

Centers for Disease Control and  
Prevention (CDC)

National Center for Environmental Health  
(NCEH)

Division of Laboratory Sciences (DLS)

**NEWBORN SCREENING AND  
MOLECULAR BIOLOGY BRANCH  
(NSMBB)**

**NEWBORN SCREENING QUALITY  
ASSURANCE PROGRAM (NSQAP)  
PORTAL**

**PROFICIENCY TESTING USER  
GUIDE**

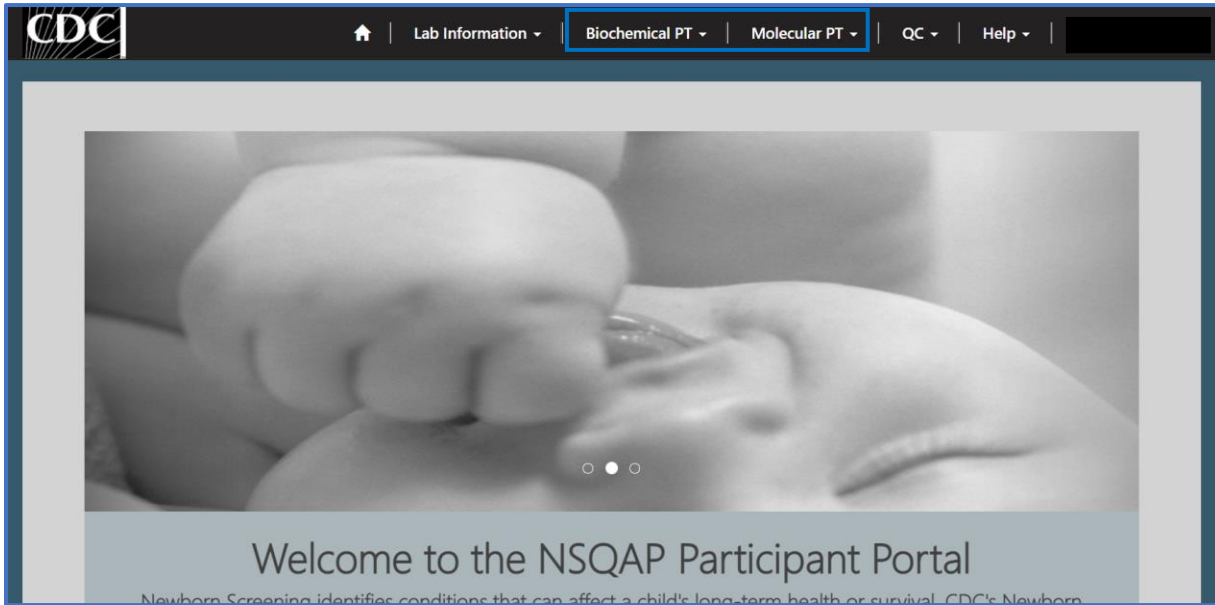
**September 2023**

## Table of Contents

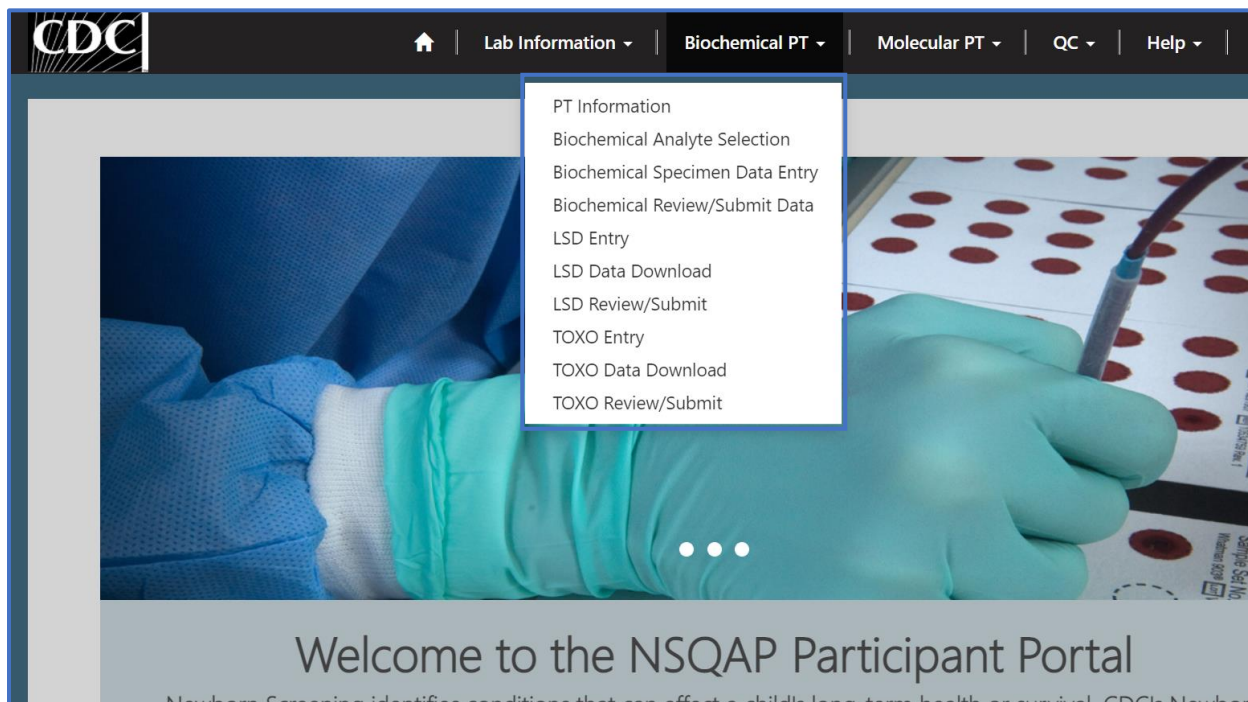
|  |           |
|--|-----------|
| <b>1. Proficiency Testing Navigation</b> .....         | <b>2</b>  |
| 1.1 PT Information Page .....                          | 4         |
| 1.2 Biochemical Analyte Selection.....                 | 6         |
| 1.3 Biochemical Specimen Data Entry .....              | 7         |
| 1.4 Biochemical Review and Submit Data .....           | 8         |
| 1.5 Program File Drop-Off .....                        | 9         |
| 1.6 Program Specific PT Pages.....                     | 10        |
| <b>2. Biochemical Data Entry</b> .....                 | <b>12</b> |
| 2.1 Analyte Selection .....                            | 12        |
| 2.2 Data Entry .....                                   | 21        |
| <b>3. Biochemical Data Review and Submission</b> ..... | <b>26</b> |
| 3.1 Data Summary .....                                 | 26        |
| 3.2 Data Submission .....                              | 31        |
| <b>4. PT Program File Drop-Off</b> .....               | <b>33</b> |
| 4.1 Download the Data Report Form .....                | 34        |
| 4.2 Upload the PT Program Data Report Form.....        | 36        |
| <b>5. Reporting</b> .....                              | <b>41</b> |
| 5.1 Quarterly Summary Report .....                     | 41        |
| 5.2 Evaluation Report .....                            | 43        |

# 1. Proficiency Testing Navigation

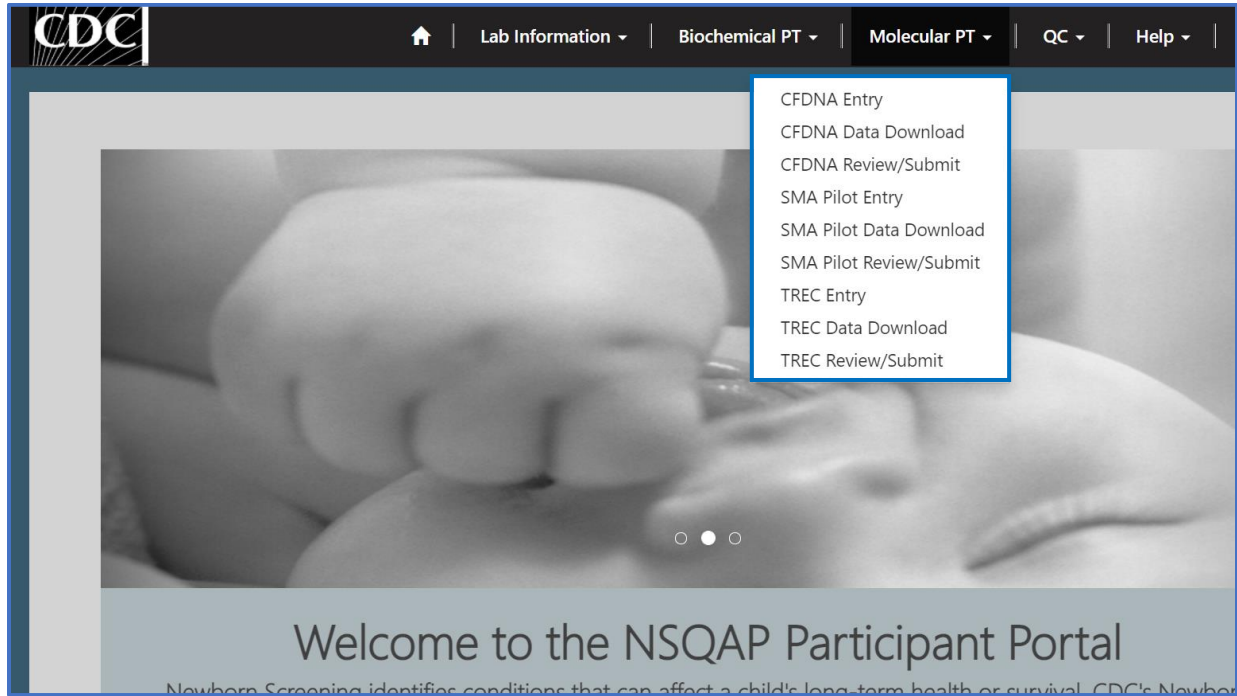
The Proficiency Testing (PT) sections of the NSQAP Portal can be accessed by clicking **‘Biochemical PT’** or **‘Molecular PT’** from the menu bar.



1. The Biochemical PT section contains the following pages: PT Information, Biochemical Analyte Selection, Biochemical Specimen Data Entry, Biochemical Review/Submit Data, and two sets of program specific pages for LSDPT and TOXOPT.

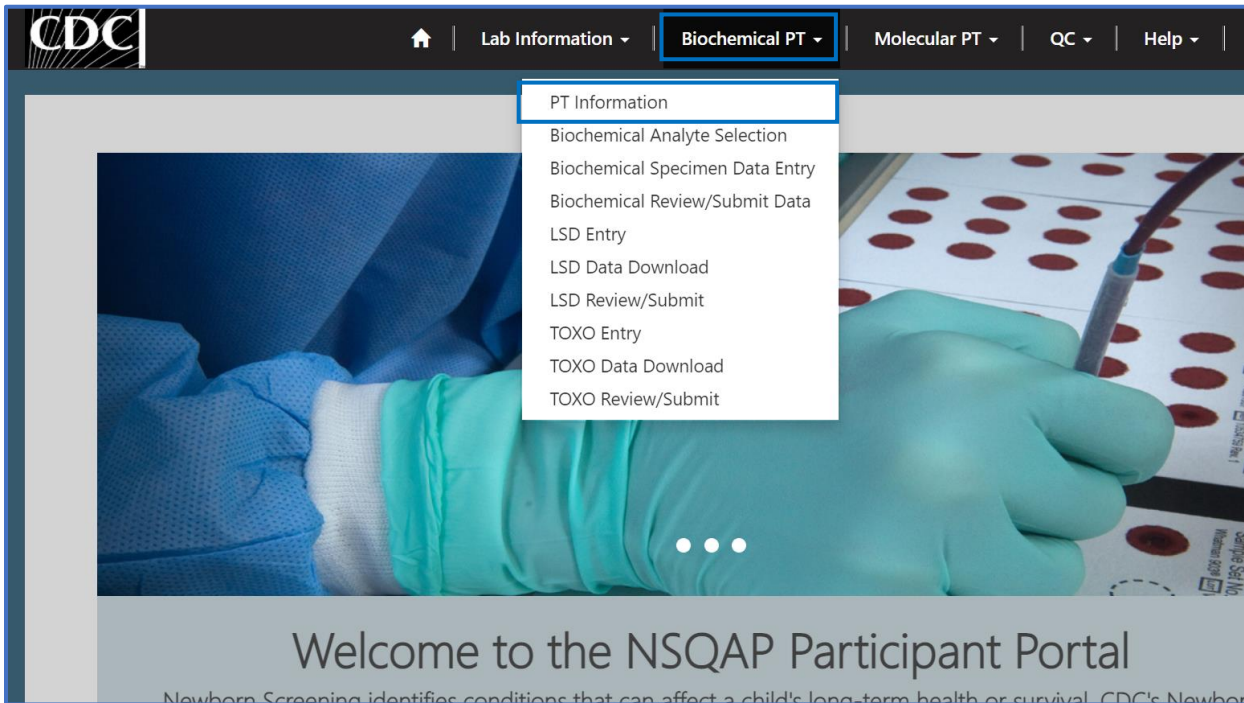


- The Molecular PT section contains three sets of program specific pages for CFDNAPT, SMAPT Pilot, and TRECPT.

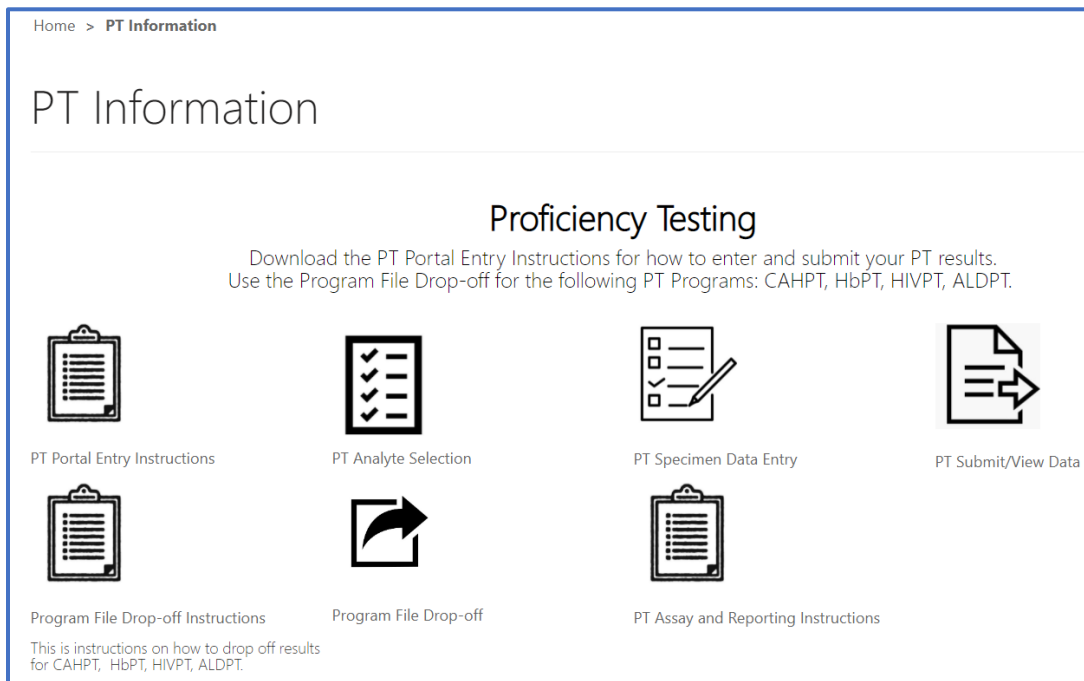


## 1.1 PT Information Page

1. Select the **'Biochemical PT'** button at the top of the page on the toolbar and select the **'PT Information'** option.



2. This page serves as the homepage and resource for all Biochemical PT related activities.



3. The PT Information homepage contains several icons that are used to navigate to the various Biochemical PT sections within the NSQAP Portal.

Home > PT Information

## PT Information

### Proficiency Testing

Download the PT Portal Entry Instructions for how to enter and submit your PT results. Use the Program File Drop-off for the following PT Programs: CAHPT, HbPT, HIVPT, ALDPT.

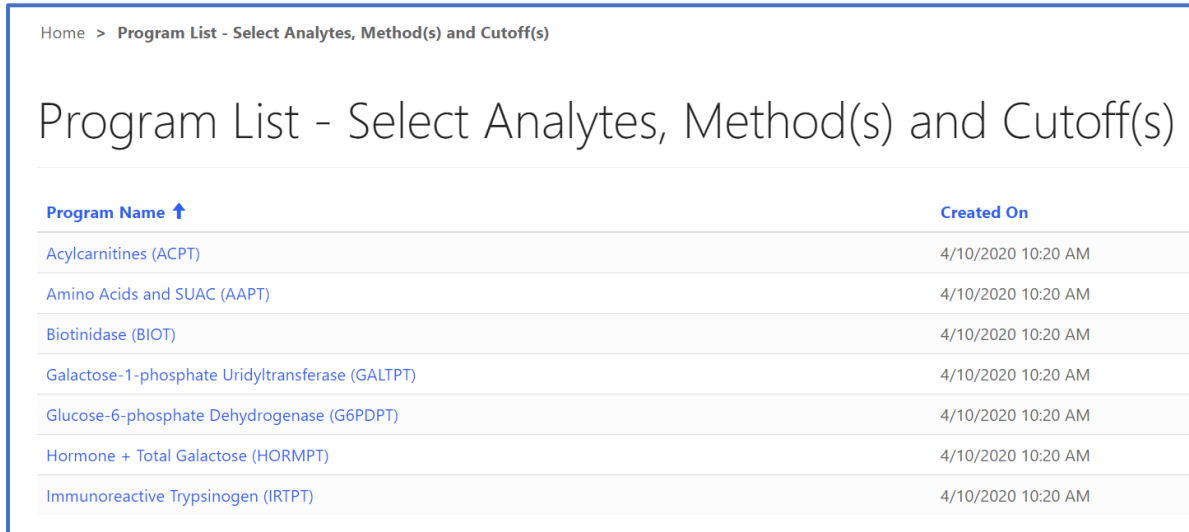
The screenshot shows a grid of seven numbered icons with their corresponding labels:

- 1** PT Portal Entry Instructions
- 2** PT Analyte Selection
- 3** PT Specimen Data Entry
- 4** PT Submit/View Data
- 5** Program File Drop-off Instructions  
This is instructions on how to drop off results for CAHPT, HbPT, HIVPT, ALDPT.
- 6** Program File Drop-off
- 7** PT Assay and Reporting Instructions

- 1. PT Portal Entry Instructions** – Downloadable instructions for completing PT data entry in the NSQAP Portal.
- 2. PT Analyte Selection** – Page for setting up the portal for PT data entry.
- 3. PT Specimen Data Entry** – Page for entering PT program data.
- 4. PT Submit/View Data** – Page for reviewing and submitting PT program data.
- 5. Program File Drop-Off Instructions**– Downloadable instructions for uploading PT program data entry forms into the NSQAP Portal.
- 6. Program File Drop-Off** – Page for uploading PT program data report forms into the NSQAP Portal.
- 7. PT Assay and Reporting Instructions** – Page for accessing NSQAP assay and reporting instructions for AAPT, ACPT, ALDPT BIOT, CAHPT, CFDNAPT, GALPT, G6PDPT, HbPT, HIVPT, HORMPT, IRTPT, LSDPT, TRECPT, and TOXOPT programs.

## 1.2 Biochemical Analyte Selection

1. Laboratories participating in the following programs should utilize the analyte selection page to set up the NSQAP portal for data entry: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.



Home > Program List - Select Analytes, Method(s) and Cutoff(s)

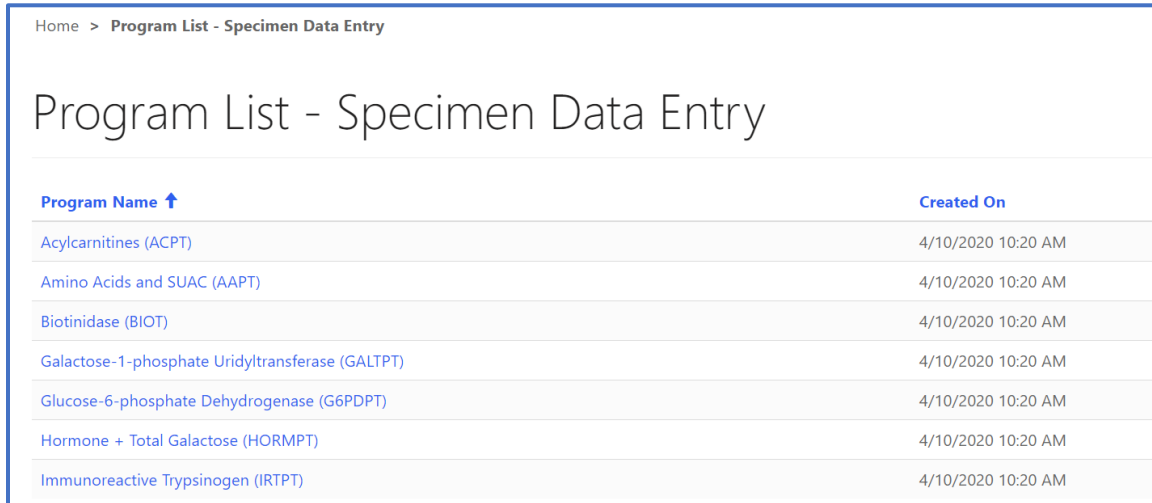
### Program List - Select Analytes, Method(s) and Cutoff(s)

| Program Name ↑                                   | Created On         |
|--|--------------------|
| Acylcarnitines (ACPT)                            | 4/10/2020 10:20 AM |
| Amino Acids and SUAC (AAPT)                      | 4/10/2020 10:20 AM |
| Biotinidase (BIOT)                               | 4/10/2020 10:20 AM |
| Galactose-1-phosphate Uridyltransferase (GALTPT) | 4/10/2020 10:20 AM |
| Glucose-6-phosphate Dehydrogenase (G6PDPT)       | 4/10/2020 10:20 AM |
| Hormone + Total Galactose (HORMPT)               | 4/10/2020 10:20 AM |
| Immunoreactive Trypsinogen (IRTPT)               | 4/10/2020 10:20 AM |

2. This page can be accessed by clicking on **'Biochemical Analyte Selection'** on the Biochemical PT drop-down menu or **'PT Analyte Selection'** on the PT Information page.
3. For additional information on analyte selection, see section 2.1.

## 1.3 Biochemical Specimen Data Entry

1. Laboratories participating in the following programs should utilize the specimen data entry page to enter data into the portal: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.



Home > Program List - Specimen Data Entry

### Program List - Specimen Data Entry

| Program Name ↑                                   | Created On         |
|--|--------------------|
| Acylcarnitines (ACPT)                            | 4/10/2020 10:20 AM |
| Amino Acids and SUAC (AAPT)                      | 4/10/2020 10:20 AM |
| Biotinidase (BIOT)                               | 4/10/2020 10:20 AM |
| Galactose-1-phosphate Uridyltransferase (GALTPT) | 4/10/2020 10:20 AM |
| Glucose-6-phosphate Dehydrogenase (G6PDPT)       | 4/10/2020 10:20 AM |
| Hormone + Total Galactose (HORMPT)               | 4/10/2020 10:20 AM |
| Immunoreactive Trypsinogen (IRTPT)               | 4/10/2020 10:20 AM |

2. This page can be accessed by clicking on **'Biochemical Specimen Data Entry'** on the Biochemical PT drop-down menu or **'PT Specimen Data Entry'** on the PT Information page.
3. For additional information on data entry, see section 2.2.



## 1.4 Biochemical Review and Submit Data

1. Laboratories participating in the following programs should utilize the biochemical summary and submission page to review and submit data: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.

| Summary and Submission                           |                |
|--|----------------|
| Program Name ↑                                   | Submitted User |
| Acylcarnitines (ACPT)                            |                |
| Amino Acids and SUAC (AAPT)                      |                |
| Biotinidase (BIOT)                               |                |
| Galactose-1-phosphate Uridyltransferase (GALTPT) |                |
| Glucose-6-phosphate Dehydrogenase (G6PDPT)       |                |
| Hormone + Total Galactose (HORMPT)               |                |
| Immunoreactive Trypsinogen (IRTPT)               |                |

2. This page can be accessed by clicking on **'Biochemical Review/Submit Data'** on the Biochemical PT drop-down menu or **'PT Submit/View Data'** on the PT Information page.
3. For additional information on reviewing and submitting data, see section 3.

## 1.5 Program File Drop-Off

1. Laboratories participating in the following programs will need to utilize the program file drop-off page to upload data report forms: CAHPT, HbPT, HIVPT, and ALDPT.

Home > Program File Drop-off

### Program File Drop-off

Note: Select the link below to access file upload folder for: CAHPT, HbPT, HIVPT, ALDPT. ([Click here to download PT template](#))

| Folder ↑                               | Created On         |
|--|--------------------|
| <a href="#">PT Drop Box - LAB-9001</a> | 8/31/2020 10:13 AM |

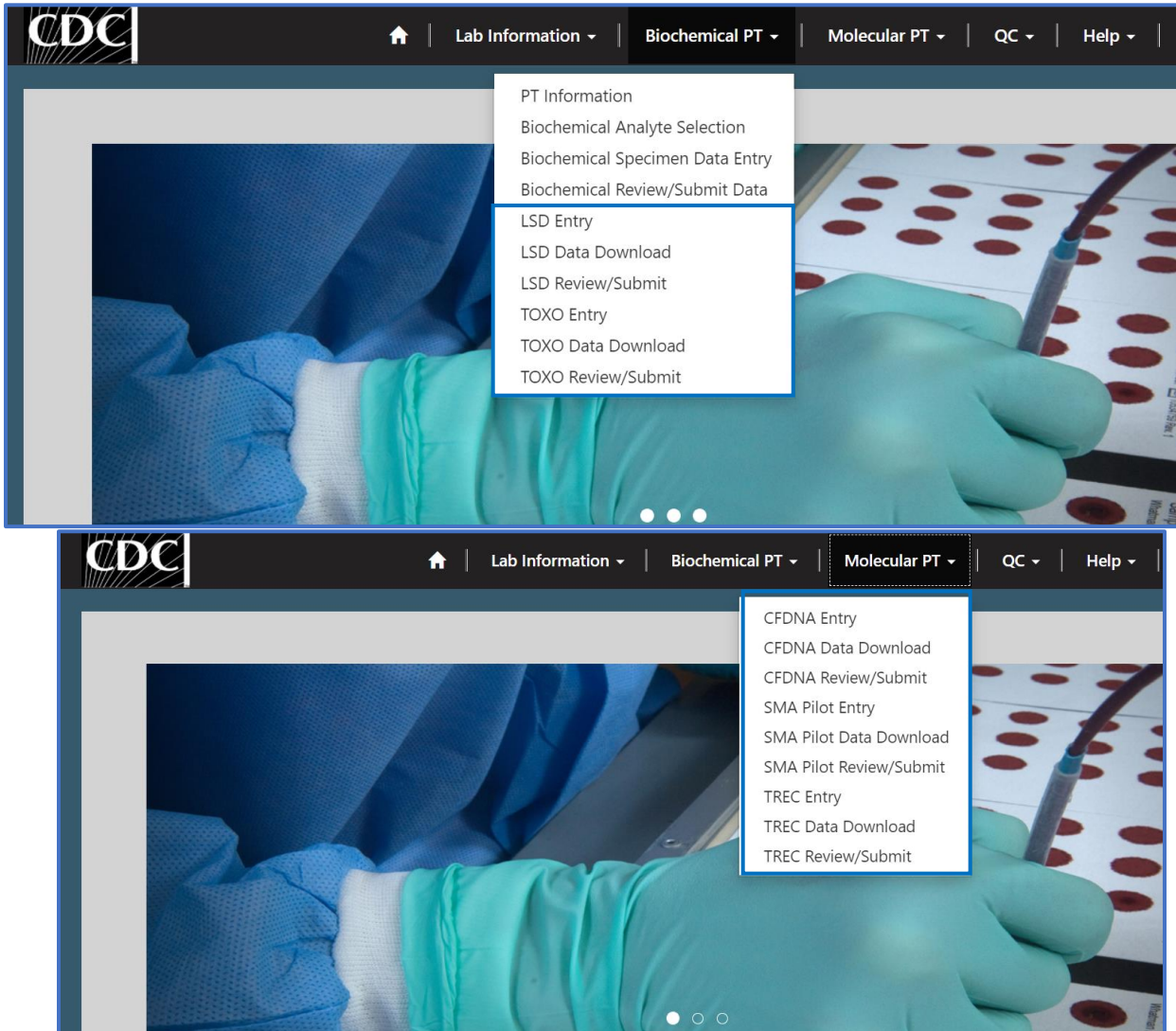
About NSQAP Self-Service Portal

This program is cosponsored by the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laboratories (APHL).

2. This page can be accessed by clicking on **'Program File Drop-Off'** on the PT Information page.
3. For additional information on program file drop-off, see section 4.

## 1.6 Program Specific PT Pages

- Laboratories participating in the following programs will need to utilize the program specific PT pages: CFDNAPT, LSDPT, SMART Pilot, TOXOPT, TRECPT, ALDPT.



- Three relevant NSQAP Portal pages exist per program (LSD, TOXO, CFDNA, SMA Pilot, and TREC): Entry, Review and Submit, and Data Download.

- **Entry** – Page for Entering and Saving Program Specific PT Program Data.
- **Review and Submit** – Page for Reviewing and Submitting Program Specific PT Program Data.
- **Data Download** – Page for Downloading Submitted Program Specific PT Program Data.

3. For additional information on any of the five sets of program specific PT pages, see the program specific PT user guide for that particular program.

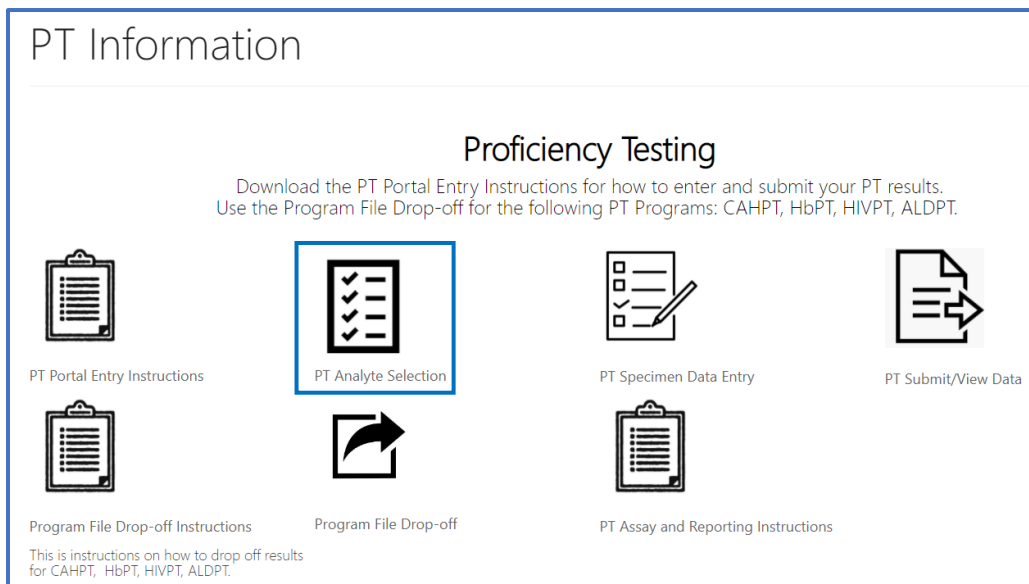
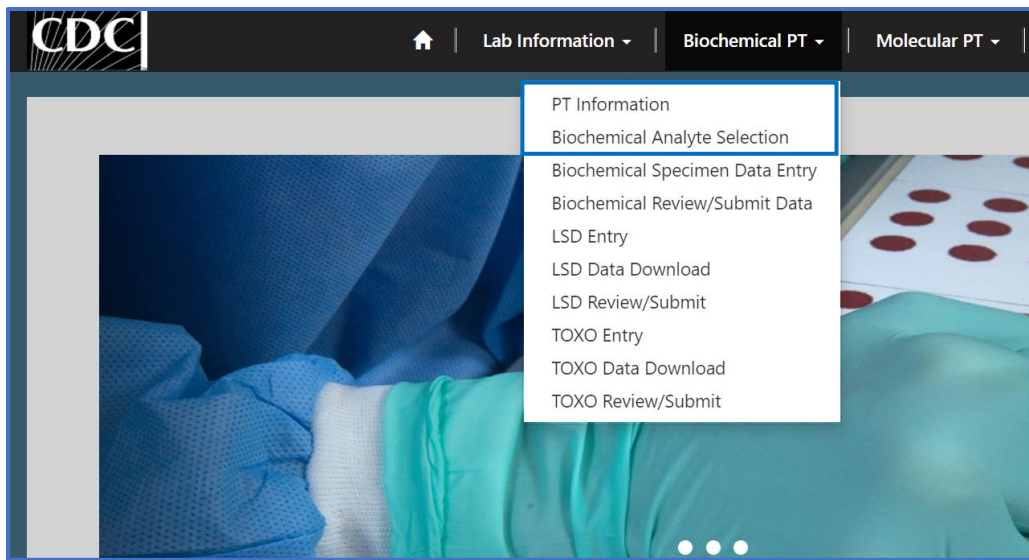
## 2. Biochemical Data Entry

### 2.1 Analyte Selection

Laboratories participating in the following programs should utilize the analyte selection page to set up the portal for data entry: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.

Enter and submit data in the NSQAP Portal by first setting up the portal for PT Data Entry.

1. Select the **'Biochemical PT'** button at the top of the page on the toolbar and select either the **'PT Information'** or the **'Biochemical Analyte Selection'** option. On the PT Information page select **'PT Analyte Selection'**.



2. Select the PT program to begin analyte selection by clicking the program hyperlink in the Program List.

Program List - Select Analytes, Method(s) and Cutoff(s)

| Program Name ↑   | Created On         |
|--|--------------------|
| <a href="#">Acylcarnitines (ACPT)</a>                            | 4/10/2020 10:20 AM |
| <a href="#">Amino Acids and SUAC (AAPT)</a>                      | 4/10/2020 10:20 AM |
| <a href="#">Biotinidase (BIOT)</a>                               | 4/10/2020 10:20 AM |
| <a href="#">Galactose-1-phosphate Uridyltransferase (GALTPT)</a> | 4/10/2020 10:20 AM |
| <a href="#">Glucose-6-phosphate Dehydrogenase (G6PDPT)</a>       | 4/10/2020 10:20 AM |
| <a href="#">Hormone + Total Galactose (HORMPT)</a>               | 4/10/2020 10:20 AM |
| <a href="#">Immunoreactive Trypsinogen (IRTPT)</a>               | 4/10/2020 10:20 AM |

3. The Method Selection page will appear for all reportable analytes within the selected program. Select the analytes for which data will be reported. To select all analytes, check the **'Select All Analytes'** box. This assumes data will be reported for every analyte in the program. To select individual analytes, select the check box next to the analytes to be reported.

## Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

Select All Analytes

- Arginine (Arg)
- Citrulline (Cit)
- Leucine (Leu)
- Methionine (Met)
- Phenylalanine (Phe)
- Succinylacetone (SUAC)
- Tyrosine (Tyr)
- Valine (Val)

Set All Methods Below

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

Method

Cutoff (µmol/L blood)

SAVE AND SET VALUES

**NOTE:** The ‘Select All Analytes’ checkbox is only present for AAPT and ACPT. All other PT Programs must have the method set for each analyte.

**NOTE:** When the ‘Select All Analytes’ is checked for ACPT, all analytes except C3DC, C3DC+C4OH, and C4OH will be checked. To choose these analytes, manually check the boxes and select a compatible method for each.

- Select the method to be used for each analyte tested. If the same method is to be used for all analytes, select the **'Magnifying Glass'** icon on the 'Set All Methods Below' field. If different methods are to be used for specific analytes, select the **'Magnifying Glass'** icon on the **'Method'** field for that specific analyte.

Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

Select All Analytes

Arginine (Arg)

Citrulline (Cit)

Leucine (Leu)

Methionine (Met)

Phenylalanine (Phe)

Succinylacetone (SUAC)

Tyrosine (Tyr)

Valine (Val)

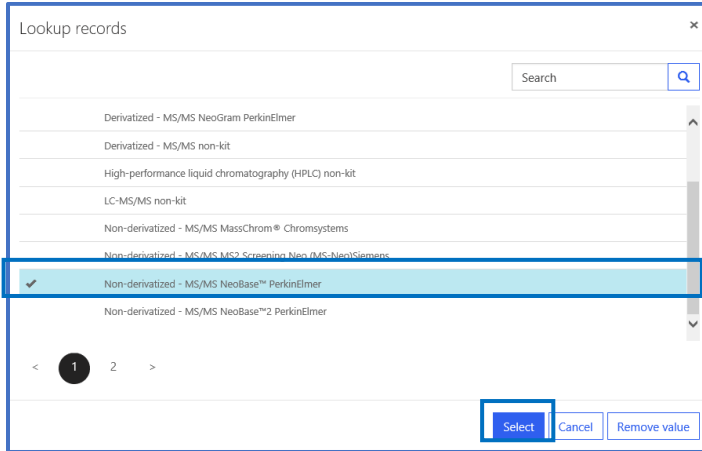
Set All Methods Below

|   |   |   |
|---|---|---|
| <input type="checkbox"/> Arginine (Arg)         | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Citrulline (Cit)       | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Leucine (Leu)          | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Methionine (Met)       | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Phenylalanine (Phe)    | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Succinylacetone (SUAC) | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Tyrosine (Tyr)         | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |
| <input type="checkbox"/> Valine (Val)           | <p>Method</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> <input style="float: right; width: 20px; height: 20px; border: 1px solid black; border-radius: 50%; text-align: center; line-height: 20px; font-size: 12px; margin-left: 5px;" type="button" value="Q"/> </p> | <p>Cutoff (µmol/L blood)</p> <p style="text-align: center;"> <input style="width: 100%; height: 20px;" type="text"/> </p> |

SAVE AND SET VALUES



- A new window will appear listing methods for the analyte(s). To select a method, click on the method, and the row will highlight with a check mark on the left side. Click the **'Select'** button at the bottom of the window to select the method for all analytes or a single analyte.



- If **'Set All Methods Below'** is used, the method will populate in the 'Method' field for all analytes on the page.

### Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

Select All Analytes

Arginine (Arg)

Citrulline (Cit)

Leucine (Leu)

Methionine (Met)

Phenylalanine (Phe)

Succinylacetone (SUAC)

Tyrosine (Tyr)

Valine (Val)

**Set All Methods Below**

Non-derivatized - MS/MS NeoBase™ PerkinElmer ✕ 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Method**  
Non-derivatized - MS/MS NeoBase™ PerkinElmer 🔍

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

**Cutoff (µmol/L blood)**

SAVE AND SET VALUES

**NOTE:** For ACPT, the method will populate for all analytes except C3DC, C3DC+C4OH, and C4OH. If these analytes are selected, the method for each must be set individually.

**NOTE:** For HORMPT, the method must be set individually for each analyte.

- If a method has been selected for an individual analyte, it will appear in the 'Method' field for the selected analyte only.

### Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

|   |  |  |
|---|--|--|
| <input type="checkbox"/> Select All Analytes            | <b>Set All Methods Below</b><br><input style="width: 90%;" type="text"/>                             |  |
| <input checked="" type="checkbox"/> Arginine (Arg)      | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">✕ 🔍</span> | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input type="checkbox"/> Citrulline (Cit)               | <b>Method</b><br><input style="width: 90%;" type="text"/>  | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input checked="" type="checkbox"/> Leucine (Leu)       | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">✕ 🔍</span> | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input type="checkbox"/> Methionine (Met)               | <b>Method</b><br><input style="width: 90%;" type="text"/>  | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input checked="" type="checkbox"/> Phenylalanine (Phe) | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">✕ 🔍</span> | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input type="checkbox"/> Succinylacetone (SUAC)         | <b>Method</b><br><input style="width: 90%;" type="text"/>  | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input type="checkbox"/> Tyrosine (Tyr)                 | <b>Method</b><br><input style="width: 90%;" type="text"/>  | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |
| <input type="checkbox"/> Valine (Val)                   | <b>Method</b><br><input style="width: 90%;" type="text"/>  | <b>Cutoff (µmol/L blood)</b><br><input style="width: 90%;" type="text"/> |

- If the method for testing is not shown in the provided list, click the **'Other'** option, then the **'Select'** button.

- If 'Other' method is selected type the name of the 'Other Method' the field.

**NOTE:** ‘Other’ methods must be set individually for each analyte in HORMPT program.

10. Enter the cutoff value for each analyte in the ‘Cutoff’ field.

### Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

|   |   |   |
|---|---|---|
| <input type="checkbox"/> Select All Analytes            | <b>Set All Methods Below</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">✕ 🔍</span> |   |
| <input type="checkbox"/> Arginine (Arg)                 | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="70.0"/>                                       |
| <input type="checkbox"/> Citrulline (Cit)               | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="55.0"/>                                       |
| <input type="checkbox"/> Leucine (Leu)                  | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="290.0"/>                                      |
| <input type="checkbox"/> Methionine (Met)               | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="75.0"/>                                       |
| <input checked="" type="checkbox"/> Phenylalanine (Phe) | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="150.0"/>                                      |
| <input type="checkbox"/> Succinylacetone (SUAC)         | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="2.2"/>  |
| <input type="checkbox"/> Tyrosine (Tyr)                 | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input type="text" value="350.0"/>                                      |
| <input type="checkbox"/> Valine (Val)                   | <b>Method</b><br>Non-derivatized - MS/MS NeoBase™ PerkinElmer <span style="float: right;">🔍</span>                  | <b>Cutoff (µmol/L blood)</b><br><input style="border: 1px solid #0070C0;" type="text" value="300.0"/> ✕ |

SAVE AND SET VALUES

**NOTE:** Cutoffs shown are for illustration only and have no clinical utility. Laboratories are expected to report their own cutoffs.

11. Complete program setup for data entry by selecting the **'Save and Set Values'** button at the bottom of the setup page.

### Amino Acid (AAPT)

Select the analyte(s) you want to report, method(s), and give the cutoff for each analyte. Report AAPT data to one decimal place. e.g. (X.X)

|   |  |                              |
|---|--|------------------------------|
| <input type="checkbox"/> Select All Analytes            | <b>Set All Methods Below</b>                 |                              |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | ✕ 🔍                          |
| <input type="checkbox"/> Arginine (Arg)                 | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 70.0                         |
| <input type="checkbox"/> Citrulline (Cit)               | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 55.0                         |
| <input type="checkbox"/> Leucine (Leu)                  | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 290.0                        |
| <input type="checkbox"/> Methionine (Met)               | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 75.0                         |
| <input checked="" type="checkbox"/> Phenylalanine (Phe) | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 150.0                        |
| <input type="checkbox"/> Succinylacetone (SUAC)         | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2.2                          |
| <input type="checkbox"/> Tyrosine (Tyr)                 | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 350.0                        |
| <input type="checkbox"/> Valine (Val)                   | <b>Method</b>                                | <b>Cutoff (µmol/L blood)</b> |
|   | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 300.0 ✕                      |

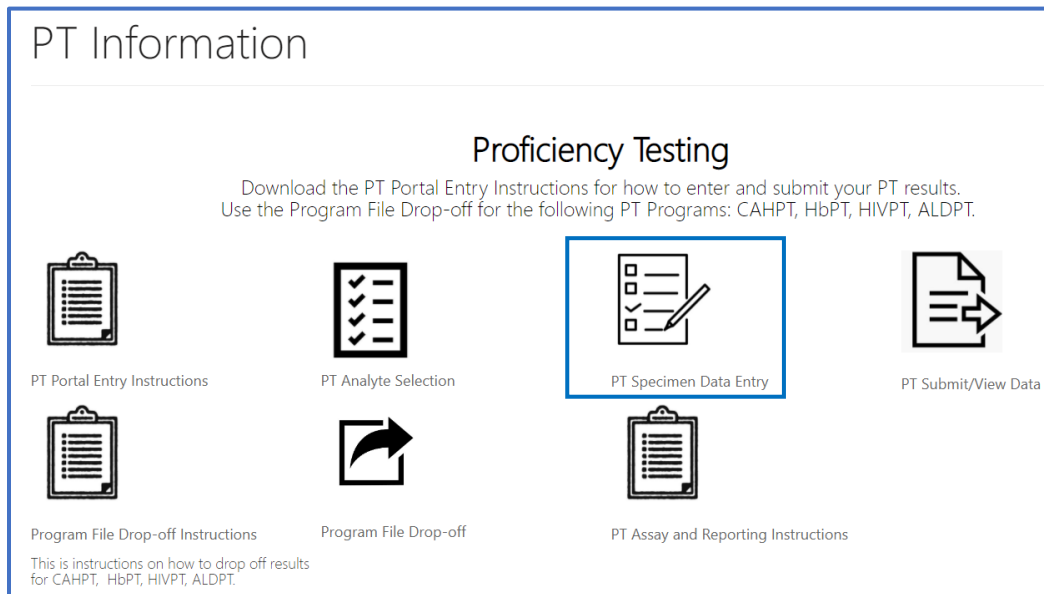
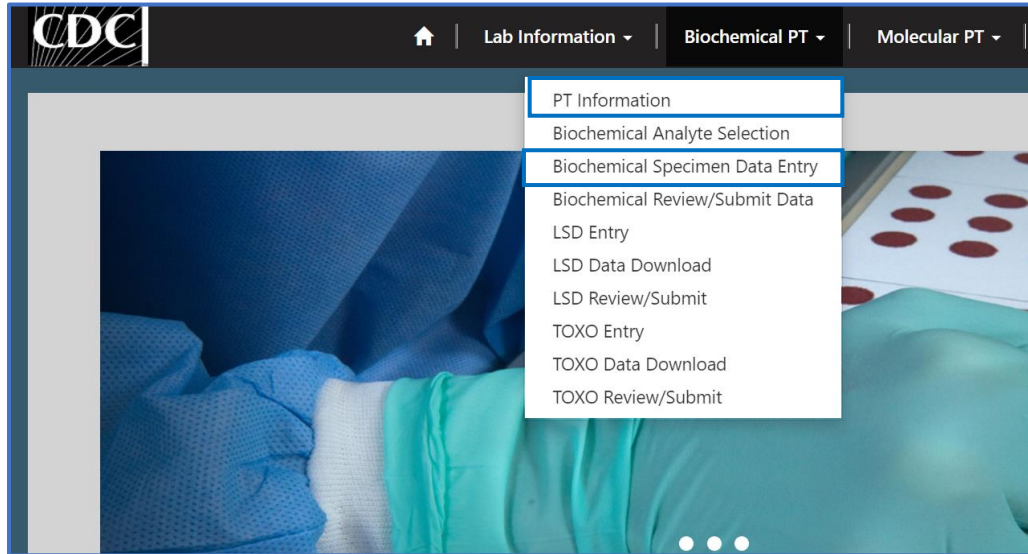
SAVE AND SET VALUES

**NOTE:** If the **'Save and Set Values'** button is not selected, data will not be retained.

## 2.2 Data Entry

Laboratories participating in the following biochemical programs should utilize the data entry page to enter data: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.

1. Select the **'Biochemical PT'** button at the top of the page on the toolbar and select either the **'PT Information'** or the **'Biochemical Specimen Data Entry'** option. On the PT Information page select **'PT Specimen Data Entry'**.



- Select the PT Program by clicking on the program hyperlink in the list of programs.

Home > Program List - Specimen Data Entry

## Program List - Specimen Data Entry

| Program Name ↑   | Created On         |
|--|--------------------|
| <a href="#">Acylcarnitines (ACPT)</a>                            | 4/10/2020 10:20 AM |
| <a href="#">Amino Acids and SUAC (AAPT)</a>                      | 4/10/2020 10:20 AM |
| <a href="#">Biotinidase (BIOT)</a>                               | 4/10/2020 10:20 AM |
| <a href="#">Galactose-1-phosphate Uridyltransferase (GALTPT)</a> | 4/10/2020 10:20 AM |
| <a href="#">Glucose-6-phosphate Dehydrogenase (G6PDPT)</a>       | 4/10/2020 10:20 AM |
| <a href="#">Hormone + Total Galactose (HORMPT)</a>               | 4/10/2020 10:20 AM |
| <a href="#">Immunoreactive Trypsinogen (IRTPT)</a>               | 4/10/2020 10:20 AM |

- The specimen list page will appear for that program.

## Specimen List

[View Summary](#)

### Specimen

| Specimen Number ↑ | Program Name | Specimen Status | Modified On       | Last Edited By |
|-------------------|--------------|-----------------|-------------------|----------------|
| 20202005001       | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| 20202005002       | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| 20202005003       | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| 20202005004       | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| 20202005005       | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |

4. To navigate to the specimen data entry page, select the ‘Specimen Number’ hyperlink.

Specimen List

[View Summary](#)

Specimen ▲

| Specimen Number ↑           | Program Name | Specimen Status | Modified On       | Last Edited By |
|-----------------------------|--------------|-----------------|-------------------|----------------|
| <a href="#">20202005001</a> | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| <a href="#">20202005002</a> | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| <a href="#">20202005003</a> | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| <a href="#">20202005004</a> | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |
| <a href="#">20202005005</a> | AAPT         | Set             | 4/13/2020 4:31 PM | ▼              |

5. Data from the PT program setup page will populate for each analyte.

**Phenylalanine (Phe)**

**Method\*** Non-derivatized - MS/MS NeoBase™ PerkinElmer **Cutoff (µmol/L blood)** 150.0

---

**Specimen Number** 20194005001 **Result µmol/L blood**  **Phe Presumptive Clinical Assessment\***

**Succinylacetone (SUAC)**

**Method\*** Non-derivatized - MS/MS NeoBase™ PerkinElmer **Cutoff (µmol/L blood)** 2.2

---

**Specimen Number** 20194005001 **Result µmol/L blood**  **SUAC Presumptive Clinical Assessment\***

**Tyrosine (Tyr)**

**Method\*** Non-derivatized - MS/MS NeoBase™ PerkinElmer **Cutoff (µmol/L blood)** 350.0

---

**Specimen Number** 20194005001 **Result µmol/L blood**  **Tyr Presumptive Clinical Assessment\***



- Enter the results for each analyte and specimen number. Choose the 'Presumptive Clinical Assessment' from the drop down list and select '1 – Within Normal Limits' or '2 – Outside Normal Limits'. Method and Presumptive Clinical Assessment must be completed for each analyte.

**Phenylalanine (Phe)**

|  |                              |
|--|------------------------------|
| <b>Method*</b>                               | <b>Cutoff (µmol/L blood)</b> |
| Non-derivatized - MS/MS NeoBase™ PerkinElmer | 150.0                        |

|                        |                                    |  |
|------------------------|------------------------------------|--|
| <b>Specimen Number</b> | <b>Result µmol/L blood</b>         | <b>Phe Presumptive Clinical Assessment*</b>                              |
| 20194005001            | <input type="text" value="134.3"/> | <input style="width: 95%;" type="text" value="1- Within normal limits"/> |

**Succinylacetone (SUAC)**

|  |                              |
|--|------------------------------|
| <b>Method*</b>                               | <b>Cutoff (µmol/L blood)</b> |
| Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2.2                          |

|                        |                                  |  |
|------------------------|----------------------------------|--|
| <b>Specimen Number</b> | <b>Result µmol/L blood</b>       | <b>SUAC Presumptive Clinical Assessment*</b>                             |
| 20194005001            | <input type="text" value="1.7"/> | <input style="width: 95%;" type="text" value="1- Within normal limits"/> |

**Tyrosine (Tyr)**

|  |                              |
|--|------------------------------|
| <b>Method*</b>                               | <b>Cutoff (µmol/L blood)</b> |
| Non-derivatized - MS/MS NeoBase™ PerkinElmer | 350.0                        |

|                        |                                    |  |
|------------------------|------------------------------------|--|
| <b>Specimen Number</b> | <b>Result µmol/L blood</b>         | <b>Tyr Presumptive Clinical Assessment*</b>                              |
| 20194005001            | <input type="text" value="334.7"/> | <input style="width: 95%;" type="text" value="1- Within normal limits"/> |

- Select the '**Save Data**' button at the bottom of the specimen data entry page to save results. Select the '**OK**' button when prompted with 'Are you sure you want to save data?'.

**Tyrosine (Tyr)**

|  |                              |
|--|------------------------------|
| <b>Method*</b>                               | <b>Cutoff (µmol/L blood)</b> |
| Non-derivatized - MS/MS NeoBase™ PerkinElmer | 350.0                        |

|                        |                                    |  |
|------------------------|------------------------------------|--|
| <b>Specimen Number</b> | <b>Result µmol/L blood</b>         | <b>Tyr Presumptive Clinical Assessment*</b>                              |
| 20194005001            | <input type="text" value="334.7"/> | <input style="width: 95%;" type="text" value="1- Within normal limits"/> |

Save Data

8. When the specimen has been saved, the specimen list page will update the ‘Specimen Status’ to ‘Saved’, show the time it was last saved, and show the last person to save the specimen data.

Specimen List

[View Summary](#)

Specimen

| Specimen Number ↑ | Program Name | Specimen Status | Modified On       | Last Edited By |
|-------------------|--------------|-----------------|-------------------|----------------|
| 20202005001       | AAPT         | Saved           | 8/27/2020 5:49 PM | Kawanda Foster |
| 20202005002       | AAPT         | Set             | 4/13/2020 4:31 PM |                |
| 20202005003       | AAPT         | Set             | 4/13/2020 4:31 PM |                |
| 20202005004       | AAPT         | Set             | 4/13/2020 4:31 PM |                |
| 20202005005       | AAPT         | Set             | 4/13/2020 4:31 PM |                |

9. In order to submit the data for the program, all specimen numbers must be completed and in a ‘Saved’ or ‘Saved (Edited)’ specimen status.

Specimen List

[View Summary](#)

Specimen

| Specimen Number ↑ | Program Name | Specimen Status | Modified On        | Last Edited By |
|-------------------|--------------|-----------------|--------------------|----------------|
| 20193005001       | AAPT         | Saved (Edited)  | 7/10/2019 12:39 PM | Corvin Bradley |
| 20193005002       | AAPT         | Saved (Edited)  | 7/10/2019 12:40 PM | Corvin Bradley |
| 20193005003       | AAPT         | Saved (Edited)  | 7/10/2019 12:42 PM | Corvin Bradley |
| 20193005004       | AAPT         | Saved (Edited)  | 7/10/2019 12:45 PM | Corvin Bradley |
| 20193005005       | AAPT         | Saved           | 7/10/2019 12:47 PM | Corvin Bradley |

**NOTE:** The ‘Saved (Edited)’ status appears when a record is saved again, after the initial save.

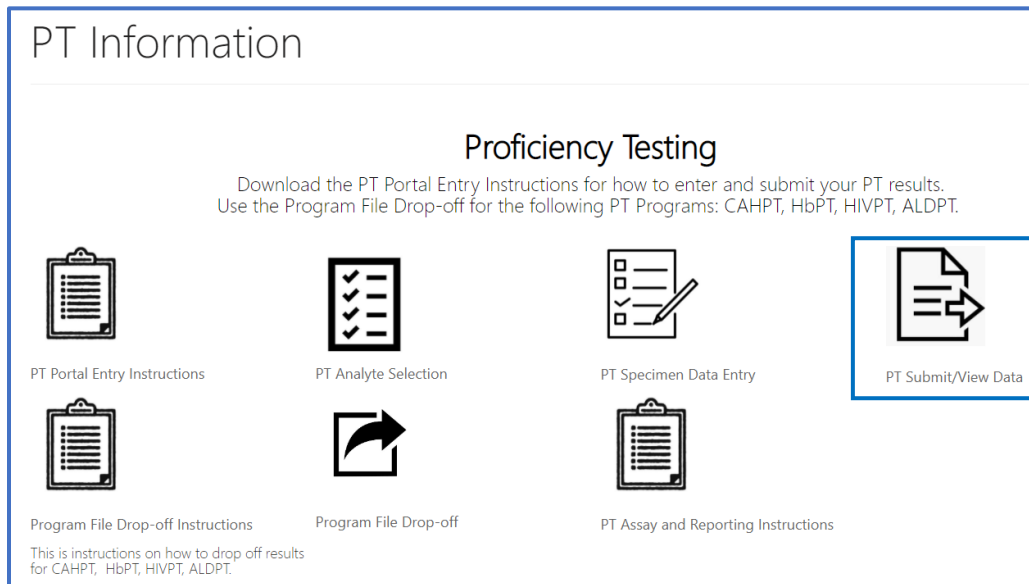
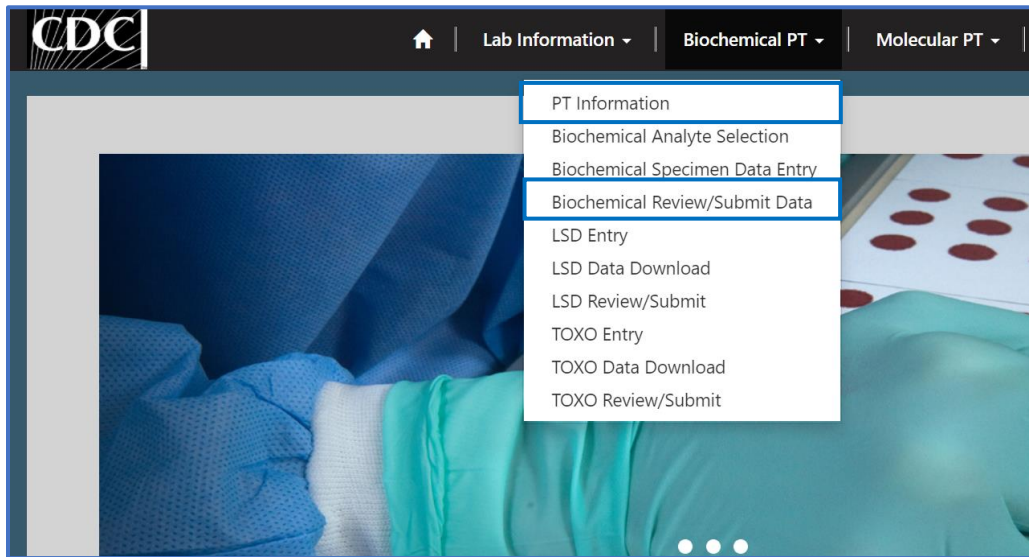
**NOTE:** Data can only be submitted if ALL specimens have a ‘Saved’ or ‘Saved (Edited)’ specimen status.

## 3. Biochemical Data Review and Submission

### 3.1 Data Summary

Laboratories participating in the following programs should utilize the review and submit page to set up the portal for data entry: ACPT, AAPT, BIOT, GALTPT, G6PDPT, HORMPT, & IRTPT.

1. Select the **'Biochemical PT'** button at the top of the page on the toolbar and select either the **'PT Information'** or the **'Biochemical Review/Submit Data'** option. On the PT Information page select **'PT Submit/View Data'**.



2. Select the PT Program by clicking on the program hyperlink.

## Summary and Submission

| Program Name ↑   | Submitted User |
|--|----------------|
| <a href="#">Acylcarnitines (ACPT)</a>                            |                |
| <a href="#">Amino Acids and SUAC (AAPT)</a>                      |                |
| <a href="#">Biotinidase (BIOT)</a>                               |                |
| <a href="#">Galactose-1-phosphate Uridyltransferase (GALTPT)</a> |                |
| <a href="#">Glucose-6-phosphate Dehydrogenase (G6PDPT)</a>       |                |
| <a href="#">Hormone + Total Galactose (HORMPT)</a>               |                |
| <a href="#">Immunoreactive Trypsinogen (IRTPT)</a>               |                |

3. The summary page will appear for that program.

### RESULTS

Select Views to Download

☰ AAPT - View All Data ▾

⬇ Download

| Specimen Number ↑ | Arg_Method   | Arg_Presumptive Clinical Assessment | Arg_Cutoff | Arg_Result | Cit_Method   | Cit_Presumptive Clinical Assessment | Cit_Cutoff | Cit_Result | Leu_Method   | Leu_Pi Clinical Assess |
|-------------------|--|-------------------------------------|------------|------------|--|-------------------------------------|------------|------------|--|------------------------|
| 20193005001       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 70.0       | 68.3       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 55.0       | 54.2       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 2- Out norma           |
| 20193005002       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 2- Outside normal limits            | 70.0       | 73.9       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 55.0       | 50.4       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Witi limits         |
| 20193005003       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 70.0       | 69.2       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 55.0       | 53.4       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Witi limits         |
| 20193005004       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 2- Outside normal limits            | 70.0       | 75.4       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 2- Outside normal limits            | 55.0       | 55.6       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Witi limits         |
| 20193005005       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 70.0       | 45.8       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Within normal limits             | 55.0       | 35.7       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | 1- Witi limits         |

- The results can be reviewed in 3 ways: 'View All Data', 'View Method(s) Only', and 'View Results Only'. Each view can be downloaded to a MS Excel spreadsheet by clicking the 'Download' button.

**RESULTS**

Select Views to Download

- AAPT - View All Data
- AAPT - View Method(s) Only
- AAPT - View Results Only

| Specimen Number | Arg_Method                                   | Arg_Presumptive Clinical Assessment | Arg_Cutoff | Arg_Result | Cit_Method                                   | Cit_Presumptive Clinical Assessment | Cit_Cutoff | Cit_Result | Leu_Method                                   | Leu_Pi Clinica Assess                        |
|-----------------|--|-------------------------------------|------------|------------|--|-------------------------------------|------------|------------|--|--|
| 20193005001     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 70.0       | 68.3       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 70.0       | 68.3       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | Non-derivatized - MS/MS NeoBase™ PerkinElmer |
| 20193005002     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Outside normal limits            | 70.0       | 73.9       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Outside normal limits            | 70.0       | 73.9       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | Non-derivatized - MS/MS NeoBase™ PerkinElmer |

View All Data

**RESULTS**

Select Views to Download

- AAPT - View All Data
- Download

| Specimen Number | Arg_Method                                   | Arg_Presumptive Clinical Assessment | Arg_Cutoff | Arg_Result | Cit_Method                                   | Cit_Presumptive Clinical Assessment | Cit_Cutoff | Cit_Result | Leu_Method                                   | Leu_Pi Clinica Assess |
|-----------------|--|-------------------------------------|------------|------------|--|-------------------------------------|------------|------------|--|-----------------------|
| 20193005001     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 70.0       | 68.3       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 55.0       | 54.2       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Out norma          |
| 20193005002     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Outside normal limits            | 70.0       | 73.9       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 55.0       | 50.4       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Witr limits        |
| 20193005003     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 70.0       | 69.2       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 55.0       | 53.4       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Witr limits        |
| 20193005004     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Outside normal limits            | 70.0       | 75.4       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 2- Outside normal limits            | 55.0       | 55.6       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Witr limits        |
| 20193005005     | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 70.0       | 45.8       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Within normal limits             | 55.0       | 35.7       | Non-derivatized - MS/MS NeoBase™ PerkinElmer | 1- Witr limits        |

View Methods Only

**RESULTS**

Select Views to Download

[AAPT - View Method\(s\) Only](#) [Download](#)

| Specimen Number ↑ | Arg_Method   | Cit_Method   | Leu_Method   | Met_Method   | Phe_Method   | SUAC_Method  | Tyr_Method   | Val_Method   |
|-------------------|--|--|--|--|--|--|--|--|
| 20193005001       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer |
| 20193005002       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer |
| 20193005003       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer |
| 20193005004       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer |
| 20193005005       | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer | Non-derivatized - MS/MS<br>NeoBase™<br>PerkinElmer |

View Results Only

**RESULTS**

Select Views to Download

[AAPT - View Results Only](#) [Download](#)

| Specimen Number ↑ | Arg_Presumptive Clinical |            | Cit_Presumptive Clinical |            | Leu_Presumptive Clinical |                          | Met   |       |                          |      |
|-------------------|--------------------------|------------|--------------------------|------------|--------------------------|--------------------------|-------|-------|--------------------------|------|
|                   | Arg_Result               | Arg_Cutoff | Cit_Result               | Cit_Cutoff | Leu_Result               | Leu_Cutoff               |       |       |                          |      |
| 20193005001       | 68.3                     | 70.0       | 1- Within normal limits  | 54.2       | 55.0                     | 1- Within normal limits  | 295.6 | 290.0 | 2- Outside normal limits | 73.2 |
| 20193005002       | 73.9                     | 70.0       | 2- Outside normal limits | 50.4       | 55.0                     | 1- Within normal limits  | 247.7 | 290.0 | 1- Within normal limits  | 67.6 |
| 20193005003       | 69.2                     | 70.0       | 1- Within normal limits  | 53.4       | 55.0                     | 1- Within normal limits  | 287.3 | 290.0 | 1- Within normal limits  | 76.8 |
| 20193005004       | 75.4                     | 70.0       | 2- Outside normal limits | 55.6       | 55.0                     | 2- Outside normal limits | 278.3 | 290.0 | 1- Within normal limits  | 67.3 |
| 20193005005       | 45.8                     | 70.0       | 1- Within normal limits  | 35.7       | 55.0                     | 1- Within normal limits  | 237.4 | 290.0 | 1- Within normal limits  | 67.8 |

<  >

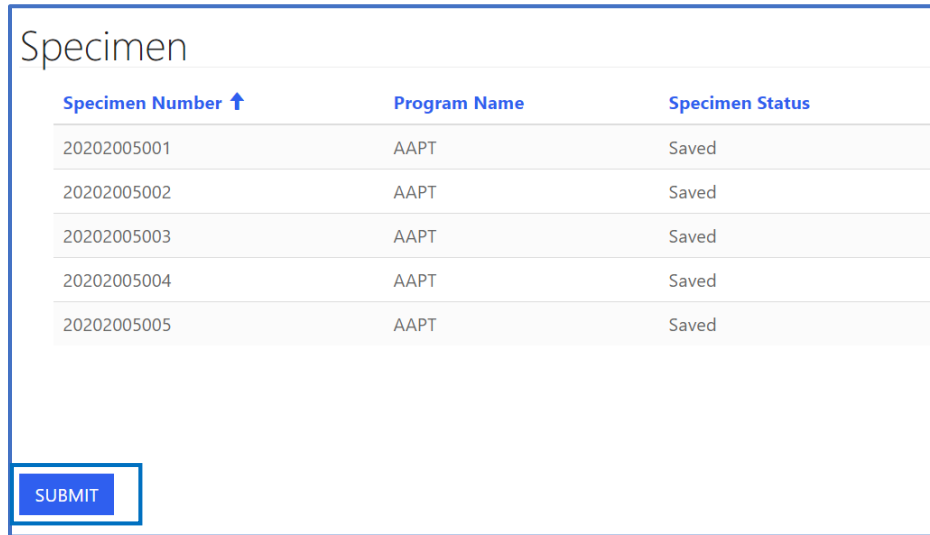
- The specimen table shows a summary view of the specimen numbers, the specimen status, when the specimen was last saved, and the last person to save the data.

Specimen

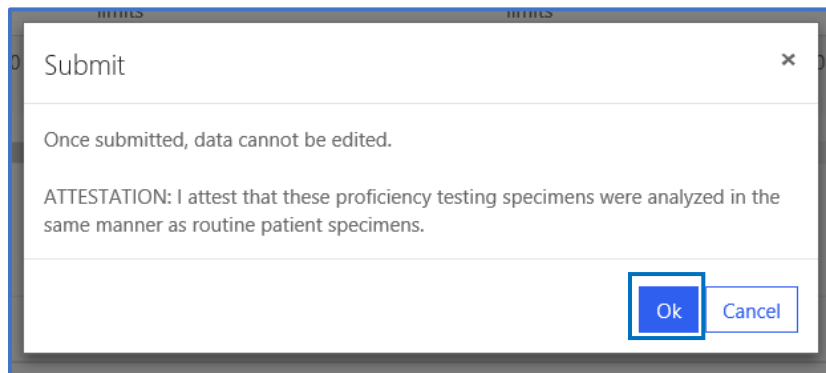
| Specimen Number ↑ | Program Name | Specimen Status | Modified On       | Last Edited By |
|-------------------|--------------|-----------------|-------------------|----------------|
| 20202005001       | AAPT         | Saved           | 8/27/2020 5:55 PM | Kawanda Foster |
| 20202005002       | AAPT         | Saved           | 8/27/2020 5:53 PM | Kawanda Foster |
| 20202005003       | AAPT         | Saved           | 8/27/2020 5:54 PM | Kawanda Foster |
| 20202005004       | AAPT         | Saved           | 8/27/2020 5:54 PM | Kawanda Foster |
| 20202005005       | AAPT         | Saved           | 8/27/2020 5:54 PM | Kawanda Foster |

## 3.2 Data Submission

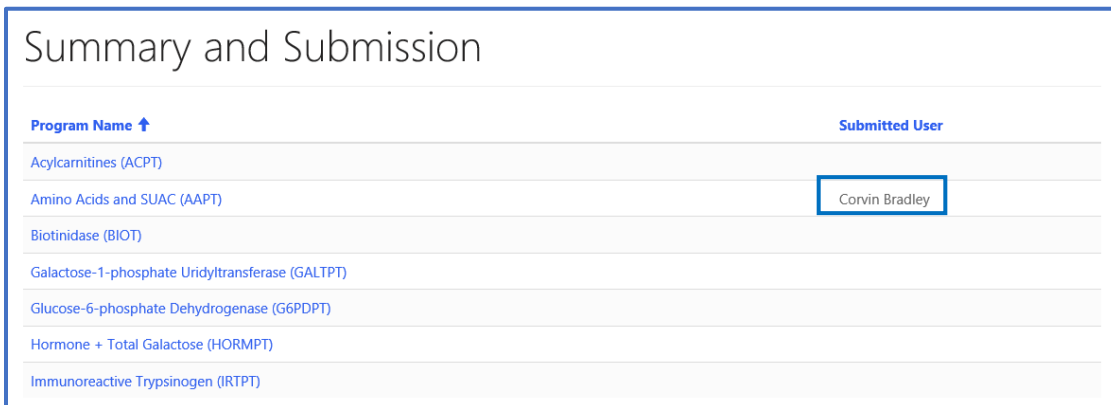
1. To submit data for the program, click the **'Submit'** button at the bottom of the summary page.



2. Select the **'OK'** button on the submission prompt.

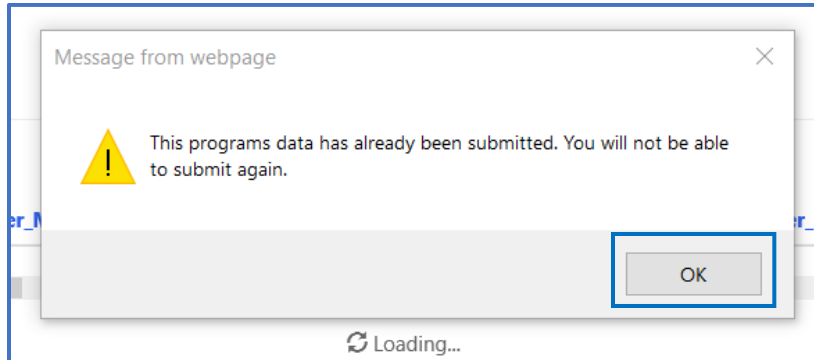


3. The user who submitted the data will appear in the program list for summary and submission.





- If you click on a submitted program's link, you will be prompted that data has already been submitted and cannot be submitted again. Click the **'Ok'** button to proceed to the summary page.



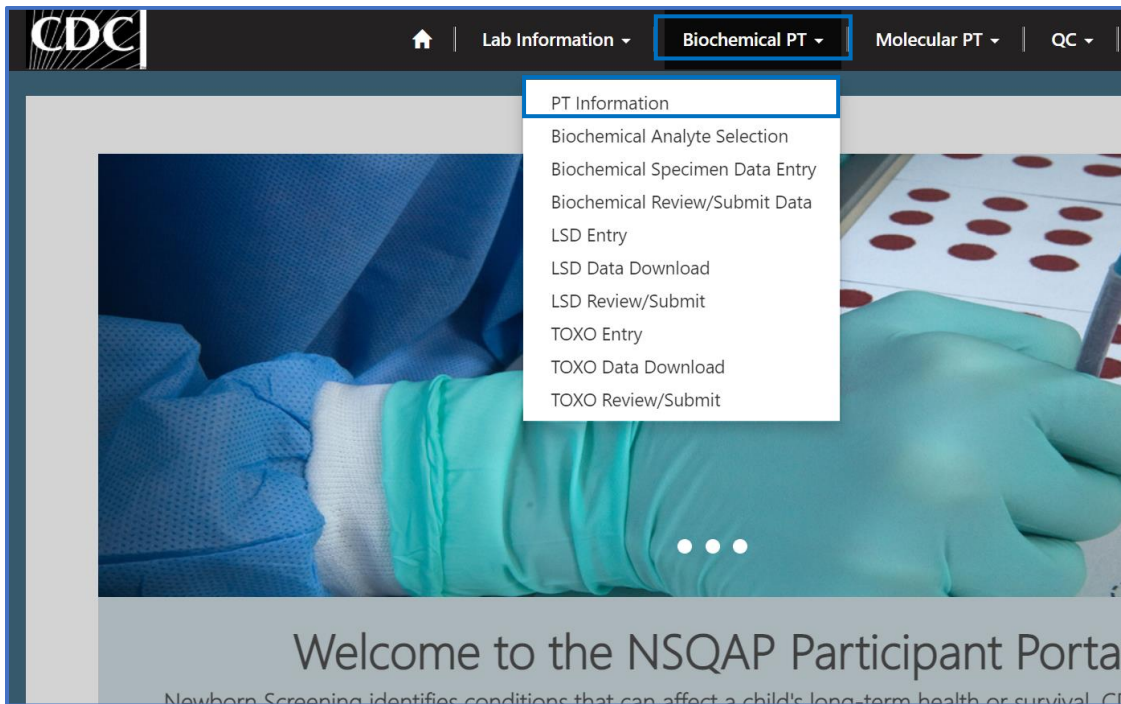
- The 'Specimen Status' for each specimen will read 'Submitted'.

| Specimen          |              |                 |
|-------------------|--------------|-----------------|
| Specimen Number ↑ | Program Name | Specimen Status |
| 20193005001       | AAPT         | Submitted       |
| 20193005002       | AAPT         | Submitted       |
| 20193005003       | AAPT         | Submitted       |
| 20193005004       | AAPT         | Submitted       |
| 20193005005       | AAPT         | Submitted       |

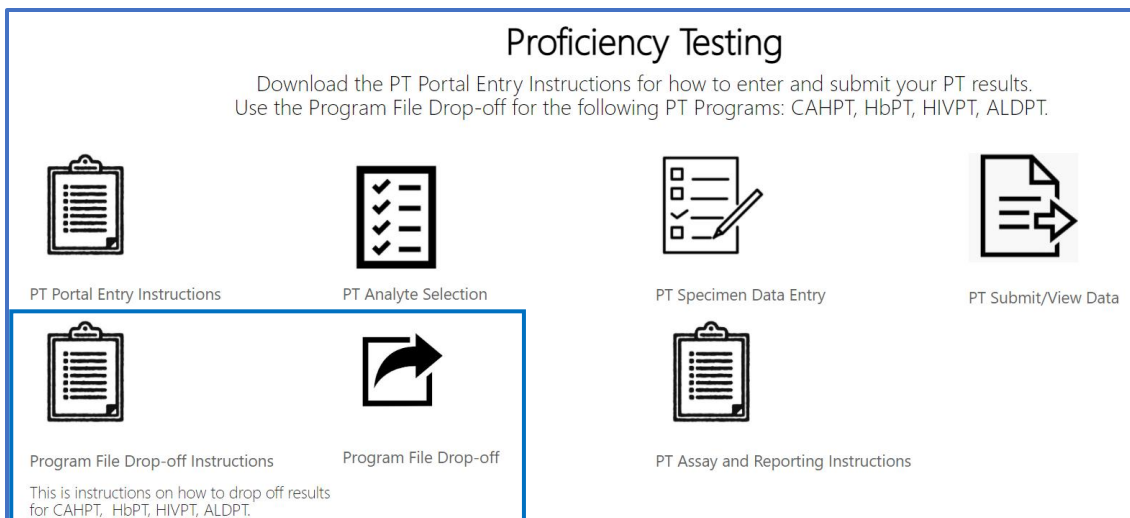
## 4. PT Program File Drop-Off

Laboratories participating in the following programs will need to utilize the PT program file drop-off page to upload data report forms: ALDPT, CAHPT, HbPT, HIVPT.

1. Navigate to the program file drop-off area by selecting the **'Biochemical PT'** tab at the top of the page on the toolbar then **'PT Information'**.



2. Select the **'Program File Drop-off Instructions'** icon for upload instructions and/or select **'Program File Drop-off'** icon to upload data entry forms.




## 4.1 Download the Data Report Form

Data report forms for the following programs can be downloaded from the NSQAP Portal: ALDPT, CAHPT, HbPT, HIVPT.


1. Select the **'Program File Drop-off'** on the PT Information page.

### Proficiency Testing


Download the PT Portal Entry Instructions for how to enter and submit your PT results. Use the Program File Drop-off for the following PT Programs: CAHPT, HbPT, HIVPT, ALDPT.




PT Portal Entry Instructions




PT Analyte Selection



PT Specimen Data Entry




PT Submit/View Data




Program File Drop-off Instructions

This is instructions on how to drop off results for CAHPT, HbPT, HIVPT, ALDPT.



Program File Drop-off



PT Assay and Reporting Instructions

2. Select **'Click here to download PT template'**.

Home > **Program File Drop-off**

## Program File Drop-off

Note: Select the link below to access file upload folder for: CAHPT, HbPT, HIVPT, ALDPT. (Click here to download PT template)

| Folder ↑               | Created On         |
|------------------------|--------------------|
| PT Drop Box - LAB-9001 | 8/31/2020 10:13 AM |

**About NSQAP Self-Service Portal**





This program is cosponsored by the Centers for Disease Control and Prevention (CDC) and the Association of Public Health Laboratories

3. Click on the Microsoft Excel icon to download the data report form(s). Click below the Excel icon to assess PT program assay and reporting instructions.

Home > PT Templates

## PT Templates

Click the "excel icon" to download the program report form and click below the icon for assay instructions.

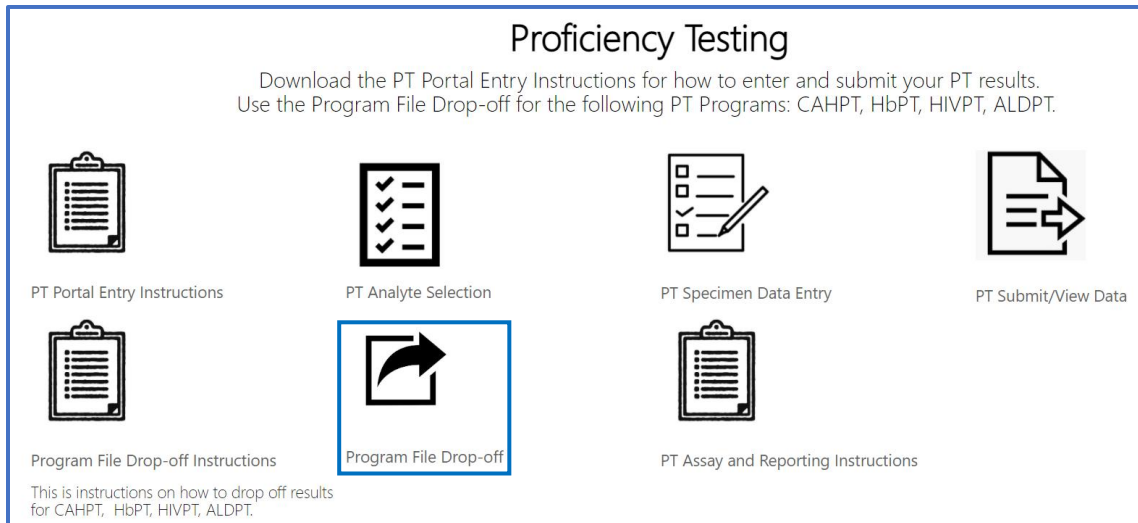
| CAHPT Form  | HbPT Form   | HIVPT Form   | ALDPT Form  |
|---|---|--|---|
|  |  |  |  |
| <a href="#">Click here for CAHPT Assay Instructions.</a>                          | <a href="#">Click here for HbPT Assay Instructions.</a>                           | <a href="#">Click here for HIVPT Assay Instructions.</a>                           | <a href="#">Click here for ALDPT Assay Instructions.</a>                            |

[About NSQAP Self-Service Portal](#)

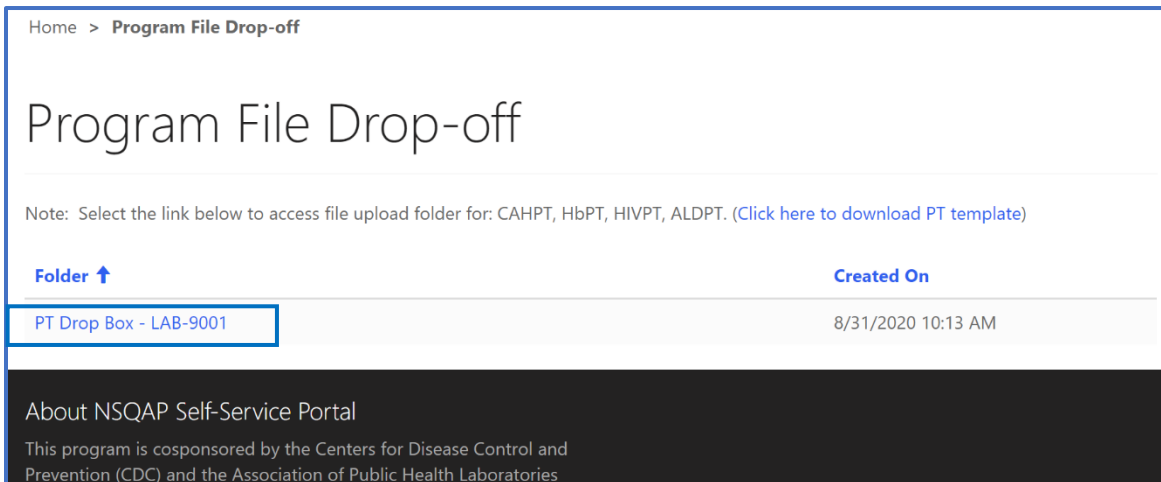
4. Complete the data report form template(s) according to the data report form instructions.

## 4.2 Upload the PT Program Data Report Form

1. Data report forms for the following programs should be uploaded to the PT Drop Box: ALDPT, CAHPT, HbPT, HIVPT.
2. Select the **'Program File Drop-off'** on the PT Information page.



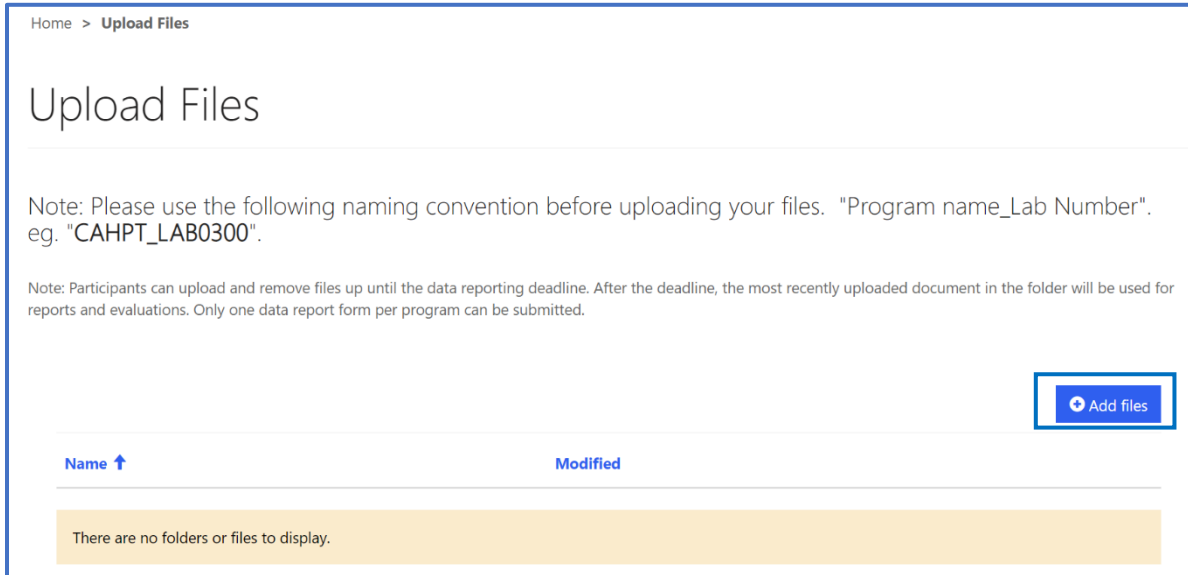
3. Select **'PT Drop Box'** to access your lab's upload folder.



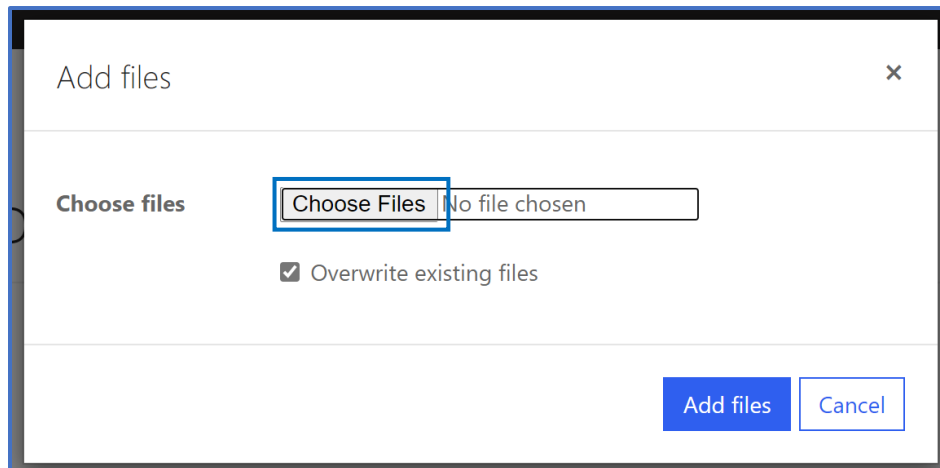
4. Upload files to your lab's folder by clicking **'+Add files'**.

**Note:** You are required to use the following naming convention before uploading your files. "Program Name\_Lab Number". eg. "CAHPT\_LAB0300"

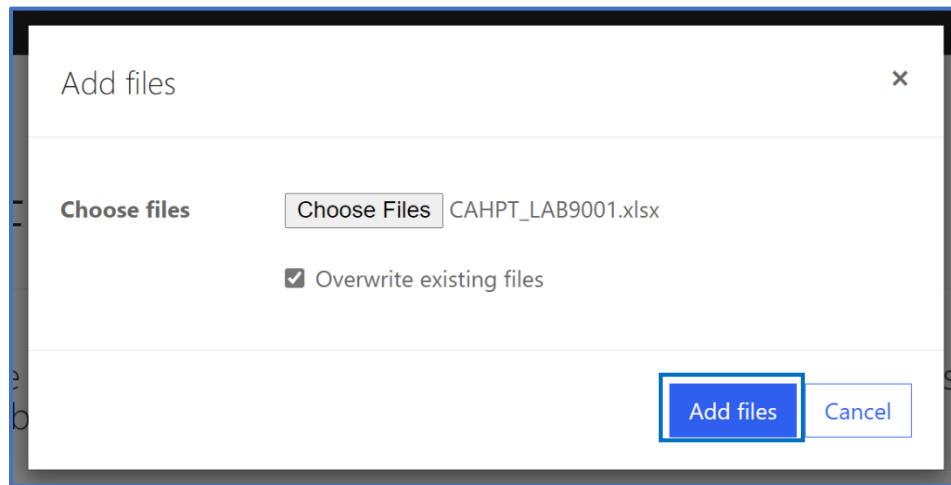
**Note:** You can upload and remove files up until the data reporting deadline. After the deadline, the most recently uploaded document in the folder will be used for reports and evaluations. Only one data report form per program can be submitted.



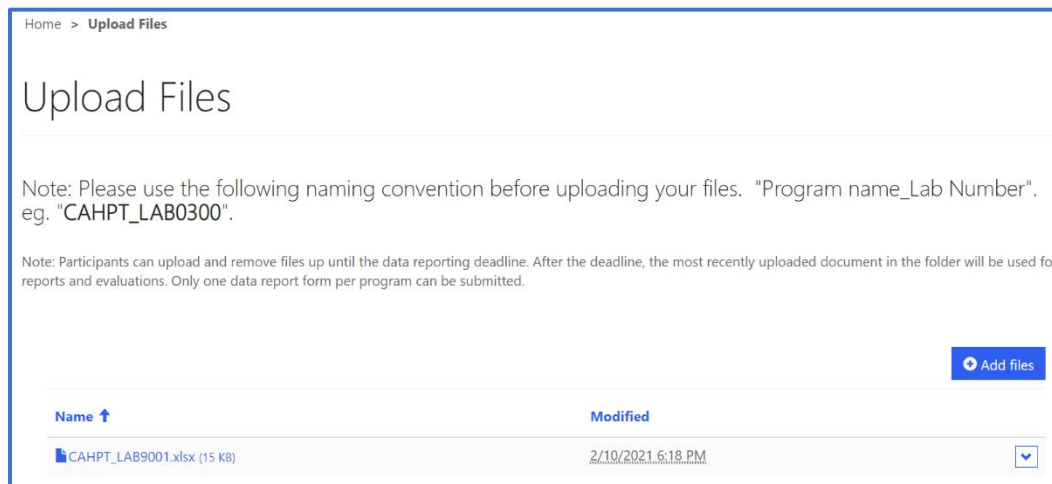
5. A small separate window **'Add Files'** will appear. Select **'Choose Files'** to locate and attach your file.



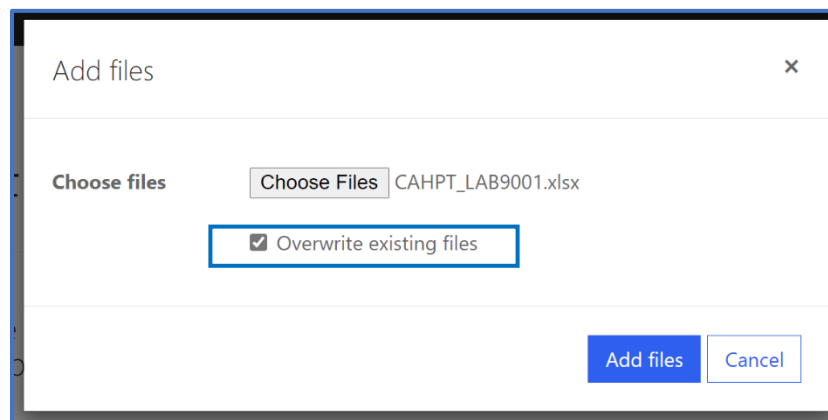
6. Select **'Add Files'** to upload your file.



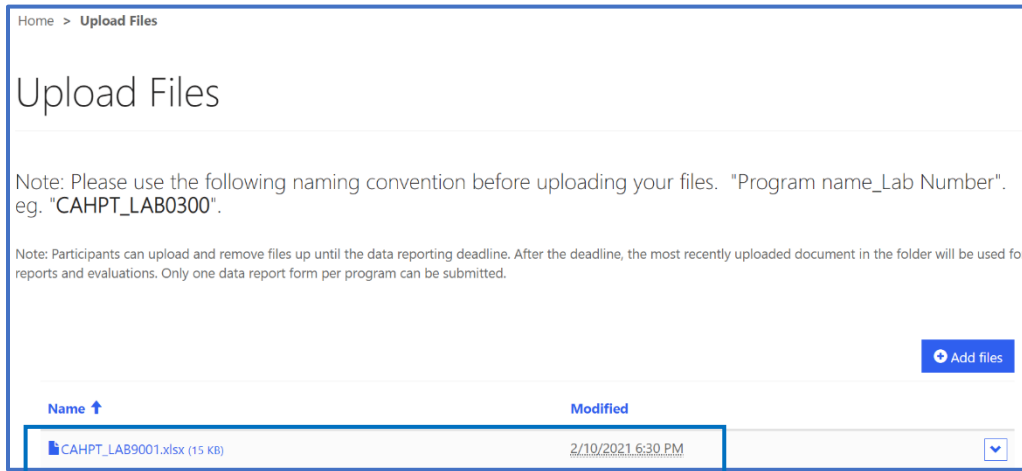
7. The file will appear in your folder once successfully uploaded.



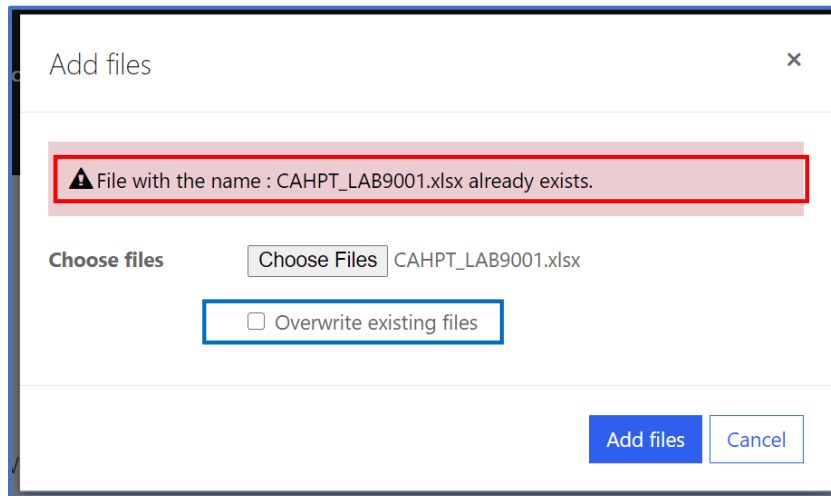
8. To replace an existing file with the same name, repeat steps 4-6 ensuring that **'overwrite existing files'** is checked.



9. The previous file of the same name will be replaced with the new file.



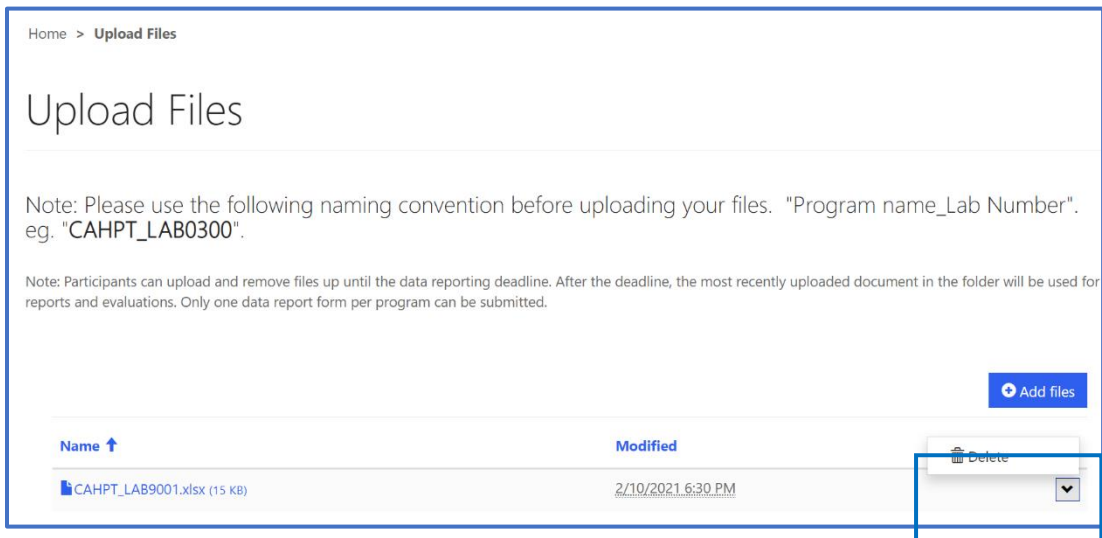
10. If the new file has the same name as an existing file and 'overwrite existing files' is not checked, an error message will appear.



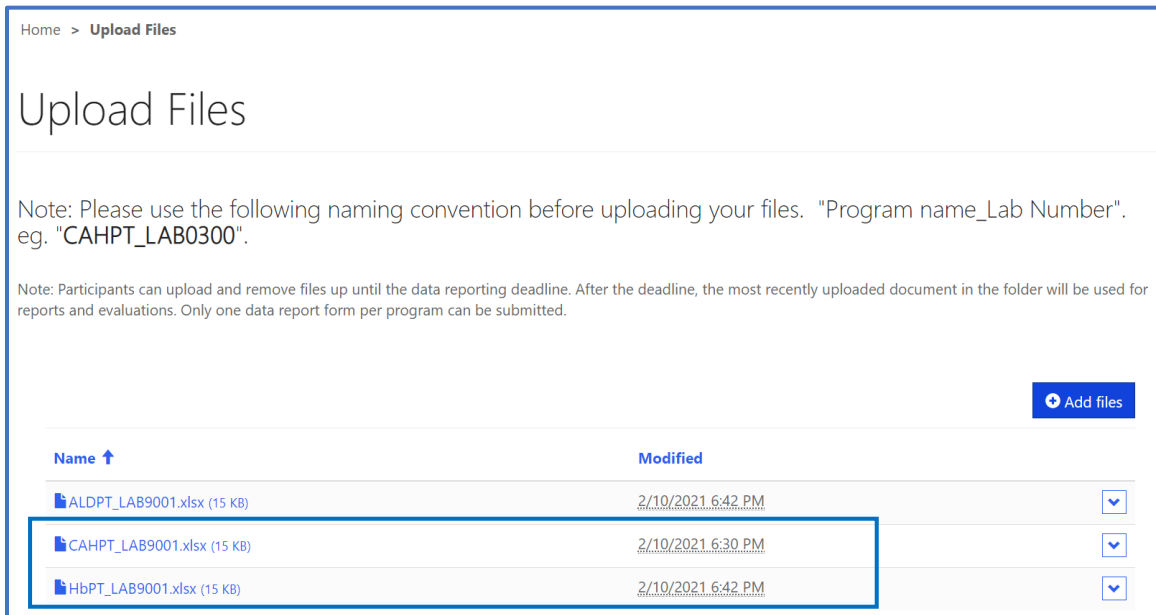
11. Select overwrite existing files or manually delete the existing file to upload the file. Ensure that all uploaded files are compliant with the required naming convention. See step 4 above.

12. To manually delete files, select the down arrow next to the file and click delete.





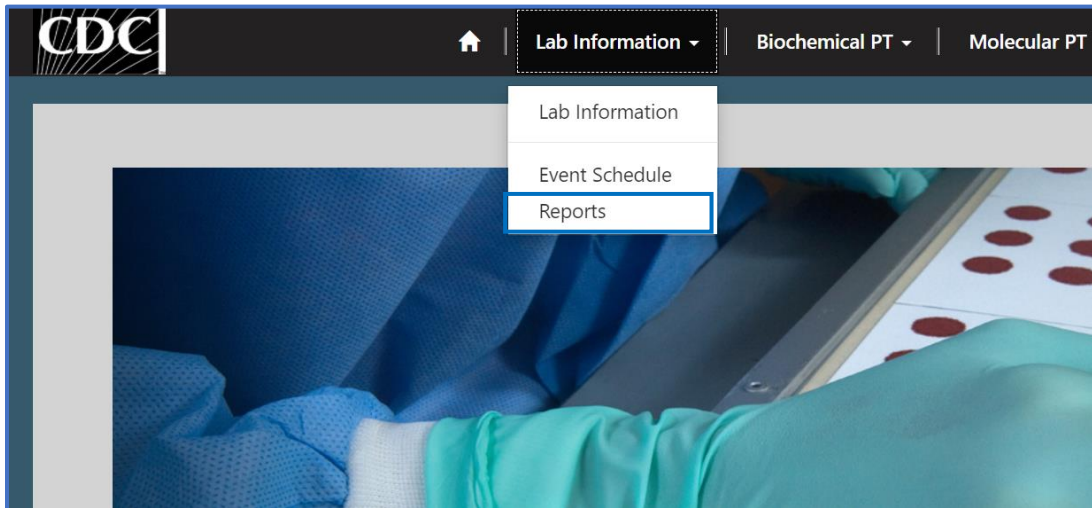
13. Follow steps 3 – 7 to upload other PT program files if necessary.



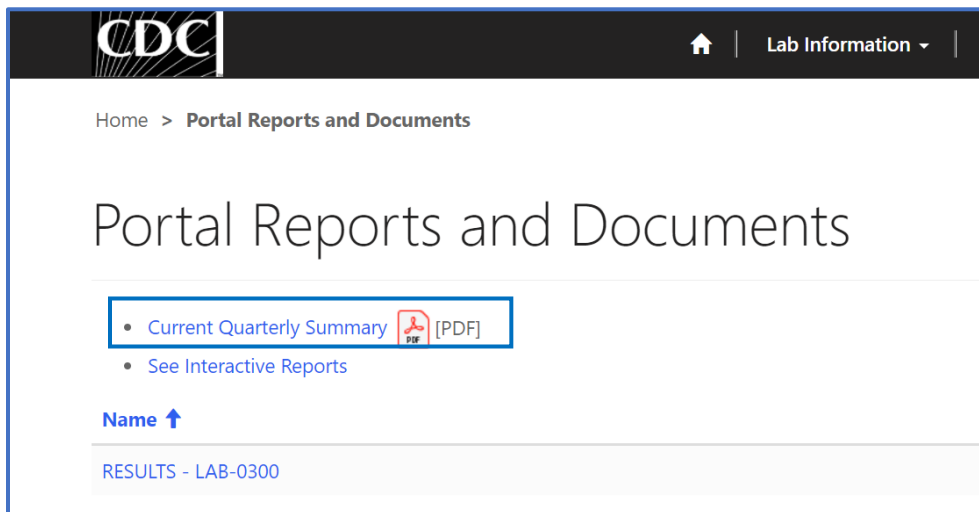
## 5. Reporting

### 5.1 Quarterly Summary Report

1. Select the **'Lab Information'** button at the top of the page on the toolbar and select the **'Reports'** option.

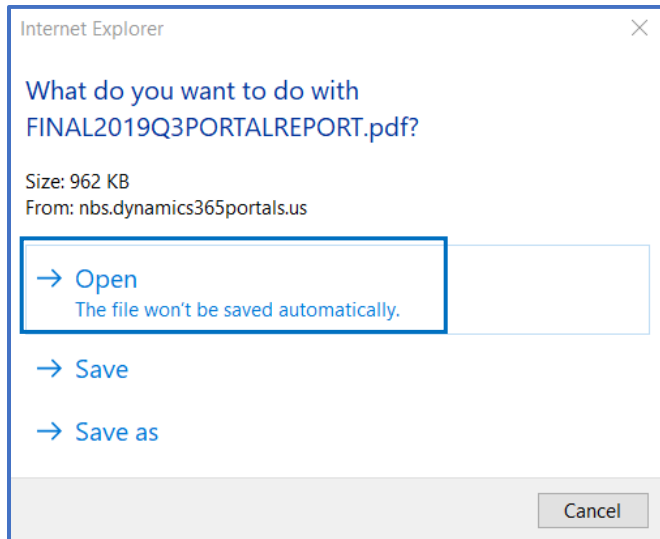


2. Select the **'Current Quarterly Summary'** link.



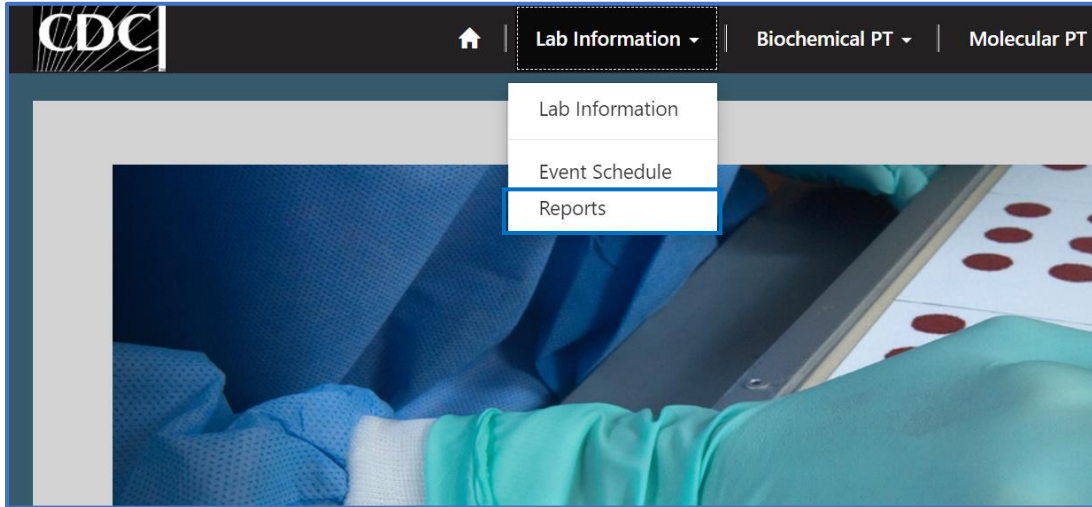
3. Click the **'Open'** option in the pop-up window to download and view the Quarterly Summary Report.

Note: The location and appearance of this window will vary depending on your web browser.

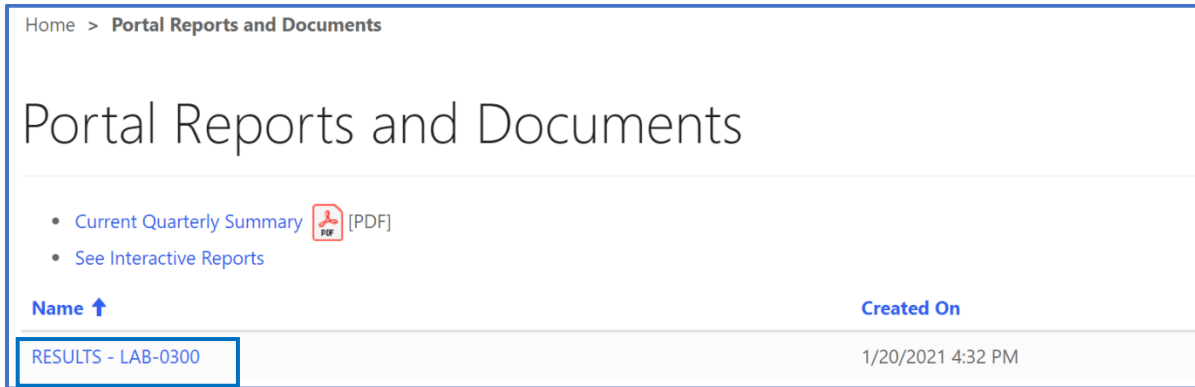


## 5.2 Evaluation Report

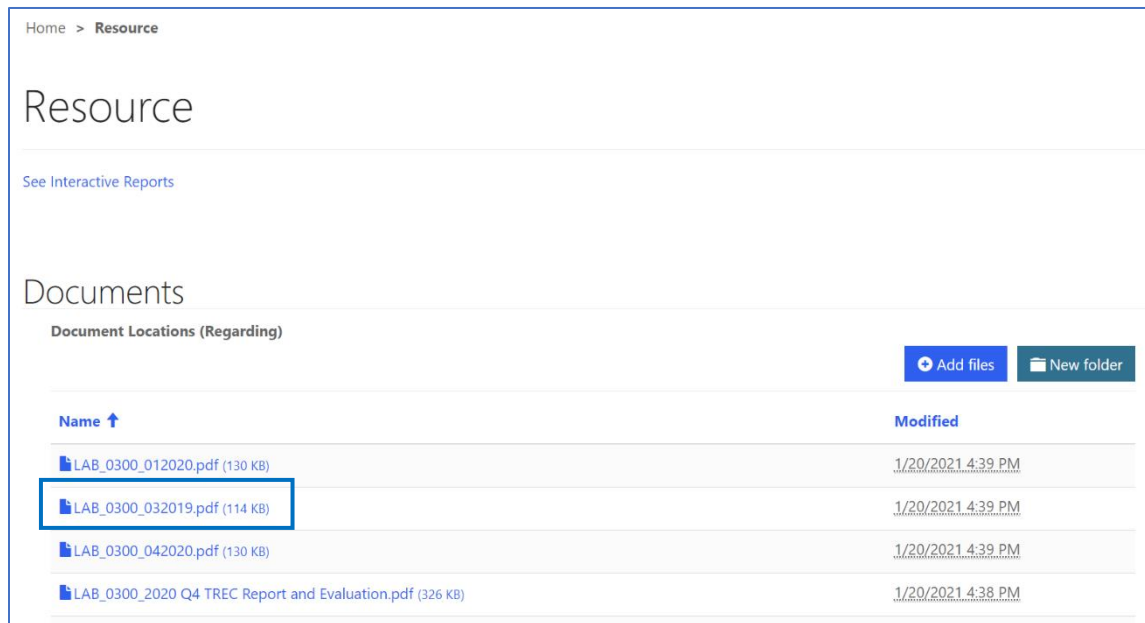
1. Select the **'Lab Information'** button at the top of the page on the toolbar and select the **'Reports'** option.



- Select the **'RESULTS – LAB - <Your Lab Number> (ex. RESULTS – LAB-0300)'** link.



- Select the Evaluation Report by clicking the file link that reads **'LAB\_<Your Lab Number>\_<Quarter><Year> (ex. LAB\_0300\_032019.pdf)'**



- Click the **'Open'** button at the bottom of the page to download and view the Evaluation Report.

