

# Council on Dairy Cattle Breeding (CDCB) Export Tool

**Publication Number** 703465 **Revision** 1

## Overview


The CDCB Export Tool is a companion application to the Axiom™ Analysis Suite. It formats your genotype export and sample sheet to enable direct uploading to the Council on Dairy Cattle Breeding website.

## Installation

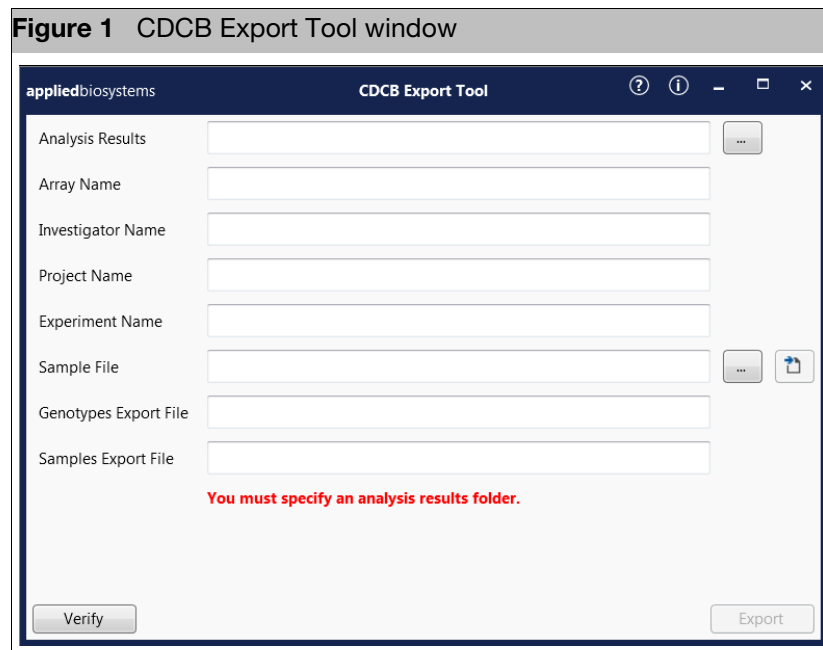
 **IMPORTANT!** You must have Axiom Analysis Suite installed on your computer BEFORE installing the CDCB Export Tool.

1. After receiving/downloading the CDCB Export Tool zip package, save it to a local (easily accessible) folder on your system.
2. Unzip the file (as you normally would), then double-click the **CDCBExportToolSetup.exe** to install it.
3. Follow the installer's instructions.

## Launching the Tool


1. Click **Start -> All Programs -> Thermo Fisher Scientific -> Axiom Analysis Suite -> CDCB Export Tool**. Alternatively (from the Axiom Analysis Suite's Viewer), click the **External Tools** window tab, then click .

The **CDCB Export Tool** window appears. (Figure 1)



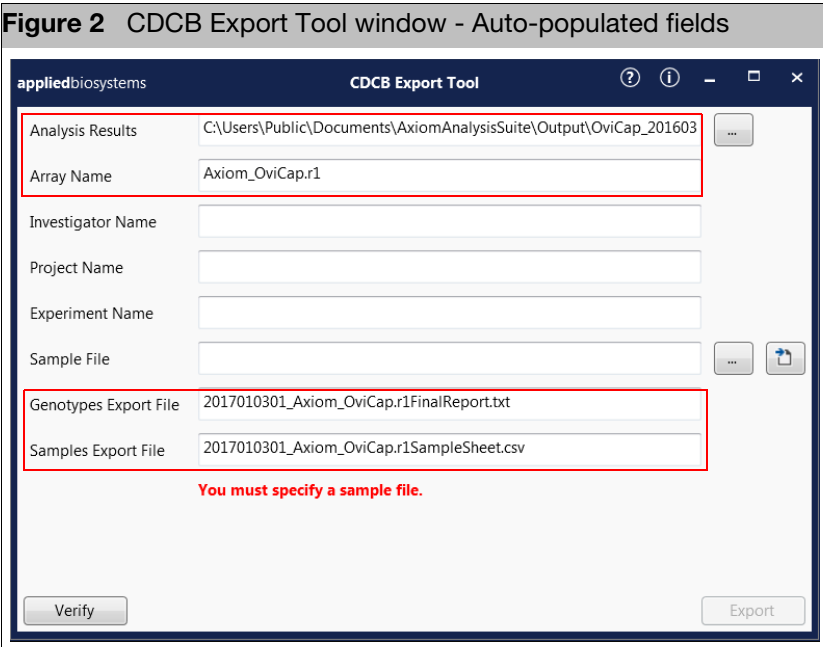
## Using the Tool

**✗ IMPORTANT!** You must have a previously run analysis to import into the CDCB Export Tool. For instructions on how to create and run an analysis, see the Axiom Analysis Suite User Guide (P/N 703307).

1. Click the **Analysis Results** field's  button.  
An Explorer window appears.
2. Navigate to your Analysis Results folder, click to highlight it, then click **Select Folder**.

The following fields auto-populate: (Figure 2)

**Figure 2** CDCB Export Tool window - Auto-populated fields




The screenshot shows the CDCB Export Tool window with the following fields and values:

- Analysis Results: C:\Users\Public\Documents\AxiomAnalysisSuite\Output\OviCap\_201603
- Array Name: Axiom\_OviCap.r1
- Investigator Name: (empty)
- Project Name: (empty)
- Experiment Name: (empty)
- Sample File: (empty)
- Genotypes Export File: 2017010301\_Axiom\_OviCap.r1FinalReport.txt
- Samples Export File: 2017010301\_Axiom\_OviCap.r1SampleSheet.csv

A red error message is displayed below the Samples Export File field: "You must specify a sample file."

If needed, you may change the auto-generated Genotypes and Samples Export filenames. To do this:


- a. Click inside the text field.  
A cursor appears.
  - b. Edit the filename, then click outside the text field to save it.
3. Click the **Sample File** field's  button.  
Your Sample File must be a tab-delimited text file with eight columns.

Each column header must use the same naming convention and be in the same (left to right) order as shown in Figure 3.

**Figure 3** Sample File - Required column order and naming conventions

	A	B	C	D	E	F	G	H
1	cel_files	sample_id	sample_name	sample_source	plate_barcode	well_position	sentrix_barcode	sentrix_position_a

OR

Click  to create a sample template file.


A **CDCBExportSampleFileTemplate.txt** now resides in your selected Analysis Results folder.

This auto-generated file is based on the information detected within the Analysis Results folder. It includes the required columns for the Sample File, as well as pre-populated CEL file, barcode, and well positions fields. (Figure 4)

**Figure 4** CDCBExportSampleFileTemplate.txt example

	A	B	C	D	E	F	G	H
1	cel_files	sample_id	sample_name	sample_source	plate_barcode	well_position	sentrix_barcode	sentrix_position_a
2	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
3	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
4	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
5	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
6	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
7	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
8	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
9	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
10	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
11	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
12	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
13	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
14	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>
15	a550627-4	<sample id>	<sample name>	<sample source>	<plate barcode>	<well position>	<sentrix barcode	<sentrix position a>

*To use the Sample File Template:*

- Navigate to your Analysis Results folder, locate the **CDCBExportSampleFileTemplate.txt** file, then open it using MS Excel.
- Complete the remaining/required fields.
- Rename the template, then save it as a tab-delimited text file.
- At the CDCB Export Tool, click the **Sample File** field's  button.
- Navigate back to your Analysis Results folder, click to highlight your saved sample file, then click **Open**.

The Sample File field is now populated.

4. Manually enter an **Investigator Name**, **Project Name**, and **Experiment Name**. (Figure 5)

**Figure 5** Completed fields example

The screenshot shows the 'CDCB Export Tool' window with the following fields filled out: Analysis Results (C:\Users\Public\Documents\AxiomAnalysisSuite\Output\OviCap\_20160308), Array Name (Axiom\_OviCap.r1), Investigator Name (Dr. J), Project Name (Project\_1), Experiment Name (Experiment\_1), Sample File (C:\Users\Public\Documents\AxiomAnalysisSuite\Output\OviCap\_20160308\CDCBExportSample), Genotypes Export File (2017010301\_Axiom\_OviCap.r1FinalReport.txt), and Samples Export File (2017010301\_Axiom\_OviCap.r1SampleSheet.csv). A red box highlights the Investigator Name, Project Name, and Experiment Name fields. The window has a 'Verify' button at the bottom left and an 'Export' button at the bottom right.

At any point, the software may detect an error or a duplicate file issue. If this is the case, an appropriate message appears, as shown in Figure 6.

**Figure 6** Error message example

The screenshot shows the 'CDCB Export Tool' window with an error message displayed in red text: 'The genotypes export file already exists. Choose a new one or delete the existing one.' The 'Verify' button is at the bottom left and the 'Export' button is at the bottom right.

Rectify the reported issue, then click **Verify** to recheck/clear the displayed message.

5. Click **Export**.

A progress bar appears, then after a few moments an Export Complete message appears.

6. Click **X** (upper right corner) to close the **CDCB Update Tool** window.

The generated Final Report (.txt) (genotype idata) and Samples Sheet (.csv) files reside in your Analysis Results folder and are ready for use.

The information in this guide is subject to change without notice.

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3 January 2017

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