLE_CALC	*E. coli* 100 mL (*option of entering this value of the primary measurements below*), maybe reported to the nearest tenth	NUMBER(20)	Required if primary measurements (shaded in gray) not entered below
FILTER1_VOLUME	Filter 1: mL of sample filtered; must be greater than 0 and may be reported to 6 decimal places	NUMBER(14,4)	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = Membrane Filtration)
FILTER1_CFU	Filter 1: Number of *E. coli* colony forming units (CFU); must be a whole number	NUMBER	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = Membrane Filtration)
FILTER2_VOLUME	Filter 2: mL of sample filtered; must be greater than 0 and may be reported to 6 decimal places	NUMBER(14,4)	Required if FILTER2_CFU != NULL
FILTER2_CFU	Filter 2: Number of *E. coli* colony forming units (CFU); must be a whole number	NUMBER	Required if FILTER2_VOLUME != NULL

Data Element Name	Data Element Description	Field Type	Requirement
FILTER3_VOLUME	Filter 3: mL of sample filtered; must be greater than 0 and may be reported to 6 decimal places	NUMBER(14,4)	Required if FILTER3_CFU != NULL
FILTER3_CFU	Filter 3: Number of *E. coli* colony forming units (CFU); must be a whole number	NUMBER	Required if FILTER3_VOLUME != NULL
FILTER4_VOLUME	Filter 4: mL of sample filtered; must be greater than 0 and may be reported to 6 decimal places	NUMBER(14,4)	Required if FILTER4_CFU != NULL
FILTER4_CFU	Filter 4: Number of *E. coli* colony forming units (CFU); must be a whole number	NUMBER	Required if FILTER4_VOLUME != NULL
VOLUME_ANALYZED	mL of sample added to tray; must be greater than 0 and may be reported to decimal places	NUMBER(14,4)	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = ONPG-MUG, 97-well or ONPG-MUG, 51-well)
COLIFORM_LARGE_WELLS	Large wells positive; Total coliform positive and UV fluorescence; must be a whole number between 0 and less than or equal to 49	NUMBER	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = ONPG-MUG, 97-well)
COLIFORM_SMALL_WELLS	Small wells positive; Total coliform positive and UV fluorescence; must be a whole number between 0 and less than or equal to 48	NUMBER	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = ONPG-MUG, 97-well)
COLIFORM_POSITIVE	Number of wells positive; Total coliform positive and UV fluorescence; must be a whole number between 0 and less than or equal to 51	NUMBER	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = ONPG-MUG, 51-well)
POSITIVE_10_TUBES	Number of positive tubes 10.0 mL; must be a whole number, less than or equal to 5	NUMBER(1)	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = 15-tube MPN)
POSITIVE_1_TUBES	Number of positive tubes 1.0 mL; must be a whole number, less than or equal to 5	NUMBER(1)	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = 15-tube MPN)
POSITIVE_01_TUBES	Number of positive tubes 0.1 mL; must be a whole number, less than or equal to 5	NUMBER(1)	Required if (SAMPLE_CALC = NULL) and (METHOD_TYPE = 15-tube MPN)
POSITIVE_001_TUBES	Number of positive tubes 0.01 mL; must be a whole number, less than or equal to 5	NUMBER(1)	Optional
POSITIVE_0001_TUBES	Number of positive tubes 0.001 mL; must be a whole number, less than or equal to 5	NUMBER(1)	Optional
VALID_STATUS_CODE	The status of the sample	VARCHAR(20)	Optional

Data Element Name	Data Element Description	Field Type	Requirement
LAB_COMMENT	Comments regarding the sample data	VARCHAR(4000)	Optional
METHOD_TYPE	The method used to analyze this *E. coli* sample	VARCHAR	Required
RESAMPLE	Displays whether the sample is a resample	VARCHAR(1)	Required
ORIG_SAMPLE_COLLECTION_DATE	The date the original sample was collected	DATE	Required if RESAMPLE = 1
LAB_RESAMPLE_EXPLANATION	The lab's justification as to why the resample was collected	VARCHAR(4000)	Required if RESAMPLE = 1

On the LT2 DCTS data entry screens, certain data elements are selected through drop-down menus where the user selects from a list of possible choices. For these data elements, one of the possible choices must be entered for the upload to work correctly. Listed in Table 6-3 are the acceptable values for these *Cryptosporidium* and *E. coli* data elements. *Note:* all data elements are case-sensitive.

Table 6-3. Acceptable Data Element Values

Analyte	Data Element Name	Acceptable Values
Both	ANALYTE	Crypto Ecoli
Cryptosporidium	SAMPLE_VOL_ANALYZED	Y/N y/n 1/0 T/F t/f
Cryptosporidium	ANALYTICAL_METHOD_NUMBER	Field MS
E. coli - Membrane Filtration	ANALYTICAL_METHOD_NUMBER	9213D (mTEC) SM 9222B/9222G (mENDO/NA-MUG) SM 9222B/9222G (LesENDO/NA-MUG) SM 9222B/9222G (mFC/NA-MUG) EPA 1603 (modified mTEC) EPA 1604 (MI Medium) mColiBlue-24
E. coli - 15-tube MPN	ANALYTICAL_METHOD_NUMBER	SM 9223 (Colilert) SM 9223 (Colilert-18) SM 9221B/9221F (LTB/EC-MUG)
E. coli - ONPG-MUG, 51-well	ANALYTICAL_METHOD_NUMBER	SM 9223 (Colilert) SM 9223 (Colilert-18)
E. coli - ONPG-MUG, 97-well	ANALYTICAL_METHOD_NUMBER	SM 9223 (Colilert) SM 9223 (Colilert-18)

Analyte	Data Element Name	Acceptable Values
E. coli - all methods	SOURCE_WATER_TYPE	Both FS and L/R Flowing stream GWUDI-FS GWUDI-LR Lake/reservoir
E. coli - all methods	METHOD_TYPE	Membrane Filtration 15-tube MPN ONPG-MUG, 51-well ONPG-MUG, 97-well
Both	VALID_STATUS_CODE	New Sample Pending Approval Approved Contested Returned to Lab

6.2.3 Legal and Security Considerations

If you choose to submit data via an XML file, that file will be the "official" copy of the data. The web entry forms provide the user with a warning, reminding the user that the sample data must be compliant with certain standards. It is assumed that the laboratory will adhere to the same standards when uploading their XML files. These standards are discussed as follows, by analyte.

***Cryptosporidium* -** Do not enter data for samples that did not meet QC requirements. You are acknowledging the following by entering *Cryptosporidium* sample data into the LT2 DCTS: all holding times for the sample were met; the sample was received by the laboratory in acceptable condition; and results for the associated method blank, ongoing precision and recovery (OPR), and positive and negative staining controls were acceptable (EPA Method 1622/1623).

***E. coli* -** Do not enter data for samples that did not meet QC requirements. You are acknowledging the following by entering *E. coli* sample data into the LT2 DCTS: all holding and incubation times and temperatures for the sample were met; the sample was received by the laboratory in acceptable condition; all method-specified QC requirements were met; and all QA/QC criteria and procedures specified in the *Manual for the Certification of Laboratories Analyzing Drinking Water* [EPA 815-R-05-004] were followed.

The XML file may be submitted with the sample in "lab approved" status. It is assumed that the laboratory is acknowledging that the following if this status is chosen:

***Cryptosporidium* -** By delivering these *Cryptosporidium* monitoring results to the PWS, you are verifying that the results were generated in accordance with all Method 1622/1623 and LT2 Rule QC requirements (these criteria are specified in Appendix B).

***E. coli* -** By delivering these *E. coli* monitoring results to the PWS, you are verifying that the results were generated in accordance with all method and LT2 Rule QC requirements (these criteria are specified in Appendix C and Appendix D).

If the file is successfully uploaded with a "lab approved" status, all the enclosed samples will move directly to the PWS review process.

6.3 User Process

After an XML file is generated, it can be uploaded through the LT2 website. Users will see a link to "UPLOAD SAMPLES" when they select "CREATE NEW SAMPLES" from the navigation toolbar on the left hand side. Figure 6-1 displays the "Create New Sample" screen.

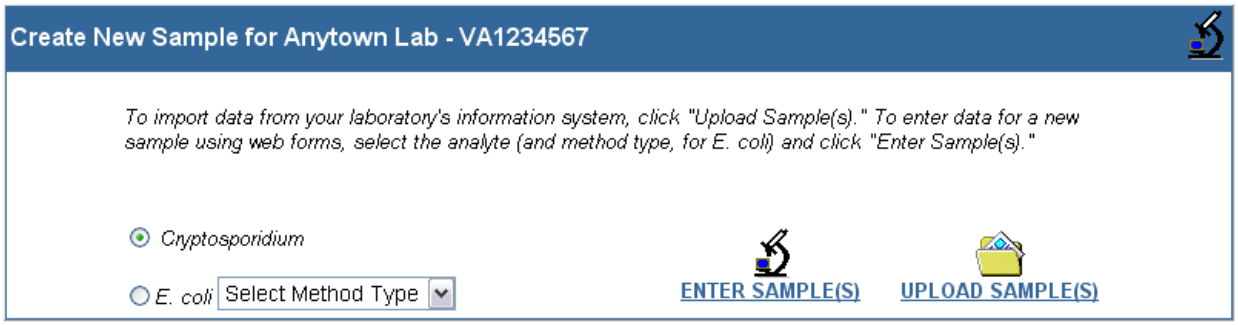

Figure 6-1. Create New Sample Screen

Lab Users that wish to upload XML files from their LIMS or data tracking systems, and that do not have a user-friendly means to convert data from their system to XML for upload should contact the LT2 Hotline, at 1-888-LT2-0020, for assistance. In addition to specific support, the LT2 Hotline staff also can provide free USEPA software for mapping a laboratory's internal database fields to the LT2 DCTS's DTD, and for translating the data to XML format for upload.

The user will then choose the "UPLOAD SAMPLE(S)" link on the right. After arriving at the "Lab Upload" page (Figure 6-2), the user can upload file(s) by clicking the "BROWSE" button. If the user knows the location of the file, they may opt to directly key this information into the text box. Otherwise, the web browser's default directory will be displayed, allowing the user to locate the desired file. The user will select the XML file from their computer to upload and click the "OPEN" button to commit the selection. After the file is selected, the user will click the "UPLOAD FILE" link to import the sample information.

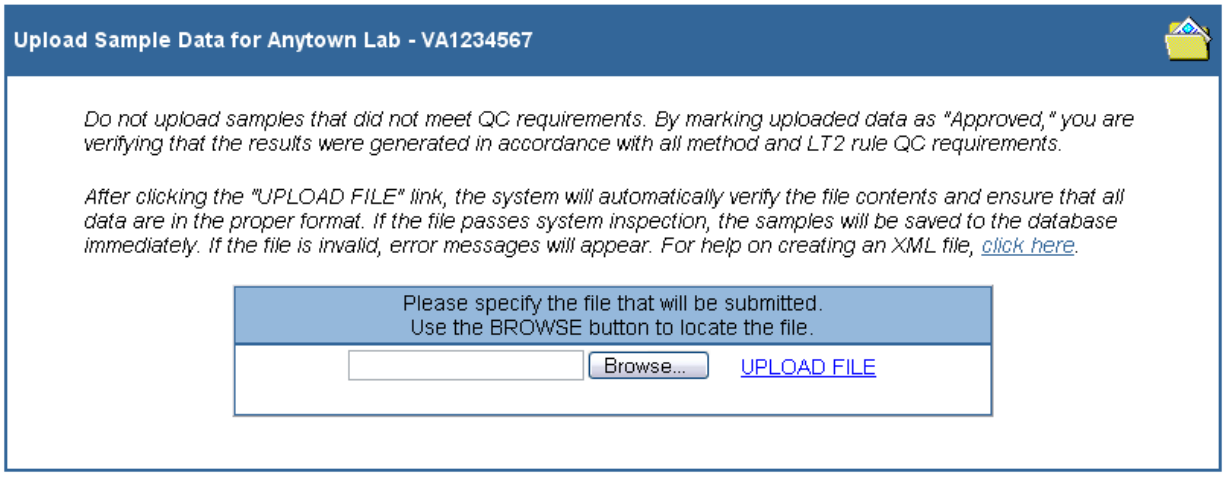

Figure 6-2. Lab Upload

Once the "UPLOAD FILE" link is clicked, the LT2 DCTS begins validating the XML file. The user must wait for the file to be validated before proceeding to other parts of the LT2 DCTS.

If the XML file passes all validation checks, the data will be loaded to the database, and the XML upload page will refresh to show the resulting success message (Figure 6-3). The samples are then available for review through the search module. If the XML file does not pass all validation checks, the XML upload page will refresh to display a list of errors (Figure 6-4). Details will describe the exact sample where an error occurred, as well as the data field containing the error. If there is an error in just one of many samples contained in the file, the entire file will be rejected.

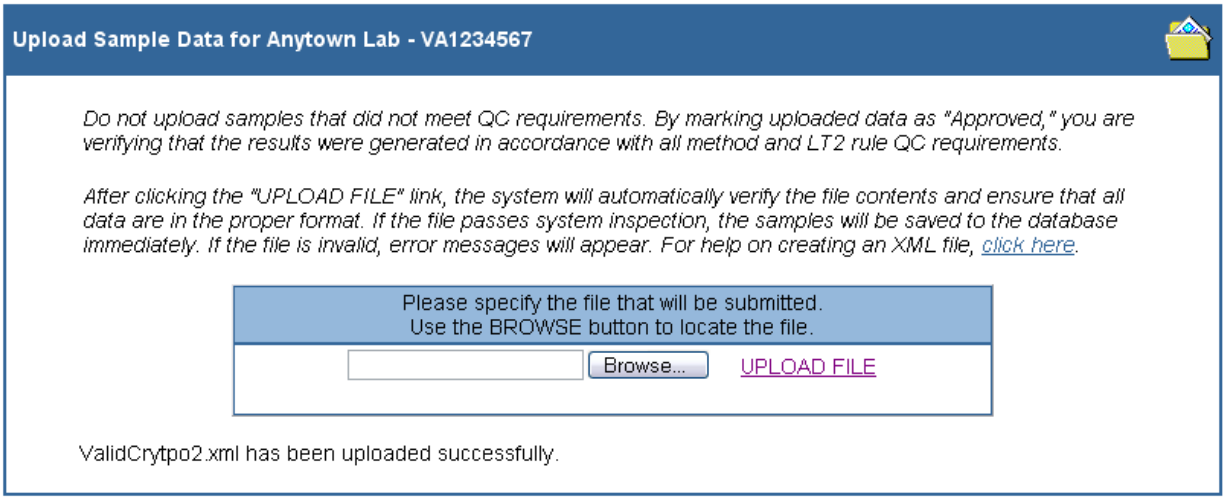

Figure 6-3. Lab Upload – Successful Upload

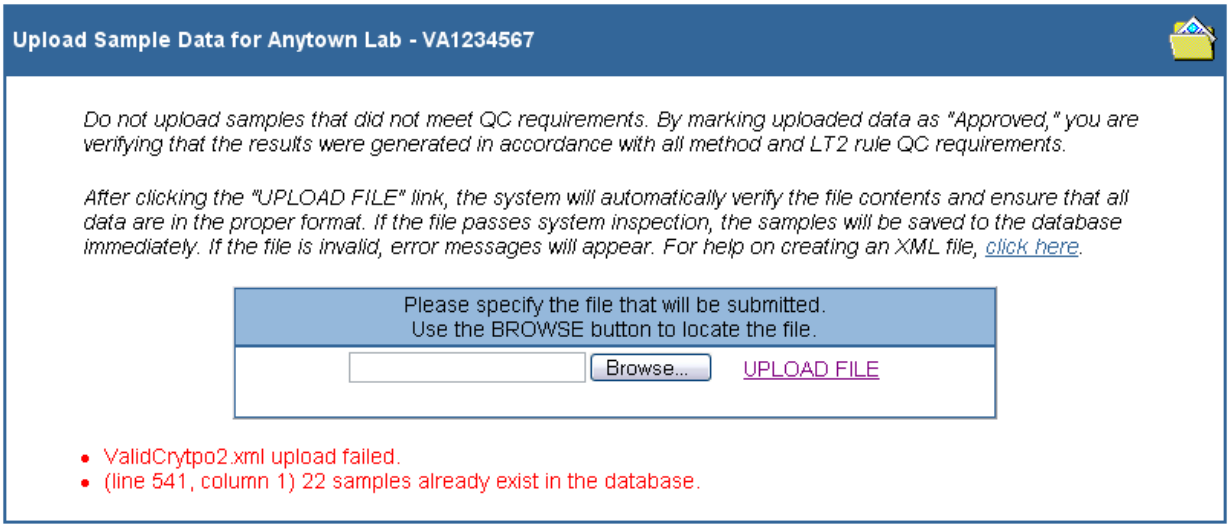

Figure 6-4. Lab Upload – Failed Upload

6.4 LT2 XML Data Flow

To create an XML document, first identify the data fields in your database that will be extracted for transmission to the LT2 DCTS. This involves reviewing the list of LT2 data elements for *Cryptosporidium* or *E. coli* and then mapping them to your database by identifying the appropriate database name, table name, and field name used to store each element. Someone familiar with the structure of the database and the location of the necessary reporting fields for LT2 should be involved in this step.

Next, extract the necessary data from your laboratory's database. Most XML transformation products have the capability of communicating directly with databases and when supplied with a DTD and mapping information, and can extract data straight from the database tables into a new XML file. Your XML software provider or LIMS developer should be consulted about the capabilities of the software. Also, consider the ability of the software to validate the XML documents. Validation ensures that the XML document conforms to XML specifications and DTD rules. When an architecture for extracting the data has been determined, the data must be parsed into an XML document according to the LT2 DTD. The LT2 DTDs are provided in Appendix A.

The validated XML document is uploaded to the LT2 DCTS as described in Section 6.2. The LT2 DCTS will send the XML file to the LT2 parser for validation and entry into LT2. If errors prevent the processing of the submission, an error message will be displayed on the screen, and the entire file will be rejected. After making the necessary corrections, the data may be resubmitted. After the data elements are loaded into LT2, you will be able to view the data through the LT2 search function.

If "entered" ("Pending Approval" status) is recorded in the status element, you will be able to make changes to the data. If "lab approved" is recorded in the status element, and you have the correct user rights, the data will be automatically sent to the PWS, and the LT2 DCTS date will be marked as the date the laboratory approved the sample. At this point, the laboratory can no longer edit the information. These samples can be viewed from the laboratory's search screen, but changes cannot be made. If the status element was left blank, the sample would be automatically placed in "Pending Approval" status. The Lab Approver User would need to enter the LT2 DCTS and manually approve the sample for PWS review.

Note: Cryptosporidium MS samples cannot be submitted in the "lab approved" status, since the user needs to verify that the MS sample is associated with a field sample. Any MS sample submitted in the "Lab Approved" status will be switched to the "Entered" status. The Lab Approver User must log in to the LT2 DCTS to manually approve these MS samples for PWS review.

6.5 Error Corrections and Resubmissions

When the LT2 DCTS determines that the XML file is not valid, a detailed error log will be displayed. The message will detail the information that is incorrect or missing. It is the user's responsibility to make the necessary changes before resubmitting the data to LT2.

Errors could occur because a sample did not pass verification checks. The following lists the verification checks for both *Cryptosporidium* and *E. coli* samples.

6.5.1 *Cryptosporidium* and *E. coli* Verification Rules

- SAMPLE_COLLECTION_DATE has an upper bound of January 1, 2009
- SAMPLE_COLLECTION_DATE and ORIG_SAMPLE_COLLECTION_DATE must not be prior to January 1, 1999
- SAMPLE_COLLECTION_DATE must be equal to or prior to the current date
- If supplied, ORIG_SAMPLE_COLLECTION_DATE must be less than the SAMPLE_COLLECTION_DATE
- SAMPLE_COLLECTION_DATE and ORIG_SAMPLE_COLLECTION_DATE will be saved as (MM/DD/YY)
- ANALYTE is 'Crypto' or 'Ecoli'
- ANALYTE is not null
- SAMPLE_COLLECTION_DATE is not null
- VALID_STATUS_CODE can be null, 'lab approved', 'or 'entered'
- If VALID_STATUS_CODE is null, then the VALID_STATUS_CODE should be written as 'entered'
- If VALID_STATUS_CODE = 'lab approved' then the LAB_APPROVAL_DATE should be written as the LT2 DCTS date
- If (VALID_STATUS_CODE = 'lab approved' AND USER_ORGANIZATION.USER_ROLE = 'lab_edit') then VALID_STATUS_CODE is saved as 'entered' and LAB_APPROVAL_DATE is null
- If a facility is inactive (FACILITY.STATUS = 'Inactive'), then the SAMPLE_COLLECTION_DATE must be less than the inactivity date (FACILITY.INACTIVE_DATE)
- Sample cannot already exist in the database. This is based on combination of PWS, facility, sampling point, sample collection date, sample type (MS or field), and analyte (*Cryptosporidium* or *E. coli*)
- RESAMPLE must be in (1, 0, 'Y', 'N', 'y', 'n', 'T', 'F', 't', 'f')
- If RESAMPLE in (1, 'Y', 'y', 'T', 't')) then ORIGINAL_SAMPLE_COLLECTION_DATE and LAB_RESAMPLE_EXPLANATION are required
- Data type and length constraints are met, including the minimum and maximum length
- All required data elements have been supplied
- All numerical data are indeed numerical

6.5.2 *Cryptosporidium* Verification Rules

- The SAMPLE_VOLUME_FILTERED cannot be null and must be greater than 0 and entered to the nearest hundredth
- NO_OF_CRYPTO must be a whole number greater than or equal to zero
- ANALYSIS_TYPE cannot be null and must be either 'MS' or 'Field'
- If ANALYSIS_TYPE = 'MS' another sample (with the same PWS, FACILITY, SAMPLING_POINT, SAMPLE_COLLECTION_DATE) should exist where ANALYSIS_TYPE = 'Field'

- If ANALYSIS_TYPE = 'MS', then VALID_STATUS_CODE must be saved as 'entered' regardless of what the user submitted
- If ANALYSIS_TYPE = 'MS', then SAMPLE_VOLUME_SPIKED and NO_OF_CRYPTO_SPIKE cannot be null
- If ANALYSIS_TYPE = 'MS', then SAMPLE_VOLUME_FILTERED must be less than or equal to SAMPLE_VOL_SPIKED
- If ANALYSIS_TYPE = 'MS', then NO_OF_CRYPTO_SPIKE must be a whole number greater than or equal to zero and entered to the nearest hundredth
- If ANALYSIS_TYPE = 'MS', then SAMPLE_VOLUME_SPIKED must be greater than zero
- SAMPLE_VOL_EXAMINED cannot be null and must be one of these ('1', '0', 'Y', 'N', 'y', 'n', 'T', 'F', 't', 'f')
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') then RESUSPENDED_CONC_VOL_IMS, RESUSPENDED_CONC_VOL, NUM_FILTERS, and PELLET_VOLUME cannot be null
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') or SAMPLE_VOLUME_FILTERED is less than 10 then PELLET_VOLUME must be greater than 0 and reported to the nearest tenth
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') then SAMPLE_VOLUME_SPIKED must be greater than 0 and reported to the nearest hundredth
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') then RESUSPENDED_CONC_VOL must be greater than or equal to 0 and entered to the nearest tenth
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') then RESUSPENDED_CONC_VOL_IMS must be greater than or equal to 0 and entered to the nearest tenth
- If SAMPLE_VOL_EXAMINED is ('0', 'N', 'n', 'F', 'f') then RESUSPENDED_CONC_VOL_IMS must be equal to or less than RESUSPENDED_CONC_VOL
- If SAMPLE_VOLUME_FILTERED is less than 10, then NUM_FILTERS and PELLET_VOLUME cannot be null
- If SAMPLE_VOLUME_FILTERED is less than 10 then NUM_FILTERS must be a whole number greater than or equal to 0
- RESUSPENDED_CONC_VOL_IMS, RESUSPENDED_CONC_VOL, NUM_FILTERS, PELLET_VOLUME, NO_OF_CRYPTO_SPIKE, NO_OF_CRYPTO, SAMPLE_VOLUME_FILTERED, SAMPLE_VOLUME_SPIKED must be numeric

6.5.3 *E. coli* Verification Rules

- METHOD_TYPE cannot be null and must be either 'Membrane Filtration', '15-Tube MPN', 'ONPG-MUG, 97-well' or 'ONPG-MUG, 51-well'
- ANALYTICAL_METHOD_NUMBER cannot be null
- If METHOD_TYPE = 'ONPG-MUG, 97-well' or 'ONPG-MUG, 51-well', ANALYTICAL_METHOD_NUMBER must be either 'SM 9223 (Colilert)' or 'SM 9223 (Colilert-18)'
- If METHOD_TYPE = '15-Tube MPN', ANALYTICAL_METHOD_NUMBER must be either 'SM 9223 (Colilert)', 'SM 9221B/9221F (LTB/EC-MUG)' or 'SM 9223 (Colilert-18)'
- If METHOD_TYPE = 'Membrane Filtration', ANALYTICAL_METHOD_NUMBER must be either 'SM 9213D (mTEC)', 'SM 9222B/9222G (mENDO/NA-MUG)', 'SM 9222B/9222G (LesENDO/NA-MUG)', 'SM 9222D/9222G (mFC/NA-MUG)', 'EPA 1603 (modified mTEC)', 'EPA 1604 (MI Medium)', or 'mColiBlue-24'
- TURBIDITY_VALUE cannot be null and must be greater than or equal to zero if the PWSs is a filtered system with a population greater than 10,000
- SOURCE_WATER_TYPE cannot be null and must be 'Both FS and L/R', 'Flowing stream', 'GWUDI-FS', 'GWUDI-LR' or 'Lake/reservoir'

- If METHOD_TYPE = 'ONPG-MUG, 97-well' and SAMPLE_CALC is null then VOLUME_ANALYZED, COLIFORM_LARGE_WELLS, and COLIFORM_SMALL_WELLS cannot be null
- If METHOD_TYPE = 'ONPG-MUG, 51-well' and SAMPLE_CALC is null then VOLUME_ANALYZED and COLIFORM_POSITIVE cannot be null
- If METHOD_TYPE = '15-Tube MPN' and SAMPLE_CALC is null then POSITIVE_10_TUBES, POSITIVE_1_TUBES, POSITIVE_01_TUBES cannot be null.
- If METHOD_TYPE = '15-Tube MPN' and SAMPLE_CALC is null then POSITIVE_10_TUBES, POSITIVE_1_TUBES, POSITIVE_01_TUBES, POSITIVE_001_TUBES, and POSITIVE_0001_TUBES can be entered.
- If METHOD_TYPE = 'Membrane Filtration' and SAMPLE_CALC is null then one pair of FILTER_VOLUME and FILTER_CFU must be supplied
- If METHOD_TYPE = 'Membrane Filtration' and SAMPLE_CALC is null then FILTER1_VOLUME, FILTER1_CFU, FILTER2_VOLUME, FILTER2_CFU, FILTER3_VOLUME, FILTER3_CFU, FILTER4_VOLUME and FILTER4_CFU can be entered
- If METHOD_TYPE = 'Membrane Filtration', SAMPLE_CALC is null and a value is supplied for a FILTER_VOLUME then the corresponding FILTER_CFU cannot be null
- If METHOD_TYPE = 'Membrane Filtration', SAMPLE_CALC is null and a value is supplied for a FILTER_CFU then the corresponding FILTER_VOLUME cannot be null
- If required, FILTER_VOLUME must be greater than 0 and less than or equal to 100
- If required, FILTER_CFU must be a whole number
- VOLUME_FILTERED for membrane filtration methods cannot exceed 100 mL
- If required, COLIFORM_POSITIVE, COLIFORM_LARGE_WELLS, and COLIFORM_SMALL_WELLS must be a whole number greater than 0
- If required, COLIFORM_POSITIVE must be less than or equal to 51
- If required, COLIFORM_LARGE_WELLS must be less than or equal to 49
- If required, COLIFORM_SMALL_WELLS must be less than or equal to 48
- If required, VOLUME_ANALYZED must be greater than 0 and less than or equal to 100
- If required, POSITIVE_10_TUBES, POSITIVE_1_TUBES, POSITIVE_01_TUBES, POSITIVE_001_TUBES, and POSITIVE_0001_TUBES must have a whole number value of ('0', '1', '2', '3', '4', '5')