

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**

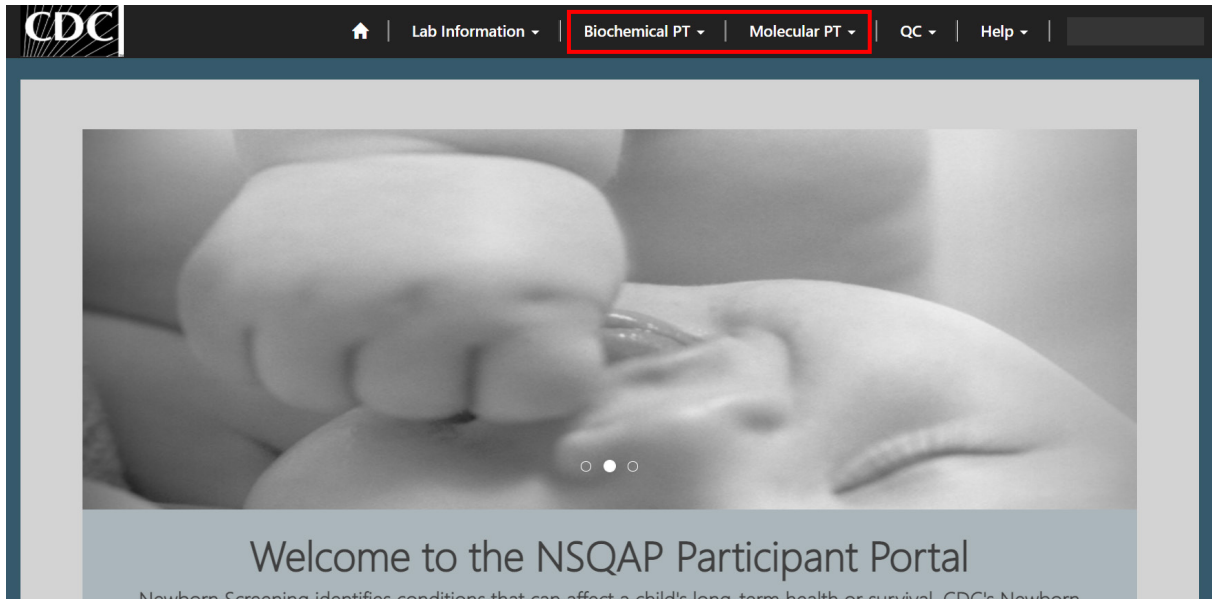
June 2021

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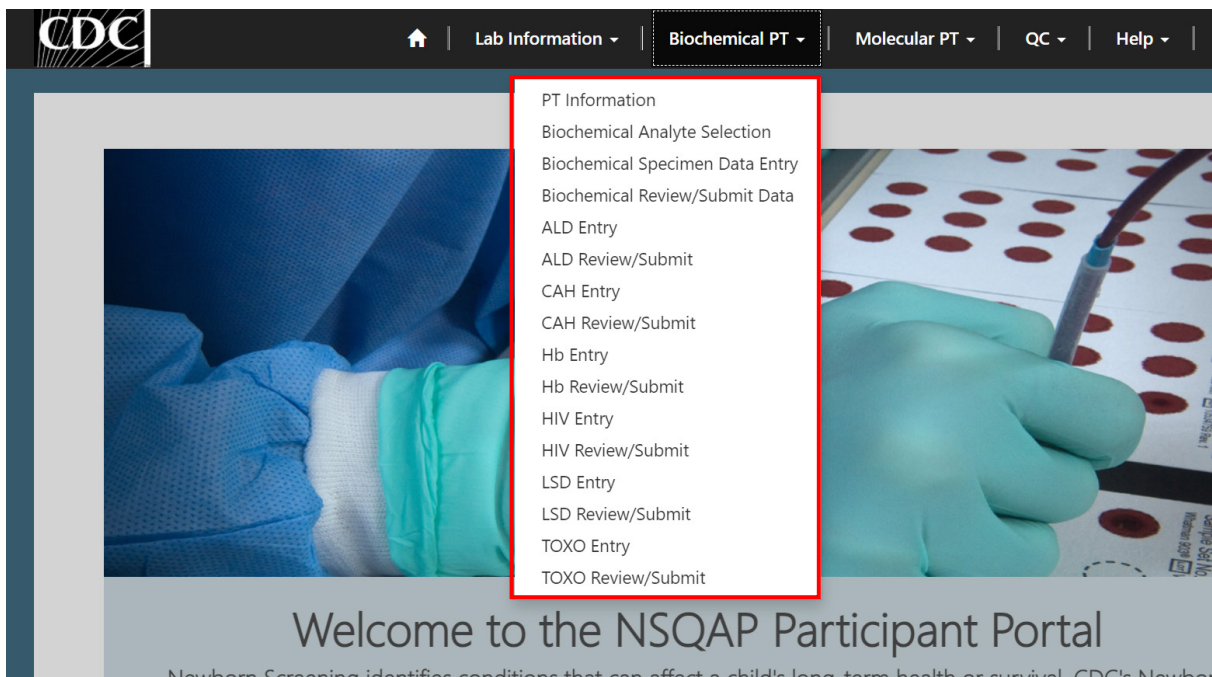
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1. Proficiency Testing Navigation

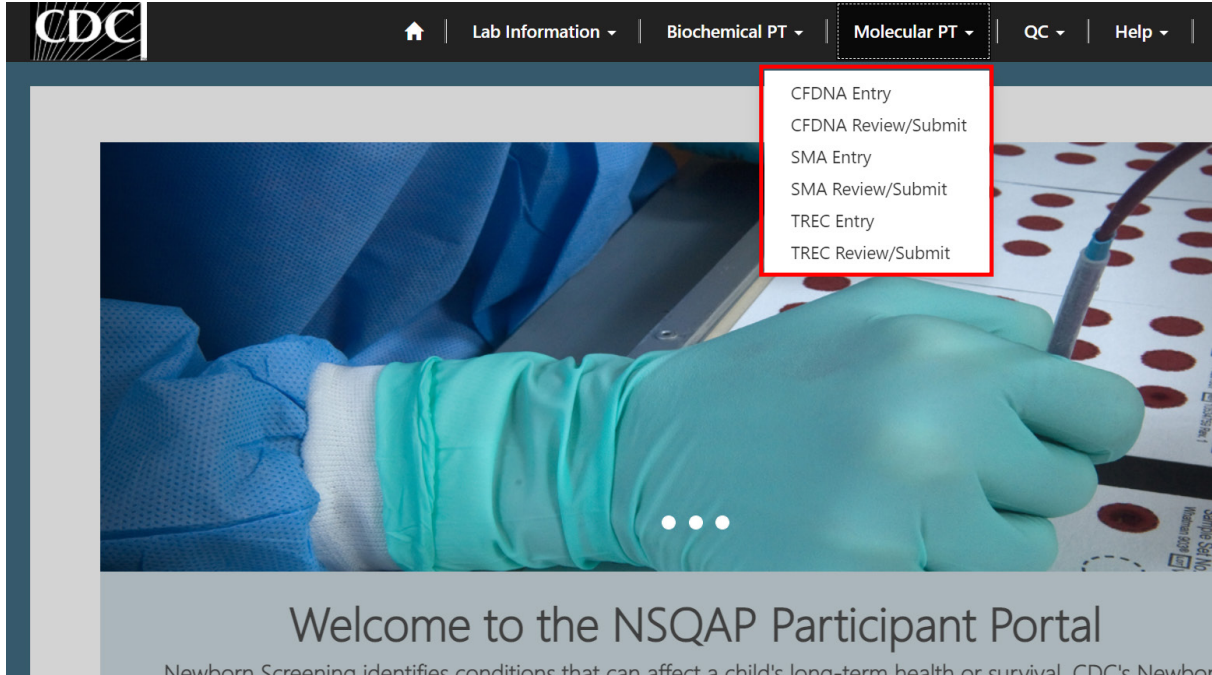
The Proficiency Testing (PT) sections of the NSQAP Portal can be accessed by clicking **'Biochemical PT'** or **'Molecular PT'** from the menu bar.



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

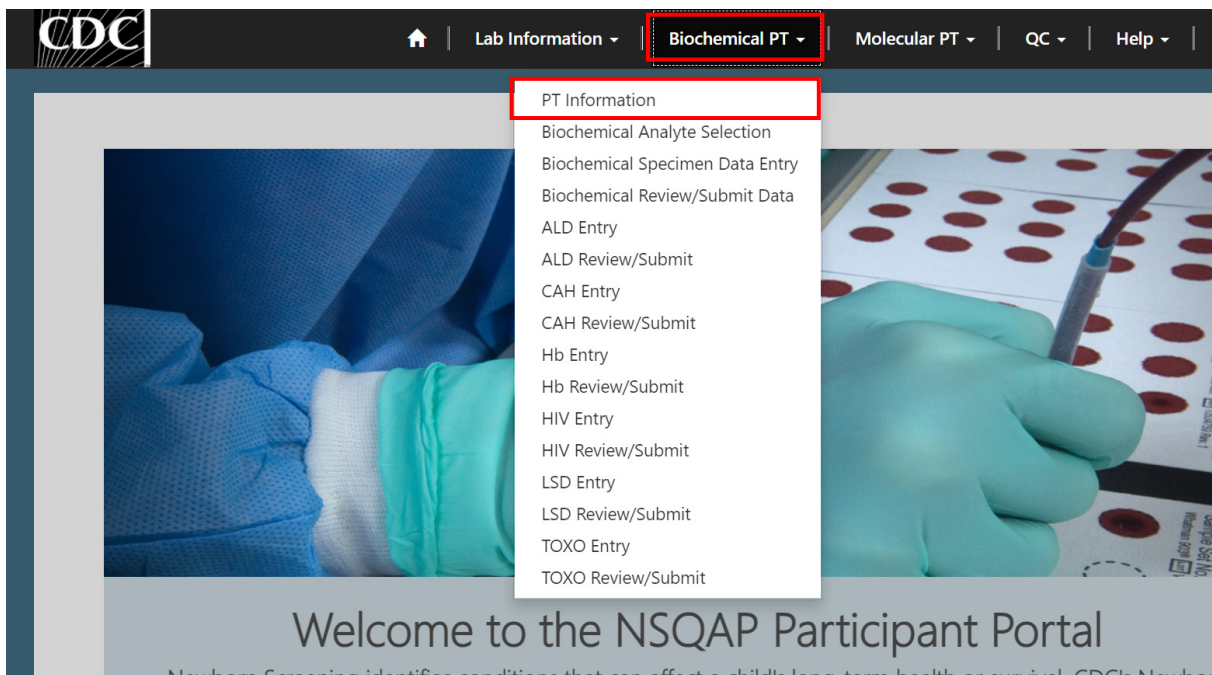


- The Molecular PT section contains three sets of program specific pages for CFDNAPT, SMAPT, and TRECPT.



1.1 PT Information Page

- 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.

Home > PT Information

PT Information

Proficiency Testing

Download the PT Portal Entry Instructions for guidance on how to enter and submit your PT results.



PT Portal Entry Instructions



PT Analyte Selection



PT Specimen Data Entry



PT Submit/View Data



PT Assay and Reporting Instructions

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

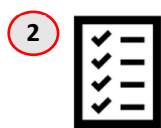
PT Information

Proficiency Testing

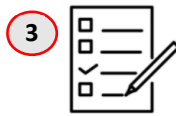
Download the PT Portal Entry Instructions for guidance on how to enter and submit your PT results.



PT Portal Entry Instructions



PT Analyte Selection



PT Specimen Data Entry



PT Submit/View Data



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. **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.

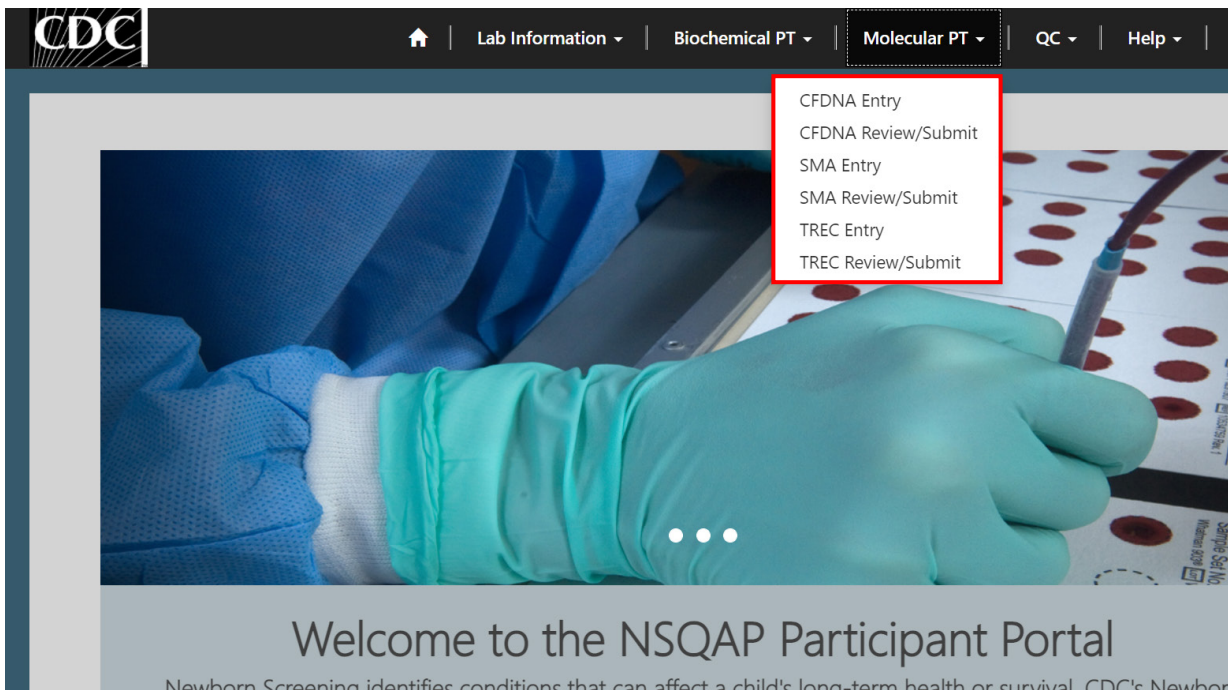
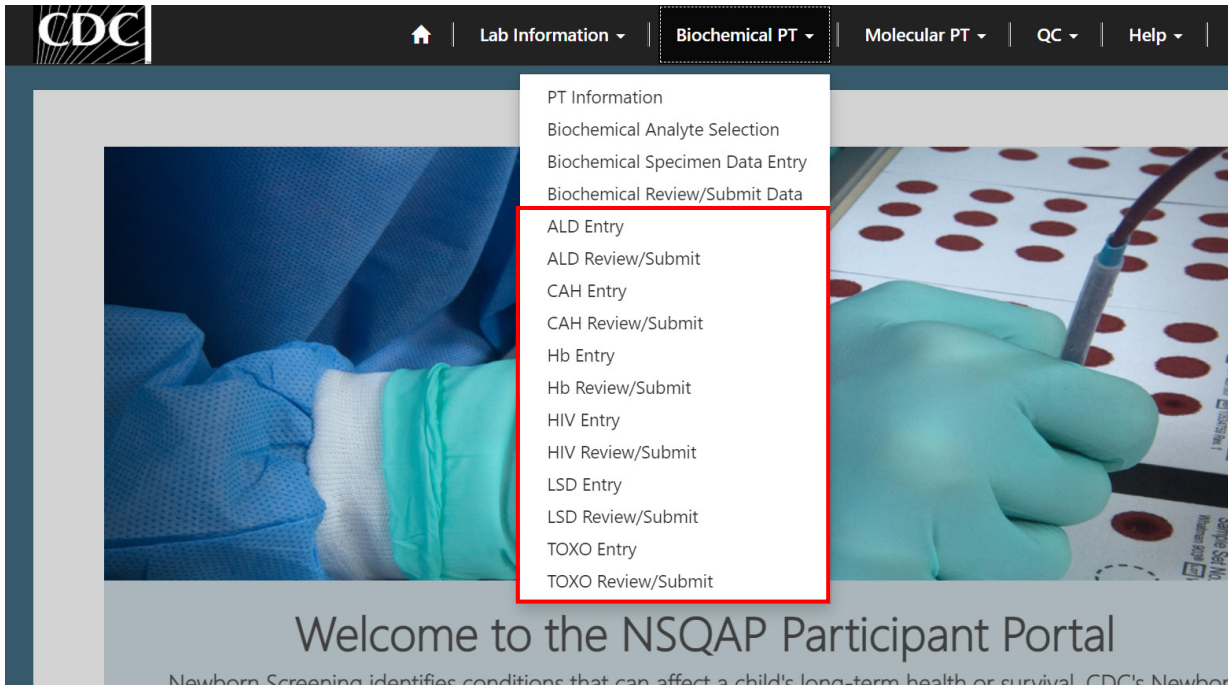
Summary and Submission

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 Disease Specific PT Pages

1. Laboratories participating in the following programs will need to utilize the disease specific PT program pages: ALDPT, CAHPT, CFDNAPT, HbPT, HIVPT, LSDPT, SMAPT, TOXOPT, and TRECPT.



2. Two relevant NSQAP Portal pages exist per program (ALDPT, CAHPT, CFDNAPT, HbPT, HIVPT, LSDPT, SMAPT, TOXOPT, and TRECPT): Entry and Review and Submit.
 - **Entry** – Page for Entering and Saving Program Specific PT Program Data.
 - **Review and Submit** – Page for Reviewing and Submitting Program Specific PT Program Data.
3. For additional information on any of the nine sets of program specific PT pages, see the program specific PT user guide for that particular program.

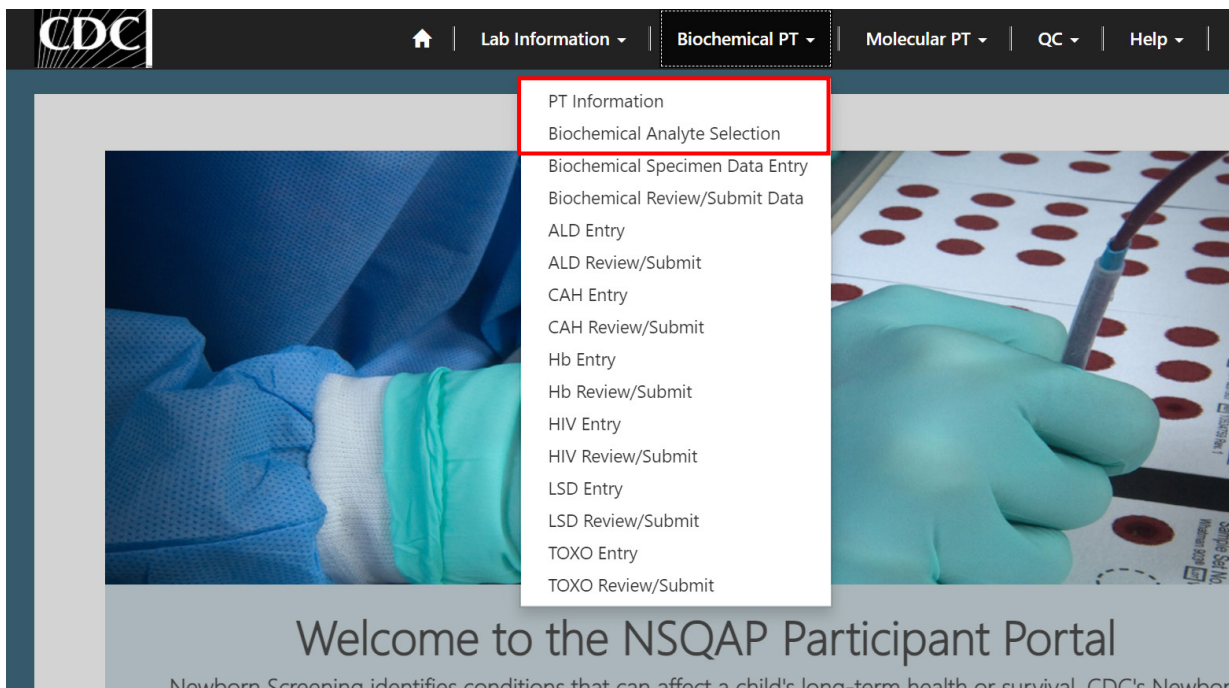
2. Biochemical Data Entry

2.1 Analyte Selection

Laboratories participating in the following programs should utilize the biochemical 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**'.



PT Information

Proficiency Testing

Download the PT Portal Entry Instructions for guidance on how to enter and submit your PT results.



PT Portal Entry Instructions



PT Analyte Selection



PT Specimen Data Entry



PT Submit/View Data



PT Assay and Reporting Instructions

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
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

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.

4. 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



Method



Method



Method



Method



Method



Method



Method



Method



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

5. 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.

Lookup records

Search

Derivatized - MS/MS NeoGram PerkinElmer
Derivatized - MS/MS non-kit
High-performance liquid chromatography (HPLC) non-kit
LC-MS/MS non-kit
Non-derivatized - MS/MS MassChrom® Chromsystems
Non-derivatized - MS/MS MS2 Screening Neo (MS-Neo)Siemens
<input checked="" type="checkbox"/> Non-derivatized - MS/MS NeoBase™ PerkinElmer
Non-derivatized - MS/MS NeoBase™2 PerkinElmer

< 1 2 >

Select Cancel Remove value

6. 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)

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	Set All Methods Below		<input type="text"/>	<input type="button" value="Q"/>
<input checked="" type="checkbox"/> Arginine (Arg)	Method	<input type="text" value="Non-derivatized - MS/MS NeoBase™ PerkinElmer"/>	<input type="button" value="x"/>	<input type="button" value="Q"/>
				Cutoff (μmol/L blood)
				<input type="text"/>
<input type="checkbox"/> Citrulline (Cit)	Method	<input type="text"/>	<input type="button" value="Q"/>	
				Cutoff (μmol/L blood)
				<input type="text"/>
<input checked="" type="checkbox"/> Leucine (Leu)	Method	<input type="text" value="Non-derivatized - MS/MS NeoBase™ PerkinElmer"/>	<input type="button" value="x"/>	<input type="button" value="Q"/>
				Cutoff (μmol/L blood)
				<input type="text"/>
<input type="checkbox"/> Methionine (Met)	Method	<input type="text"/>	<input type="button" value="Q"/>	
				Cutoff (μmol/L blood)
				<input type="text"/>
<input checked="" type="checkbox"/> Phenylalanine (Phe)	Method	<input type="text" value="Non-derivatized - MS/MS NeoBase™ PerkinElmer"/>	<input type="button" value="x"/>	<input type="button" value="Q"/>
				Cutoff (μmol/L blood)
				<input type="text"/>
<input type="checkbox"/> Succinylacetone (SUAC)	Method	<input type="text"/>	<input type="button" value="Q"/>	
				Cutoff (μmol/L blood)
				<input type="text"/>
<input type="checkbox"/> Tyrosine (Tyr)	Method	<input type="text"/>	<input type="button" value="Q"/>	
				Cutoff (μmol/L blood)
				<input type="text"/>
<input type="checkbox"/> Valine (Val)	Method	<input type="text"/>	<input type="button" value="Q"/>	
				Cutoff (μmol/L blood)
				<input type="text"/>

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

Lookup records ×

Search Q

Method Name ↑

Non-derivatized - MS/MS non-kit

Other

< 1 2 >

Select Cancel Remove value

9. If 'Other' method is selected type the name of the 'Other Method' the 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)

☐ Select All Analytes

☐ Arginine (Arg)

☐ Citrulline (Cit)

☐ Leucine (Leu)

☐ Methionine (Met)

☒ Phenylalanine (Phe)

☐ Succinylacetone (SUAC)

☐ Tyrosine (Tyr)

☐ Valine (Val)

Set All Methods Below

Other × Q

Method

Other Q

Method

Other Q

Method

Other Q

Method

Other Q

Method

Other Q

Method

Other Q

Method

Other Q

Method

Other Q

Other Method *

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)

Cutoff (μmol/L blood)

SAVE AND SET VALUES

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

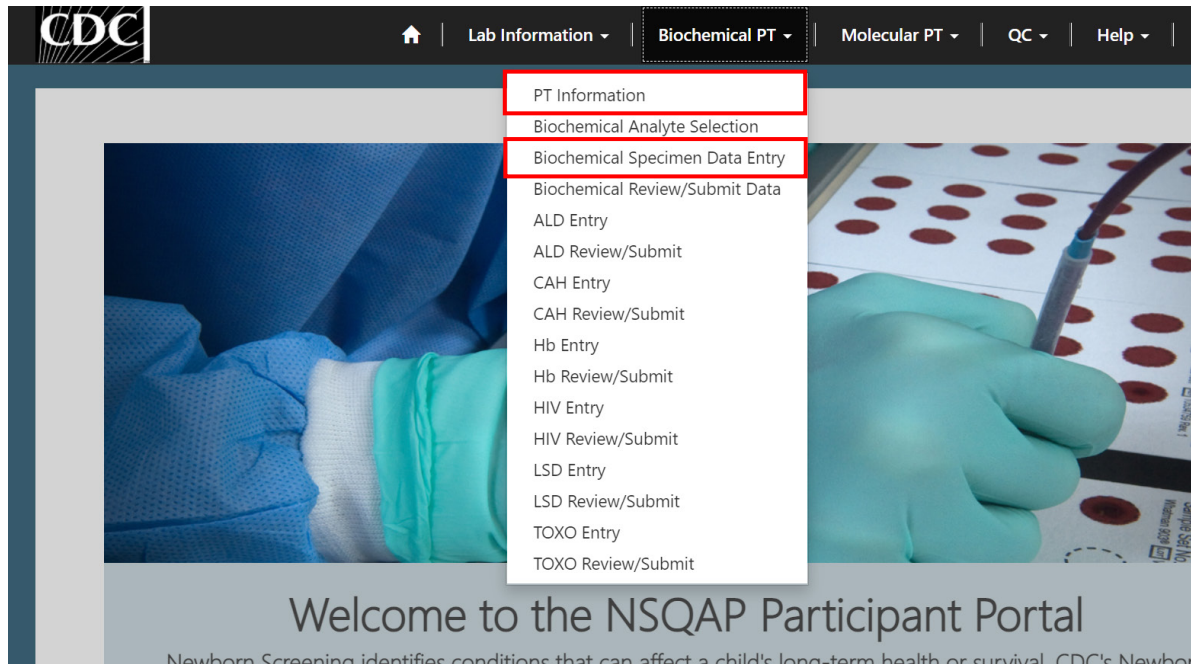
SAVE AND SET VALUES

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 biochemical specimen 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'**.



Home > PT Information

PT Information

Proficiency Testing

Download the PT Portal Entry Instructions for guidance on how to enter and submit your PT results.



PT Portal Entry Instructions



PT Analyte Selection



PT Specimen Data Entry



PT Submit/View Data



PT Assay and Reporting Instructions

2. 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
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

3. 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
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	▼

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

Phenylalanine (Phe)

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

Specimen Number	Result μmol/L blood	Phe Presumptive Clinical Assessment*
20194005001	<input type="text"/>	<input type="text" value="▼"/>

Succinylacetone (SUAC)

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

Specimen Number	Result μmol/L blood	SUAC Presumptive Clinical Assessment*
20194005001	<input type="text"/>	<input type="text" value="▼"/>

Tyrosine (Tyr)

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

Specimen Number	Result μmol/L blood	Tyr Presumptive Clinical Assessment*
20194005001	<input type="text"/>	<input type="text" value="▼"/>

6. 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)

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

Specimen Number	Result μmol/L blood	Phe Presumptive Clinical Assessment*
20194005001	134.3	1- Within normal limits ▼

Succinylacetone (SUAC)

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

Specimen Number	Result μmol/L blood	SUAC Presumptive Clinical Assessment*
20194005001	1.7	1- Within normal limits ▼

Tyrosine (Tyr)

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

Specimen Number	Result μmol/L blood	Tyr Presumptive Clinical Assessment*
20194005001	334.7	1- Within normal limits ▼

7. 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)

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

Specimen Number	Result μmol/L blood	Tyr Presumptive Clinical Assessment*
20194005001	334.7	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.

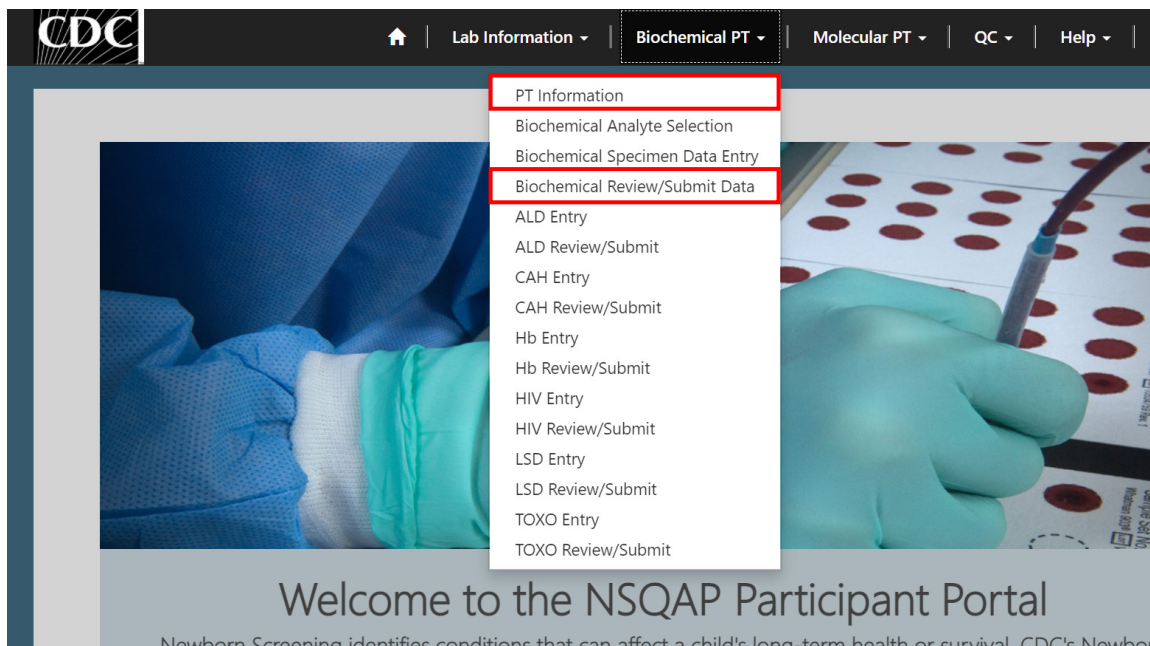
NOTE: Data can only be submitted if ALL specimens have a 'Saved' or 'Saved (Edited)' specimen status.

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'**.



Home > PT Information

PT Information

Proficiency Testing

Download the PT Portal Entry Instructions for guidance on how to enter and submit your PT results.



PT Portal Entry Instructions



PT Analyte Selection



PT Specimen Data Entry



PT Submit/View Data



PT Assay and Reporting Instructions

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

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)	

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 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- Witi 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- Witi 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- Witi 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- Witi limits

4. 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 All Data

AAPT - View Method(s) Only

AAPT - View Results Only

		Arg_Presumptive Clinical Assessment	Arg_Cutoff	Arg_Result	Cit_N
20193005001	Non-derivatized - MS/MS NeoBase™ PerkinElmer	1- Within normal limits	70.0	68.3	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

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 Clinical 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- Witi 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- Witi 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- Witi 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- Witi 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 NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer
20193005002	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer
20193005003	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer
20193005004	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer
20193005005	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer	Non-derivatized - MS/MS NeoBase™ PerkinElmer

View Results Only

RESULTS

Select Views to Download

AAPT- View Results Only ▾

Download

Specimen Number ↑	Arg_Result	Arg_Cutoff	Arg_Presumptive Clinical Assessment	Cit_Result	Cit_Cutoff	Cit_Presumptive Clinical Assessment	Leu_Result	Leu_Cutoff	Leu_Presumptive Clinical Assessment	Met
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

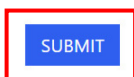
Specimen Number ↑	Program Name	Specimen Status	Modified On	Last Edited By
20202005001	AAPT	Saved	8/27/2020 5:55 PM	Kawanda Foster
20202005002	AAPT	Saved	8/27/2020 5:53 PM	Kawanda Foster
20202005003	AAPT	Saved	8/27/2020 5:54 PM	Kawanda Foster
20202005004	AAPT	Saved	8/27/2020 5:54 PM	Kawanda Foster
20202005005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

3.2 Data Submission

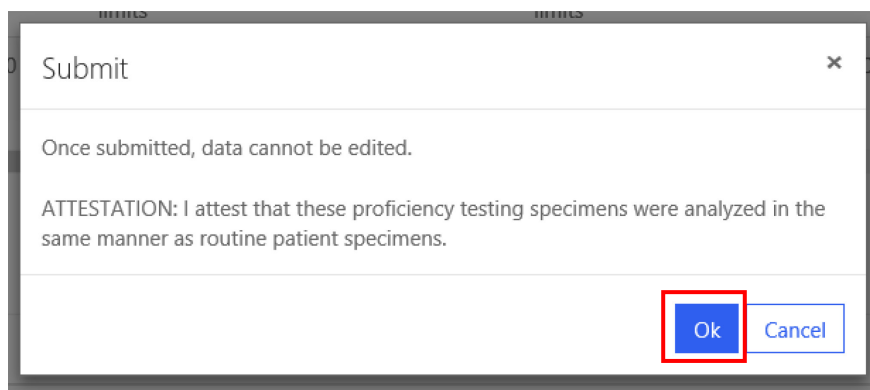
- To submit data for the program, click the **'Submit'** button at the bottom of the summary page.

Specimen

Specimen Number ↑	Program Name	Specimen Status
20202005001	AAPT	Saved
20202005002	AAPT	Saved
20202005003	AAPT	Saved
20202005004	AAPT	Saved
20202005005	AAPT	Saved



- Select the **'Ok'** button on the submission prompt.

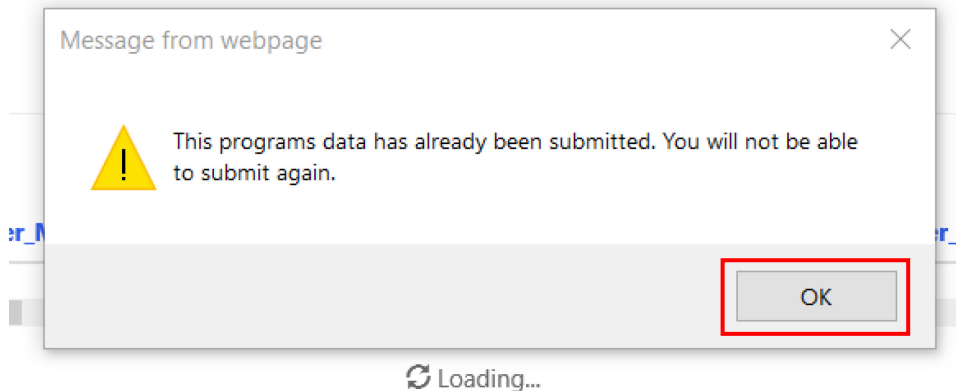


3. The user who submitted the data will appear in the program list for summary and submission.

Summary and Submission

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

4. 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.



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

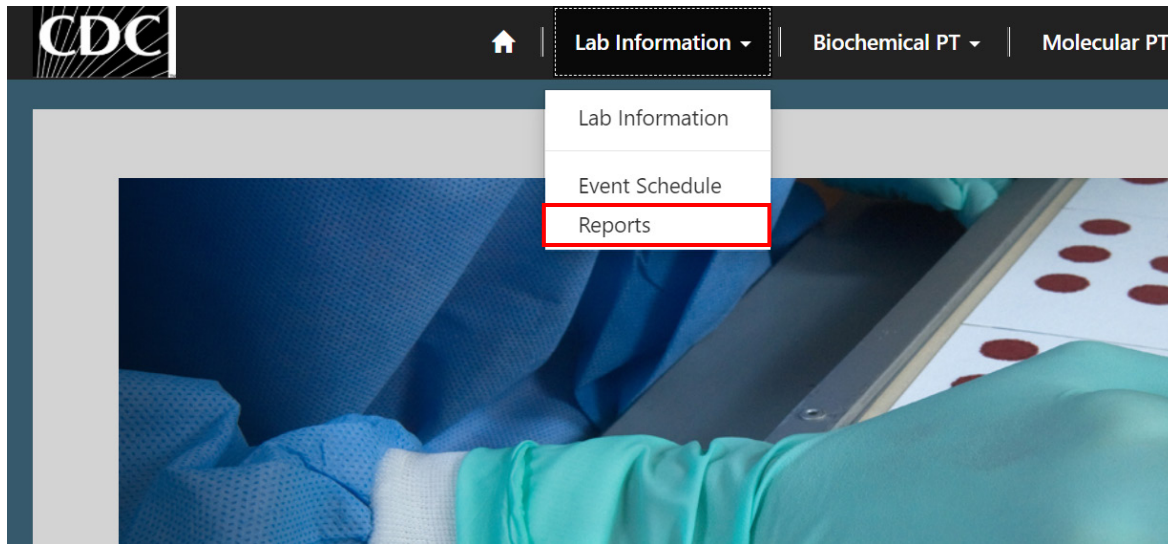
Specimen

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

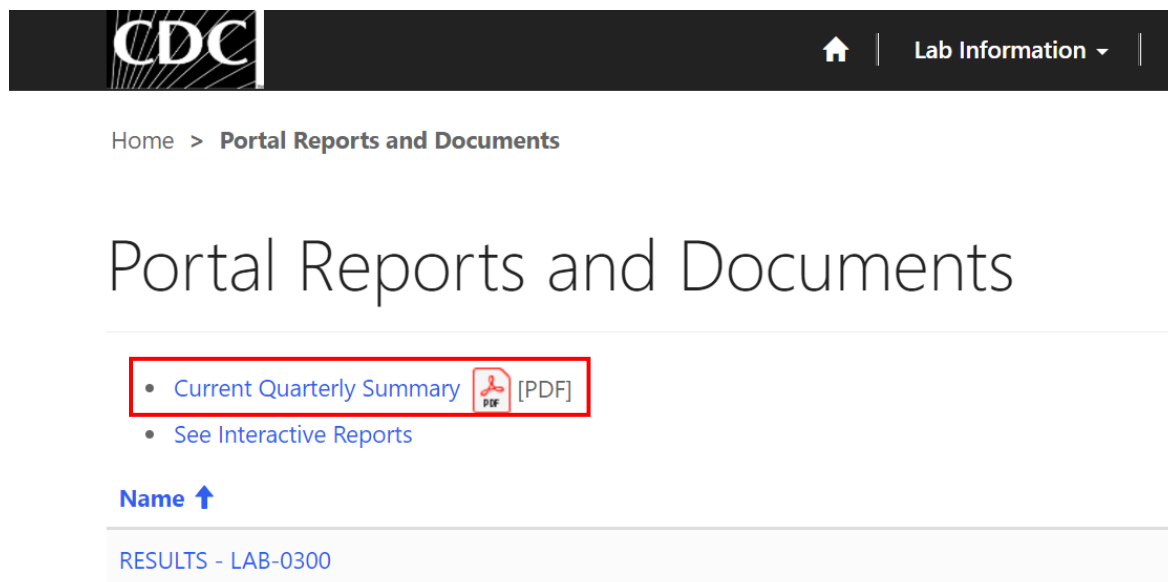
4. Reporting

4.1 Quarterly Summary Report

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

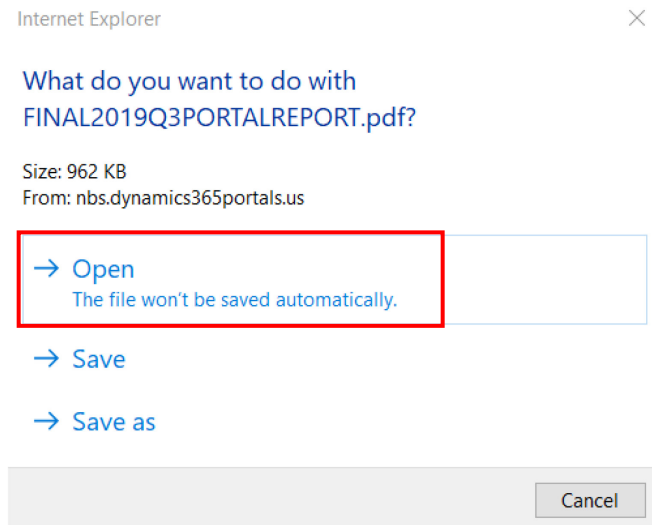


2. Select the **'Current Quarterly Summary'** link.



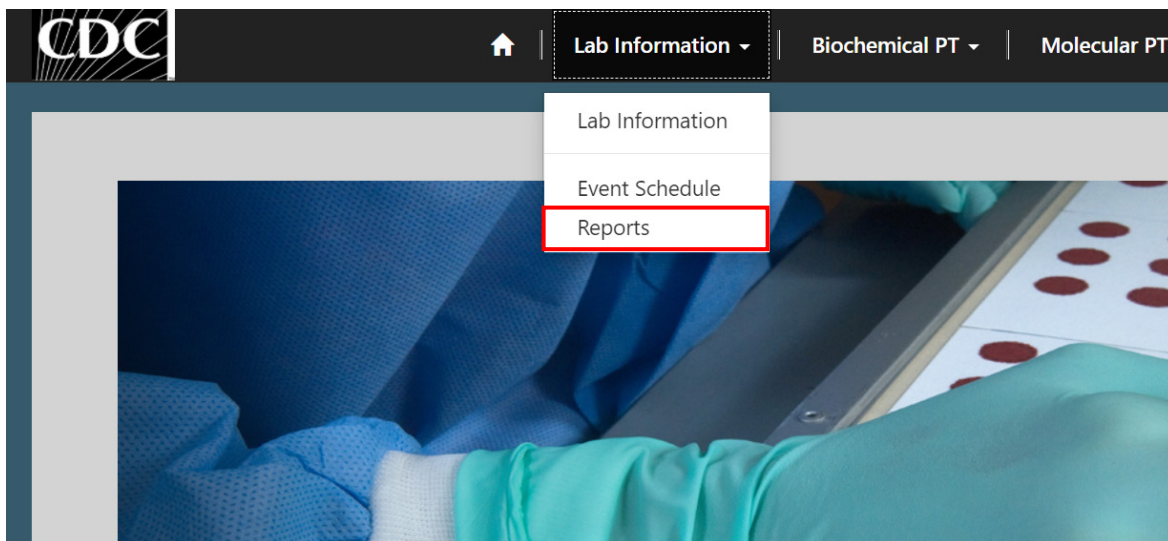
3. Click the **'Open'** option in the pop-up window to download and view the Quarterly Summary Report.

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



4.2 Evaluation Report

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



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

Home > Portal Reports and Documents

Portal Reports and Documents

- Current Quarterly Summary  [PDF]
- See Interactive Reports

Name ↑

Created On

RESULTS - LAB-0300

1/20/2021 4:32 PM

3. Select the Evaluation Report by clicking the file link that reads **'LAB_<Your Lab Number>_<Quarter><Year> (ex. LAB_0300_032019.pdf)'**


Home > Resource

Resource

[See Interactive Reports](#)

Documents

Document Locations (Regarding)

 Add files

 New folder

Name ↑

Modified

 LAB_0300_012020.pdf (130 KB)

1/20/2021 4:39 PM

 LAB_0300_032019.pdf (114 KB)

1/20/2021 4:39 PM

 LAB_0300_042020.pdf (130 KB)

1/20/2021 4:39 PM

 LAB_0300_2020 Q4 TREC Report and Evaluation.pdf (326 KB)

1/20/2021 4:38 PM

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

