This quick start tutorial walks you through analyzing and adding your first data files to CPAS.

For this example, we used the files in the Sample Data directory provided as part of the CPAS distribution.
Step 1: Create a CPAS Project and subfolder for your data

If your Project and subfolder already exist, skip to step 2.

• To Create a Project in CPAS:
  – Click Create Project in the Site Administration section of the left navigation
  – Type the name of the new Project and click Create New Project. You will go directly to the Permissions page for your new Project where you can manage Groups and Permissions.

• To Create a Subfolder in CPAS:
  – Click Manage Folders in the left navigation section and select the Project where you want to add a subfolder
  – Click Create Subfolder
  – Type the subfolder name and click Create New Folder.
Step 2: Add the Data Pipeline Web Part

After you create your new folder, select Data Pipeline from the drop down list of web parts. Click Add Web Part.
Step 3: Set up the data pipeline

Click Setup.
Step 4: Set your data pipeline root directory

Type the path to the root directory where your MS/MS data files are stored in the field provided.

Click Set.
Step 5: Complete Setup

Click Done.
Step 6: Process and Upload Data

Click the Process and Upload Data button.
Step 7: Select folder with your data

The files found in the root directory will be listed on the page.

Click the folder that contains your data (here, the bov_sample folder).
Step 8: Begin Analysis

Click the "Search for Peptides" button next to the data file you want to analyze.
Step 9: Describe your MS2 run

This page allows you to add information about your MS2 runs. Start by clicking selecting <New Protocol> from the Protocol drop down list.
Step 10: Create a new MS2 Sample Protocol

Name your sample preparation protocol.

Add text to the fields provided to describe the steps of your sample preparation and LC-MS/MS protocols.

When you finish, click Submit.
Step 11: Finish describing your run

Name your run and enter a Sample ID.

You will soon be able to add more information, such as Excel spreadsheets, about your sample using the Sample Set field.

Click Submit when you finish.
Step 12: Describe your analysis protocol

Name your analysis protocol and add a text description.

The mzXML and FASTA files in your directory will automatically be listed.

Select the FASTA file(s) you want to search against.

Add X!Tandem search parameters.

Click Search.
Step 13: Refresh the browser until the analysis is complete.

The run being analyzed will appear in the Data Pipeline area of the page. Click your browser’s Refresh button periodically until the analysis is complete.
Step 14: View your MS2 run

When the analysis is complete, a new MS2 Runs area will appear with your run listed. Click the links in the protocol column to view the experiment summary and analysis protocols (see steps 15 and 16). Click the description to view and analyze the run using the CPAS MS2 module (see steps 17 and 18).
Step 15: View the experiment summary flow chart

Click a node in the flow chart to view more detailed information about that step, file, or data element.
Step 16: View the analysis flow chart

Click a node in the flow chart to view more detailed information about that step, file, or data element.
Step 17: View and analyze your MS2 run

Details of the run are listed at the top of the page.

Use the View section to customize the appearance of the Peptides section and apply filters. Here we selected “Default View” from the drop down list and clicked Go - see step 18).

The results are listed in the Peptides section of the page.
Step 18: View filtered MS2 data

The details of the filter are displayed in the View section, and the filtered results are displayed in the Peptides section.