

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**

July 2026

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0. Using this Guide

This guide contains instructions for using the NSQAP Portal to report PT results and access PT reporting documents. Screenshots are provided as a reference, but experiences are customized for each individual participating lab. Individual users may see different menus and programs depending on their enrollment. Cutoffs shown are for illustration only and have no clinical utility. Laboratories are expected to report their own cutoffs.

1. Proficiency Testing Navigation

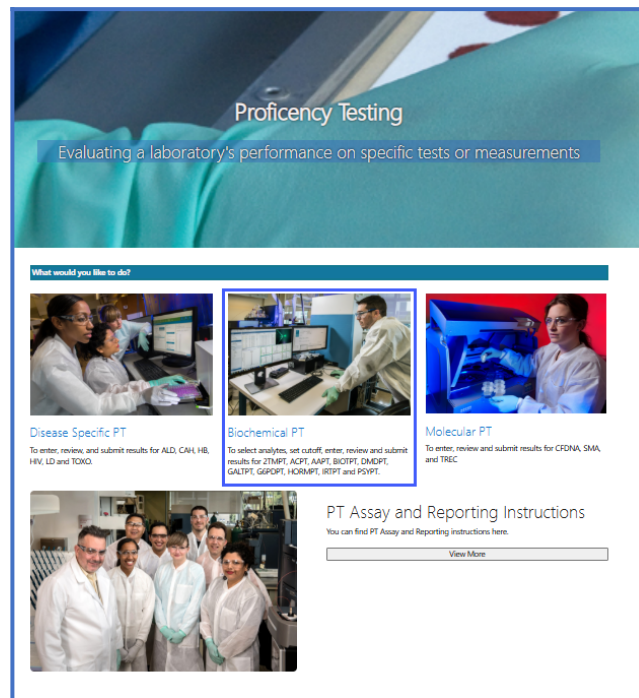
The Proficiency Testing (PT) sections of the NSQAP Portal can be accessed by clicking **'PT Information'** from the menu bar.

The screenshot shows the NSQAP Participant Portal. At the top is the CDC logo and the text "U.S. CENTERS FOR DISEASE CONTROL AND PREVENTION". Below this is a navigation bar with links: Home, Lab Information, PT Information (highlighted with a blue box), QC Information, My Support, and USERNAME. The main header area features a background image of a hand holding a finger, with the text "NSQAP Participant Portal" overlaid. Below the header, there is a paragraph of text about the Newborn Screening Quality Assurance Program (NSQAP). To the left of the main content area is a table titled "Announcements". To the right is a "Calendar" section showing a collage of colorful calendar cards.

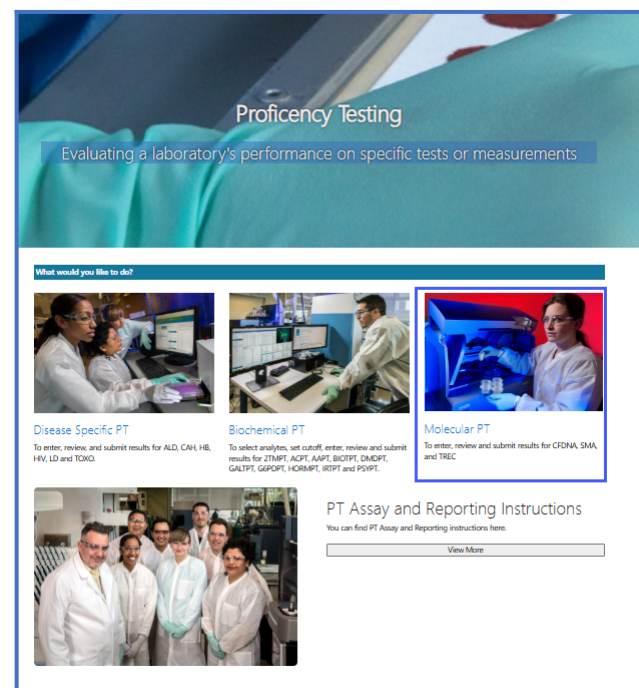
Title	Date ↑
Welcome to NSQAP Participation Portal	5/11/2026

[View All Announcements](#)

1. The Biochemical PT section contains the program specific pages for biochemical PT programs.



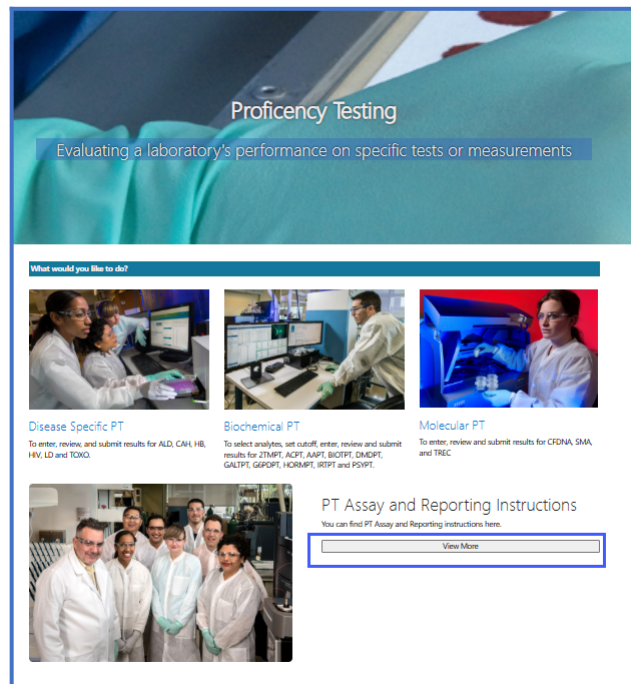
2. The Molecular PT section contains program specific pages for molecular PT programs.



3. The Disease Specific PT section contains program specific pages for disease specific PT programs.

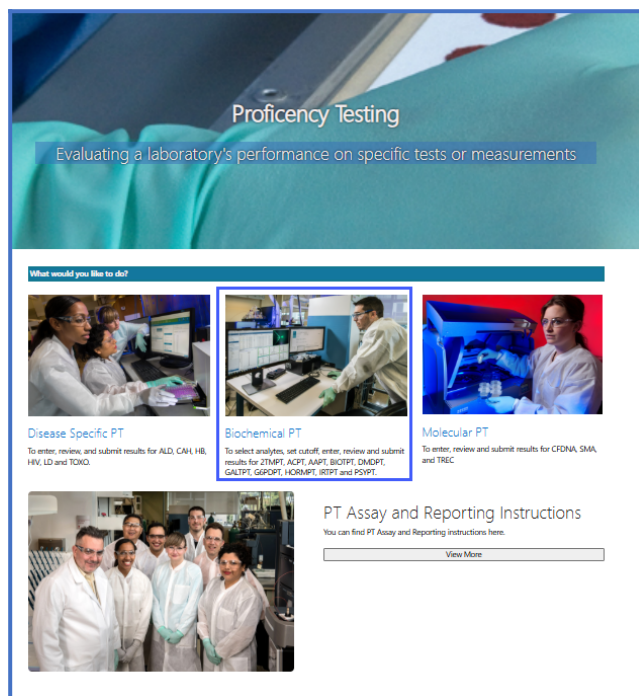


4. The PT Assay and Reporting Instructions section contains PT assay and reporting informational documents.



1.1 Biochemical PT Page

1. Select the **'Biochemical PT'** button at the center of the page.



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

Step 1 - Analyte Selection		Step 2 - Specimen Data Entry	
Program Name ↑ Acylcarnitines (ACPT) Amino Acids and SUAC (AAPT) Biotinidase (BIOT) Galactose-1-phosphate Uridyltransferase (GALTPT) Hormone + Total Galactose (HORMPT) Immunoreactive Trypsinogen (IRTPT)		Program Name ↑ Acylcarnitines (ACPT) Amino Acids and SUAC (AAPT) Biotinidase (BIOT) Galactose-1-phosphate Uridyltransferase (GALTPT) Hormone + Total Galactose (HORMPT) Immunoreactive Trypsinogen (IRTPT)	
Step 3 - Review and Submit			
Program Name ↑	Submitted User	Submission Date	
Acylcarnitines (ACPT)			
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM	
Biotinidase (BIOT)			
Galactose-1-phosphate Uridyltransferase (GALTPT)			
Hormone + Total Galactose (HORMPT)			
Immunoreactive Trypsinogen (IRTPT)			

1.2 Biochemical Analyte Selection

1. Laboratories participating in Biochemical PT programs should utilize the analyte selection section to set up the NSQAP portal for data entry.

Step 1 - Analyte Selection

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 2 - Specimen Data Entry

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 3 - Review and Submit

Program Name ↑	Submitted User	Submission Date
Acylcarnitines (ACPT)		
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		
Immunoreactive Trypsinogen (IRTPT)		

2. Programs shown are for example purposes only. Labs will see programs corresponding to their individual enrollment. For additional information on analyte selection, see section 2.1.

1.3 Biochemical Specimen Data Entry

1. Laboratories participating in Biochemical PT programs should utilize the specimen data entry section to enter data into the portal.

Step 1 - Analyte Selection

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 2 - Specimen Data Entry

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 3 - Review and Submit

Program Name ↑	Submitted User	Submission Date
Acylcarnitines (ACPT)		
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		
Immunoreactive Trypsinogen (IRTPT)		

2. Programs shown are for example purposes only. Labs will see programs corresponding to their individual enrollment. For additional information on data entry, see section 2.2.

1.4 Biochemical Review and Submit Data

1. Laboratories participating in Biochemical PT programs should utilize the biochemical review and submit section to review and submit data.

Step 1 - Analyte Selection

Program Name ↑
Acylcarnitines (ACPI)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridytransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 2 - Specimen Data Entry

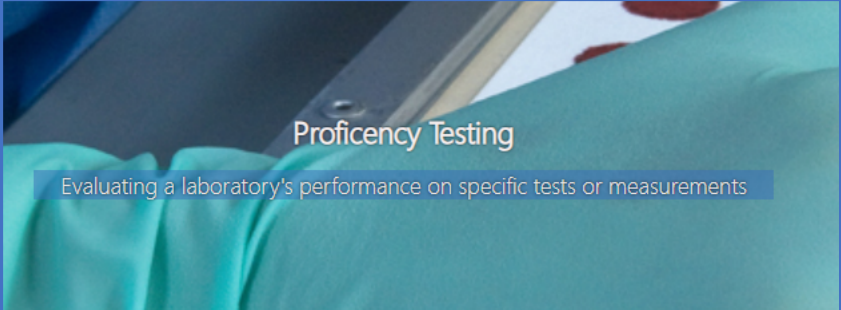
Program Name ↑
Acylcarnitines (ACPI)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 3 - Review and Submit

2. Programs, names and dates shown are for example purposes only. Labs will see programs corresponding to their individual enrollment. For additional information on reviewing and submitting data, see section 3.

1.5 Disease Specific PT Pages

1. Laboratories participating in disease specific PT programs will need to utilize the disease specific PT page.



Proficiency Testing

Evaluating a laboratory's performance on specific tests or measurements

What would you like to do?



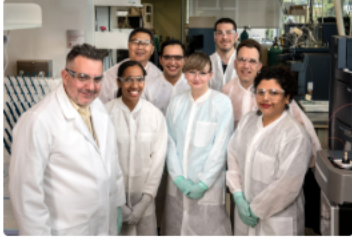
Disease Specific PT
To enter, review, and submit results for ALD, CAH, HB, HIV, LD and TOXO.



Biochemical PT
To select analytes, set cutoff, enter, review and submit results for 2TMPT, ACPT, AAPT, BIOTPT, DMDPT, GALTPT, GGPT, HORMPT, IRTPT and PSYPT.



Molecular PT
To enter, review and submit results for CFDNA, SMA, and TREC



PT Assay and Reporting Instructions
You can find PT Assay and Reporting instructions here.

[View More](#)

2. Three relevant NSQAP Portal pages exist per program: Analyte Selection, Entry, and Review/Submit.

ALD ENTRY		ALD REVIEW/SUBMIT		
Name ↑	Saved By	Name ↑	Submitted By	IsSubmitted
ALD		ALD		

CAH ENTRY		CAH REVIEW/SUBMIT		
Name ↑	Saved By	Name ↑	Submitted By	IsSubmitted
There are no records to display.		There are no records to display.		

HB ENTRY		HB REVIEW/SUBMIT		
Name ↑	Saved By	Name ↑	Submitted By	IsSubmitted
Hb		Hb		

HIV Entry		HIV REVIEW/SUBMIT		
Name ↑	Saved By	Name ↑	Submitted By	IsSubmitted
There are no records to display.		There are no records to display.		

TOXO Entry		TOXO REVIEW/SUBMIT		
Name ↑	Saved By	Name ↑	Submitted By	IsSubmitted
There are no records to display.		There are no records to display.		

LD Analyte Selection		LD Entry	
Program Name ↑	Created On	Program Name ↑	Created On
LDPT	5/26/2026 11:48 AM	LDPT	5/26/2026 11:48 AM

LD Review and Submit	
Program Name ↑	Created On
LDPT	5/26/2026 11:48 AM

- **Analyte Selection** – Pages for Selecting and saving analytes to be used when entering program data.
- **Entry** – Pages for Entering and Saving Disease Specific PT Program Data.
- **Review and Submit** – Pages for Reviewing and Submitting Program Specific PT Program Data.

NOTE: Programs shown are for demonstration purposes only. Each lab will see pages only for programs they participate in.

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

1.6 Molecular PT Pages

1. Laboratories participating in molecular PT programs will need to utilize the molecular PT page.



2. Two relevant NSQAP Portal pages exist per program: Entry and Review/Submit.

CFDNA Entry

Name ↑	Saved By
CFDNA	

CFDNA Review/Submit

Name ↑	Submitted By	isSubmitted
CFDNA		No

SMA Entry

Name	Saved By
SMA	

SMA Review/Submit

Name ↑	Submitted By	isSubmitted
SMA		No

TREC Entry

Name ↑	Saved By
TREC	

TREC Submit/Review

Name ↑	Submitted By	isSubmitted
TREC		Yes

- **Entry** – Pages for Entering and Saving Disease Specific PT Program Data.
- **Review and Submit** – Pages for Reviewing and Submitting Program Specific PT Program Data.

NOTE: *Programs shown are for demonstration purposes only. Each lab will see pages only for programs they participate in.*

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

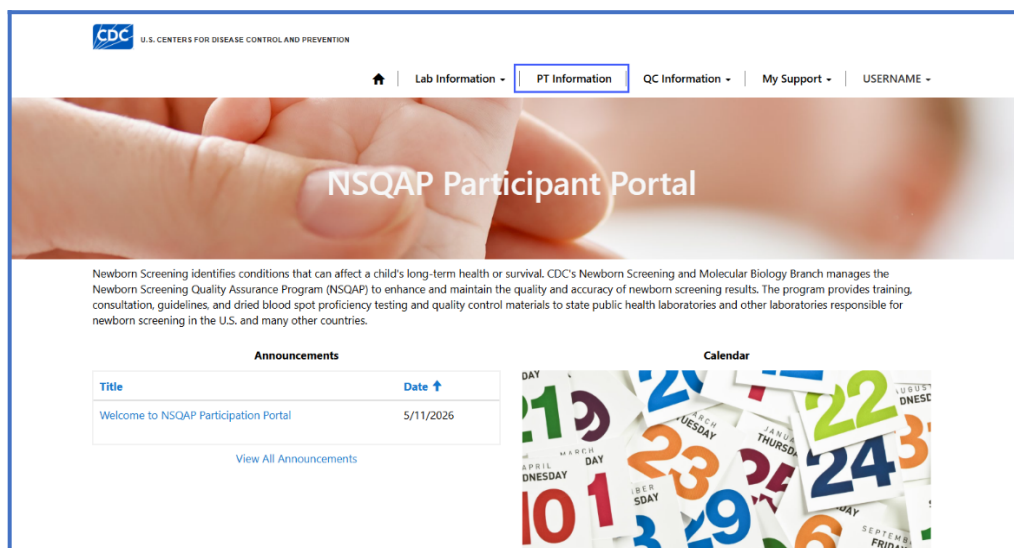
2. Biochemical Data Entry

2.1 Analyte Selection

Laboratories participating in Biochemical PT programs should utilize the analyte selection pages to set up the portal for data entry.

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

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





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

Step 1 - Analyte Selection		Step 2 - Specimen Data Entry	
Program Name	Program Name	Program Name	Program Name
Acylcarnitines (ACPT)	Acylcarnitines (ACPT)	Acylcarnitines (ACPT)	Acylcarnitines (ACPT)
Amino Acids and SUAC (AAP)	Amino Acids and SUAC (AAP)	Amino Acids and SUAC (AAP)	Amino Acids and SUAC (AAP)
Biotinidase (BIOT)	Biotinidase (BIOT)	Biotinidase (BIOT)	Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)	Galactose-1-phosphate Uridyltransferase (GALTPT)	Galactose-1-phosphate Uridyltransferase (GALTPT)	Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)	Hormone + Total Galactose (HORMPT)	Hormone + Total Galactose (HORMPT)	Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTP)	Immunoreactive Trypsinogen (IRTP)	Immunoreactive Trypsinogen (IRTP)	Immunoreactive Trypsinogen (IRTP)

Step 3 - Review and Submit		
Program Name	Submitted User	Submission Date
Acylcarnitines (ACPT)		
Amino Acids and SUAC (AAP)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		

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)	Method	Cutoff (μmol/L blood)
☐ Citrulline (Cit)	Method	Cutoff (μmol/L blood)
☐ Leucine (Leu)	Method	Cutoff (μmol/L blood)
☐ Methionine (Met)	Method	Cutoff (μmol/L blood)
☐ Phenylalanine (Phe)	Method	Cutoff (μmol/L blood)
☐ Succinylacetone (SUAC)	Method	Cutoff (μmol/L blood)
☐ Tyrosine (Tyr)	Method	Cutoff (μmol/L blood)
☐ Valine (Val)	Method	Cutoff (μmol/L blood)

SAVE AND SET VALUES

NOTE: The **'Select All Analytes'** checkbox is only present for some programs. 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

Set All Methods Below

Q

Method

Q

Method

Q

Method

Q

Method

Q

Method

Q

Method

Q

Method

Q

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)

☐ Arginine (Arg)

☐ Citrulline (Cit)

☐ Leucine (Leu)

☐ Methionine (Met)

☐ Phenylalanine (Phe)

☐ Succinylacetone (SUAC)

☐ Tyrosine (Tyr)

☐ Valine (Val)

SAVE AND SET VALUES

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

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)

17

7. 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)

☐ Select All Analytes

☒ Arginine (Arg)

☐ Citrulline (Cit)

☒ Leucine (Leu)

☐ Methionine (Met)

☒ Phenylalanine (Phe)

☐ Succinylacetone (SUAC)

☐ Tyrosine (Tyr)

☐ Valine (Val)

Set All Methods Below

Method

Non-derivatized - MS/MS NeoBase™ PerkinElmer

×

Q

Method

Q

Method

Non-derivatized - MS/MS NeoBase™ PerkinElmer

×

Q

Method

Q

Method

Non-derivatized - MS/MS NeoBase™ PerkinElmer

×

Q

Method

Q

Method

Q

Method

Q

Cutoff (μmol/L blood)

Cutoff (μmol/L blood)

Cutoff (μmol/L blood)

Cutoff (μmol/L blood)

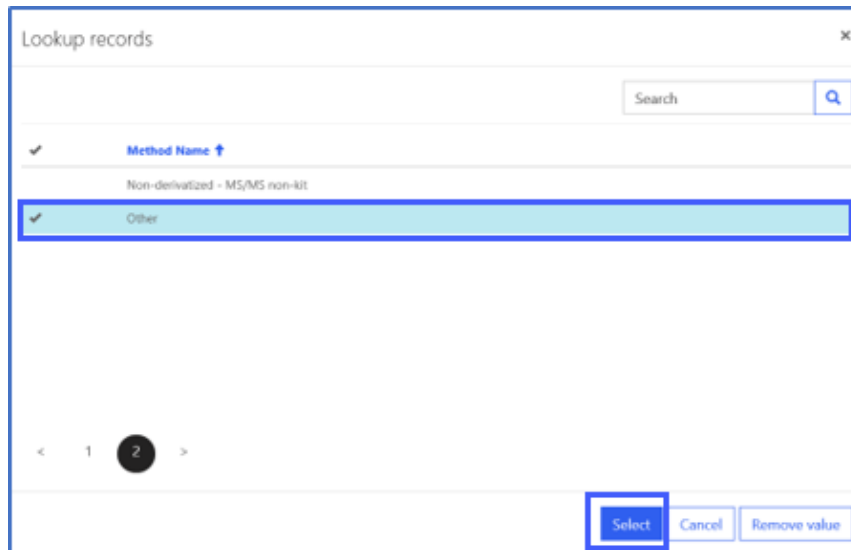
Cutoff (μmol/L blood)

Cutoff (μmol/L blood)

Cutoff (μmol/L blood)

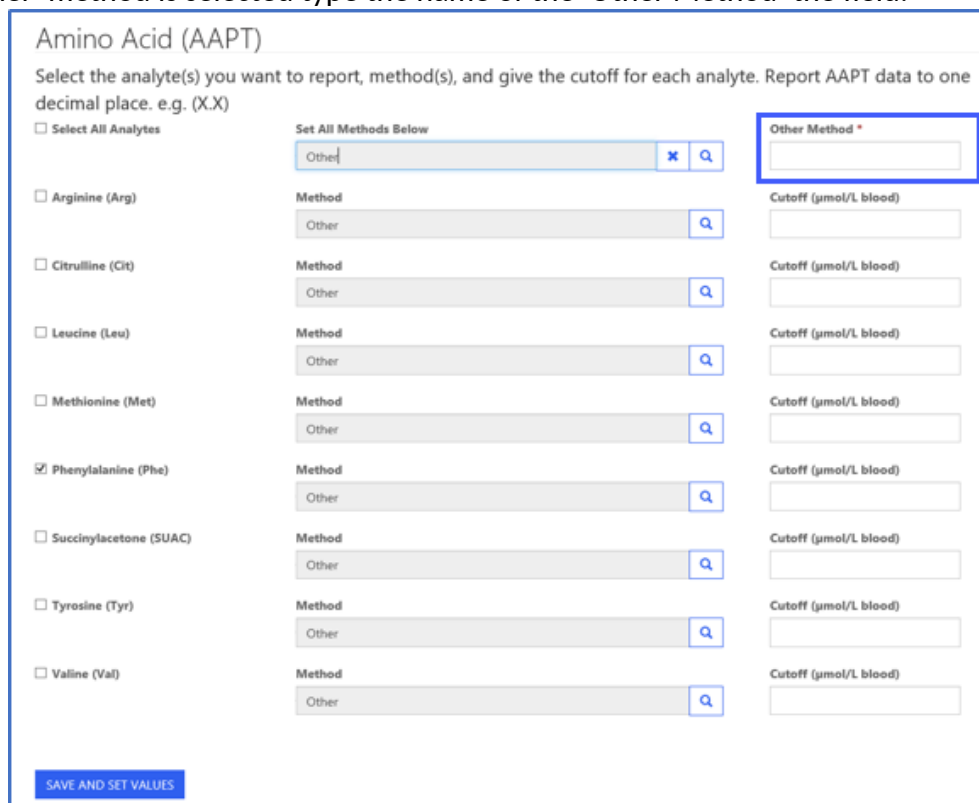
SAVE AND SET VALUES

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



The screenshot shows a 'Lookup records' window with a search bar and a table. The table has a header 'Method Name' and a single row with the value 'Other'. The 'Other' row is highlighted. At the bottom right, there are three buttons: 'Select', 'Cancel', and 'Remove value'. The 'Select' button is highlighted with a red box.

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



The screenshot shows the 'Amino Acid (AAPT)' form. It has a title 'Amino Acid (AAPT)' and a subtitle '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)'. There are checkboxes for 'Select All Analytes', 'Arginine (Arg)', 'Citrulline (Cit)', 'Leucine (Leu)', 'Methionine (Met)', 'Phenylalanine (Phe)', 'Succinylacetone (SUAC)', 'Tyrosine (Tyr)', and 'Valine (Val)'. The 'Phenylalanine (Phe)' checkbox is checked. There are three columns: 'Set All Methods Below', 'Method', and 'Cutoff (μmol/L blood)'. The 'Set All Methods Below' column has a search bar with 'Other' entered. The 'Method' column has a search bar with 'Other' entered. The 'Cutoff (μmol/L blood)' column has a search bar with 'Other' entered. The 'Other Method' field is highlighted with a red box.

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)

☐ Select All Analytes

☐ Arginine (Arg)	Set All Methods Below Non-derivatized - MS/MS NeoBase™ PerkinElmer Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 70.0
☐ Citrulline (Cit)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 55.0
☐ Leucine (Leu)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 290.0
☐ Methionine (Met)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 75.0
☒ Phenylalanine (Phe)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 150.0
☐ Succinylacetone (SUAC)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 2.2
☐ Tyrosine (Tyr)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 350.0
☐ Valine (Val)	Method Non-derivatized - MS/MS NeoBase™ PerkinElmer Cutoff (μmol/L blood) 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)

☐ 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	Cutoff (μmol/L blood)
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	70.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	55.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	290.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	75.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	150.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	2.2
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	350.0
Non-derivatized - MS/MS NeoBase™ PerkinElmer Q	300.0 x

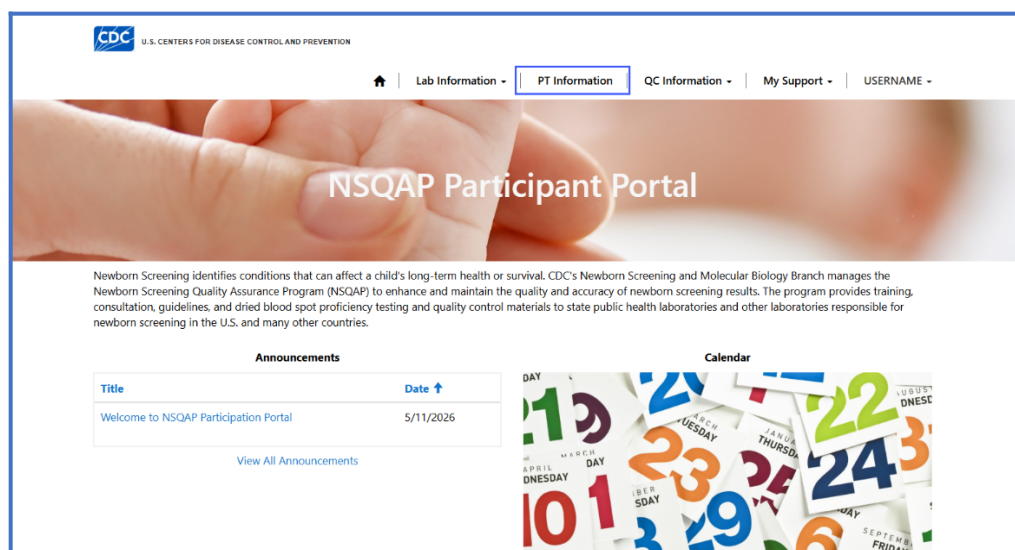
SAVE AND SET VALUES

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

2.2 Data Entry

Laboratories participating in biochemical programs should utilize the data entry page to enter data.

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



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

Step 1 - Analyte Selection

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 2 - Specimen Data Entry

Program Name ↑
Acylcarnitines (ACPT)
Amino Acids and SUAC (AAPT)
Biotinidase (BIOT)
Galactose-1-phosphate Uridyltransferase (GALTPT)
Hormone + Total Galactose (HORMPT)
Immunoreactive Trypsinogen (IRTPT)

Step 3 - Review and Submit

Program Name ↑	Submitted User	Submission Date
Acylcarnitines (ACPT)		
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		
Immunoreactive Trypsinogen (IRTPT)		

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		▼
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		▼
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		▼

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.

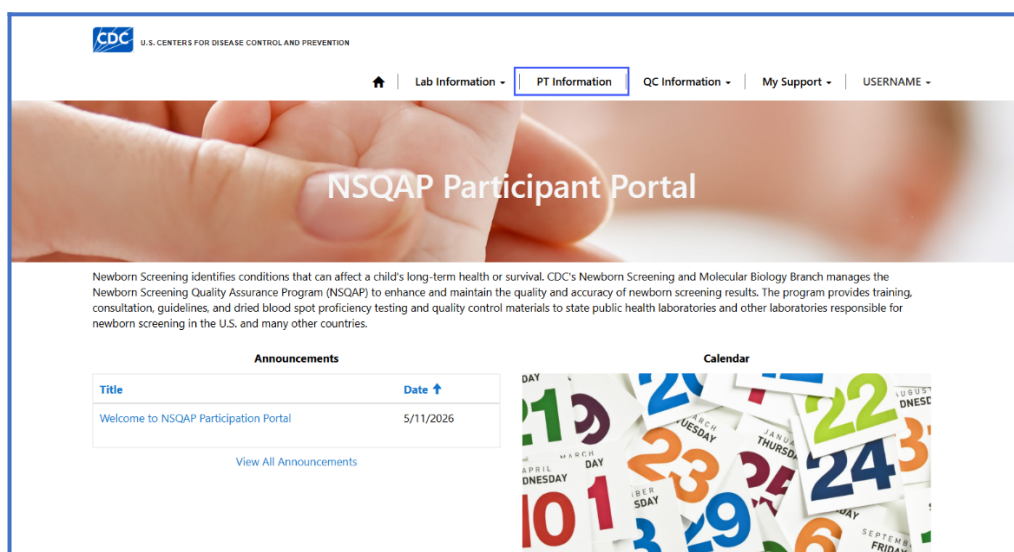
NOTE: Data can only be submitted if ALL specimens have a 'Saved' or 'Saved (Edited)' specimen status.

3. Biochemical Data Review and Submission

3.1 Data Summary

Laboratories participating in biochemical PT programs should utilize the review and submit page for data submission.

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



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

Step 1 - Analyte Selection

Program Name ↑

- Acylcarnitines (ACPT)
- Amino Acids and SUAC (AAPT)
- Biotinidase (BIOT)
- Galactose-1-phosphate Uridyltransferase (GALTPT)
- Hormone + Total Galactose (HORMPT)
- Immunoreactive Tyrosinogen (IRTP)

Step 2 - Specimen Data Entry

Program Name ↑

- Acylcarnitines (ACPT)
- Amino Acids and SUAC (AAPT)
- Biotinidase (BIOT)
- Galactose-1-phosphate Uridyltransferase (GALTPT)
- Hormone + Total Galactose (HORMPT)
- Immunoreactive Tyrosinogen (IRTP)

Step 3 - Review and Submit

Program Name ↑	Submitted User	Submission Date
Acylcarnitines (ACPT)		
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		
Immunoreactive Tyrosinogen (IRTP)		

- 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

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_Presumptive Clinical Assessment	Leu_Cutoff	Leu_Result
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	1- Within normal limits	70.0	68.3
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	2- Outside normal limits	70.0	73.9

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_Presumptive Clinical Assessment	Leu_Cutoff	Leu_Result
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 normal limits	70.0	68.3
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- Within normal limits	70.0	73.9
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- Within normal limits	70.0	69.2
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- Within normal limits	70.0	75.4
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- Within normal limits	70.0	45.8

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

< >

5. 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.

Specimen

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

SUBMIT

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

Submit

Once submitted, data cannot be edited.

ATTESTATION: I attest that these proficiency testing specimens were analyzed in the same manner as routine patient specimens.

Ok Cancel

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

Step 1 - Analyte Selection

Program Name ↑

Acylcamitines (ACPT)

Amino Acids and SUAC (AAPT)

Biotinidase (BIOT)

Galactose-1-phosphate Uridyltransferase (GALTPT)

Hormone + Total Galactose (HORMPT)

Immunoreactive Trypsinogen (IRTP)

Step 2 - Specimen Data Entry

Program Name ↑

Acylcamitines (ACPT)

Amino Acids and SUAC (AAPT)

Biotinidase (BIOT)

Galactose-1-phosphate Uridyltransferase (GALTPT)

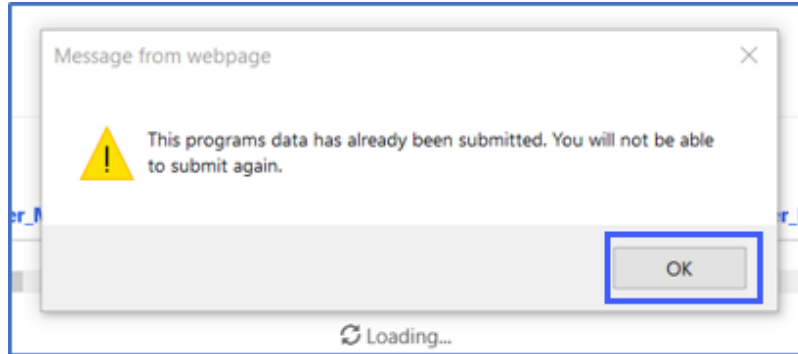
Hormone + Total Galactose (HORMPT)

Immunoreactive Trypsinogen (IRTP)

Step 3 - Review and Submit

Program Name ↑	Submitted User	Submission Date
Acylcamitines (ACPT)		
Amino Acids and SUAC (AAPT)	Username	5/22/2026 1:46 PM
Biotinidase (BIOT)		
Galactose-1-phosphate Uridyltransferase (GALTPT)		
Hormone + Total Galactose (HORMPT)		
Immunoreactive Trypsinogen (IRTP)		

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.



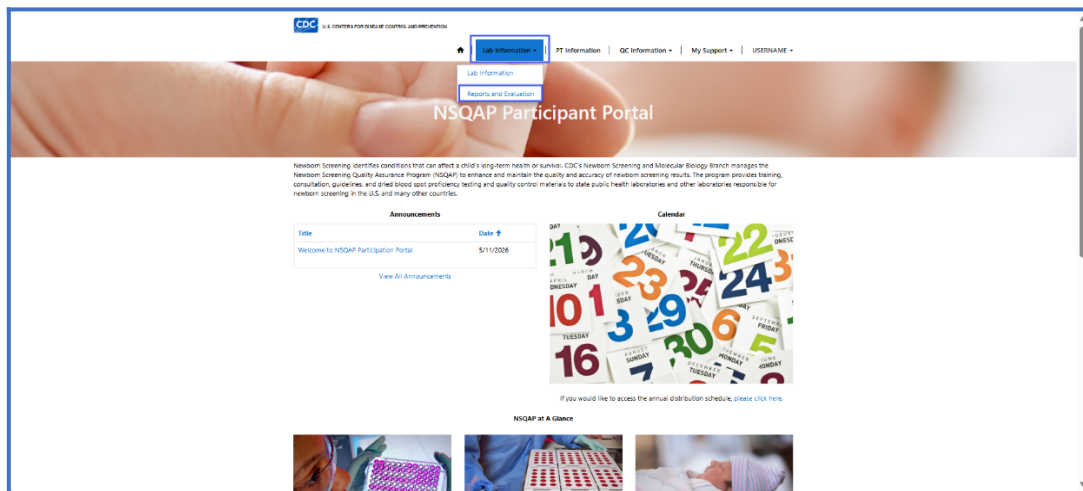
4. The 'Specimen Status' for each specimen will read 'Submitted'.

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

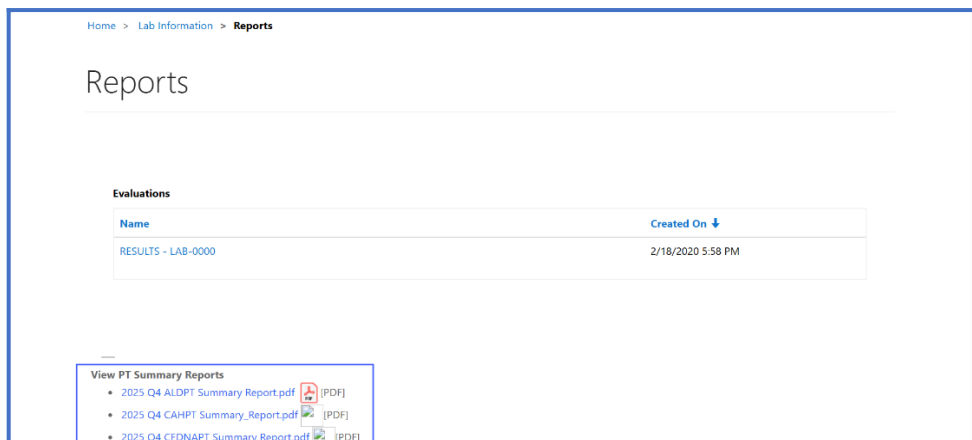
4. Reporting

4.1 Quarterly Summary Report

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

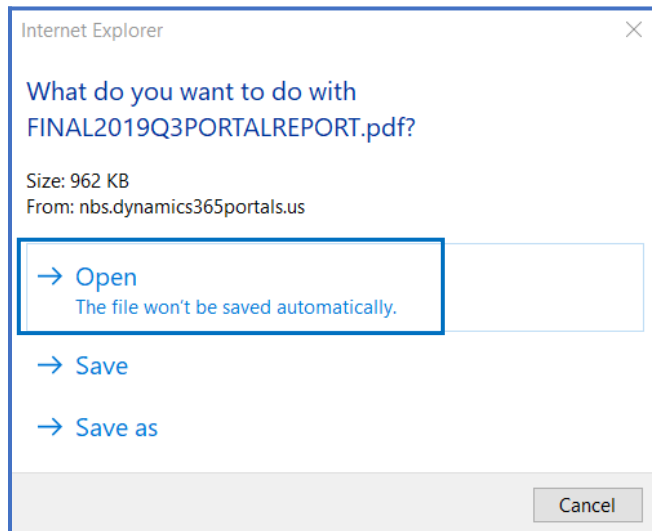


2. Select the **Summary Report** link for the report you wish to view.



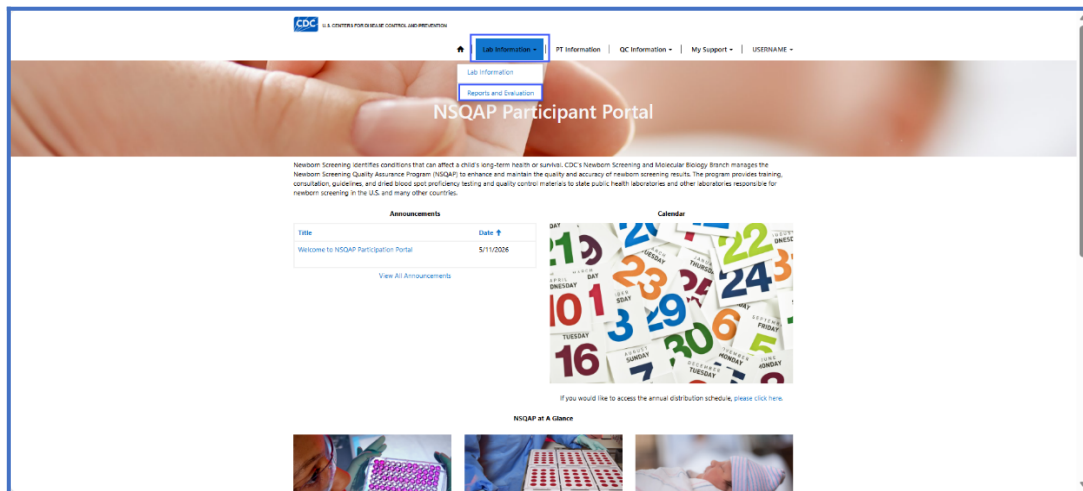
3. Click the '**Open**' option in the pop-up window to download and view the Quarterly Summary Report.

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

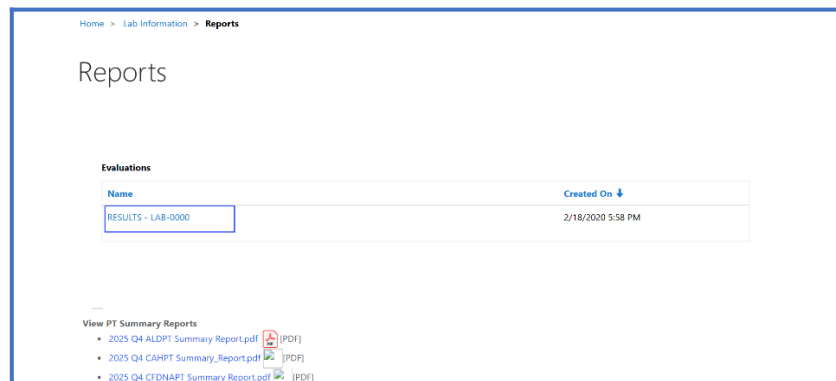


5.2 Evaluation Report

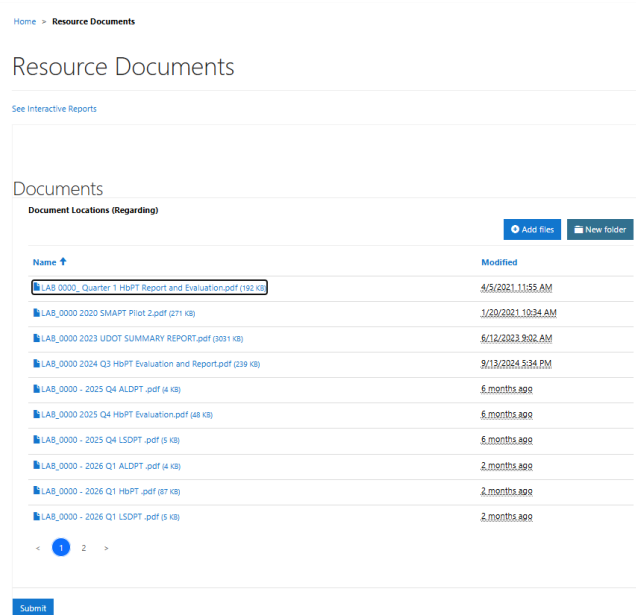
1. Select the **'Lab Information'** button at the top of the page on the toolbar and select the **'Reports and Evaluations'** option.



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



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



4. If required for your browser, click the '**Open**' button at the bottom of the page to download and view the Evaluation Report.