

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**

**SMA AND TREC QUALITY
CONTROL USER GUIDE**

July 2026

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1. Introduction

The NSMBB Newborn Screening Quality Assurance Program (NSQAP) Portal SMA/TREC QC Program has been designed to accept participant Quality Control (QC) data using the manual data entry option. Participants are advised to consider the following before entering data:

1. Participants are permitted to only use manual upload data entry option for this program.
2. The review feature enables participants to review and edit manually entered data in the Portal directly from the review page.

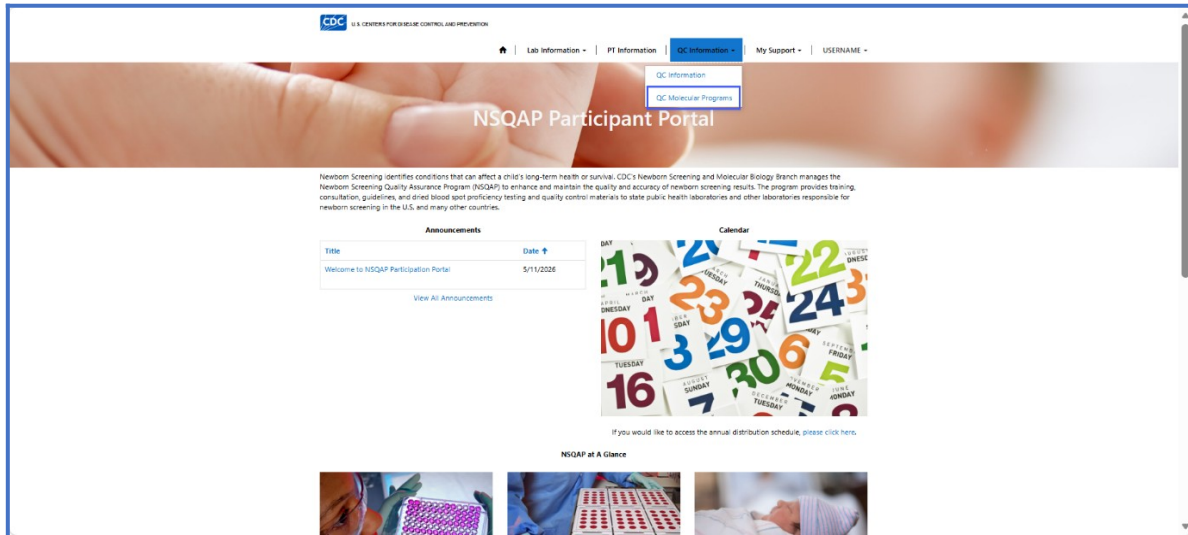
The following pages describe how to enter data into the NSQAP Portal.

2. QC Manual Data Entry

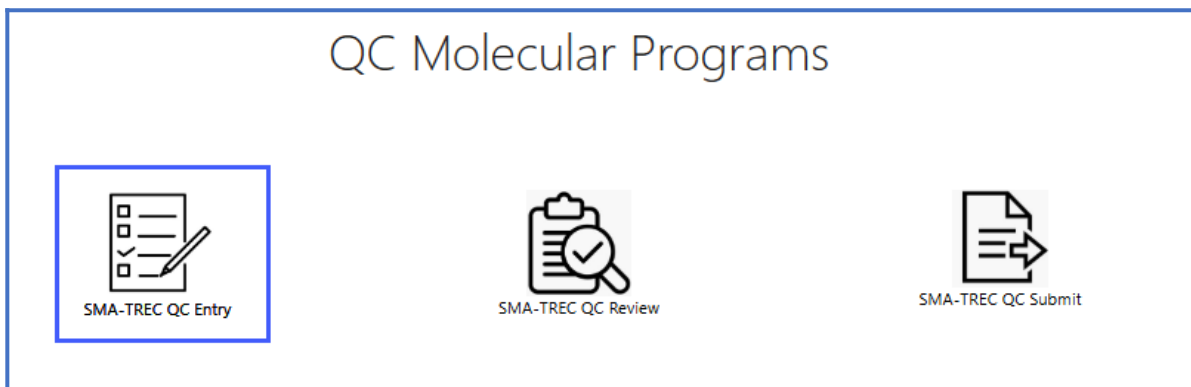
QC Programs data can be manually entered into the NSQAP Portal from the QC Information section of the Portal.

2.1 Manual Data Entry

1. Navigate to the 'QC Molecular Programs' under the 'QC Information' dropdown menu.



2. Click 'SMA-TREC QC Entry' to proceed to the entry page.



3. Select the **'Spinal Muscular Atrophy + T-cell Receptor Excision Circle (SMA and TREC QC)** by clicking on the program hyperlink.

Home > QC Molecular Programs

QC Molecular Programs

Name ↑	Created On
Spinal Muscular Atrophy + T-cell Receptor Excision Circle (SMA and TREC QC)	7/16/2022 5:34 PM

*-Required Field.

Form Approved
OMB No. 0920-1389
Exp. Date 03/31/2026

4. Select the Analyte by clicking on the analyte abbreviation hyperlink.

Home > Analytes List - (DATA ENTRY)

Analytes List - (DATA ENTRY)

Program Name *

Spinal Muscular Atrophy + T-cell Receptor Excision Circle (SMA and TREC QC)

Analytes

Abbreviation	Name ↑
SMN1 E7	Survival Muscular Neuron Gene 1 Exon 7
TREC	T-Cell Receptor Excision Circle

5. Select the **'Magnifying Glass'** icon on the 'DNA Extraction Method' field.

Molecular QC Data Entry

Save Method Information

Analyte Name *

Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *

Instrumentation

SMN1 E7 Primary Testing Method *

Other DNA Extraction Method *

Other Instrumentation *

Other SMN1 E7 Testing Method *

- A new window will appear listing methods for the analyte. 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 choose the method and close the window.

Lookup records

Search

Q

Choose one record and click Select to continue

✓

Name ↑

☐	Extracta™ DBS
☐	Extracta™ DBS with one wash
☐	Generation™ DNA Elution Solution (S2 only)
☐	Generation™ DNA Purification and Elution Solutions (S1/S2)
☐	ImmunoIVD SPOT-it™ TREC & SMN1 Screening Kit reagents
☐	In situ/on card (DNA is NOT extracted)
☐	Other

Select

Cancel

Remove value

- If **'Other'** was chosen, enter the other method in the **'Other DNA Extraction Method'** field that appears.

Molecular QC Data Entry

Save Method Information

Analyte Name *

Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *

x

Q

Instrumentation

x

Q

SMN1 E7 Primary Testing Method *

x

Q

Other DNA Extraction Method *

Other Instrumentation *

Other SMN1 E7 Testing Method *

8. Select the **'Magnifying Glass'** icon on the 'Instrumentation' field.

Molecular QC Data Entry

Save Method Information

Analyte Name *
Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *
[Text Field] x [Magnifying Glass Icon]

Other DNA Extraction Method *
[Text Field]

Instrumentation
[Text Field] x [Magnifying Glass Icon]

Other Instrumentation *
[Text Field]

SMN1 E7 Primary Testing Method *
[Text Field] x [Magnifying Glass Icon]

Other SMN1 E7 Testing Method *
[Text Field]

9. A new window will appear listing instrumentation for the analyte. Click on the instrumentation, and the row will highlight with a check mark on the left side. Click the **'Select'** button at the bottom of the window to choose the instrumentation and close the window.

Lookup records

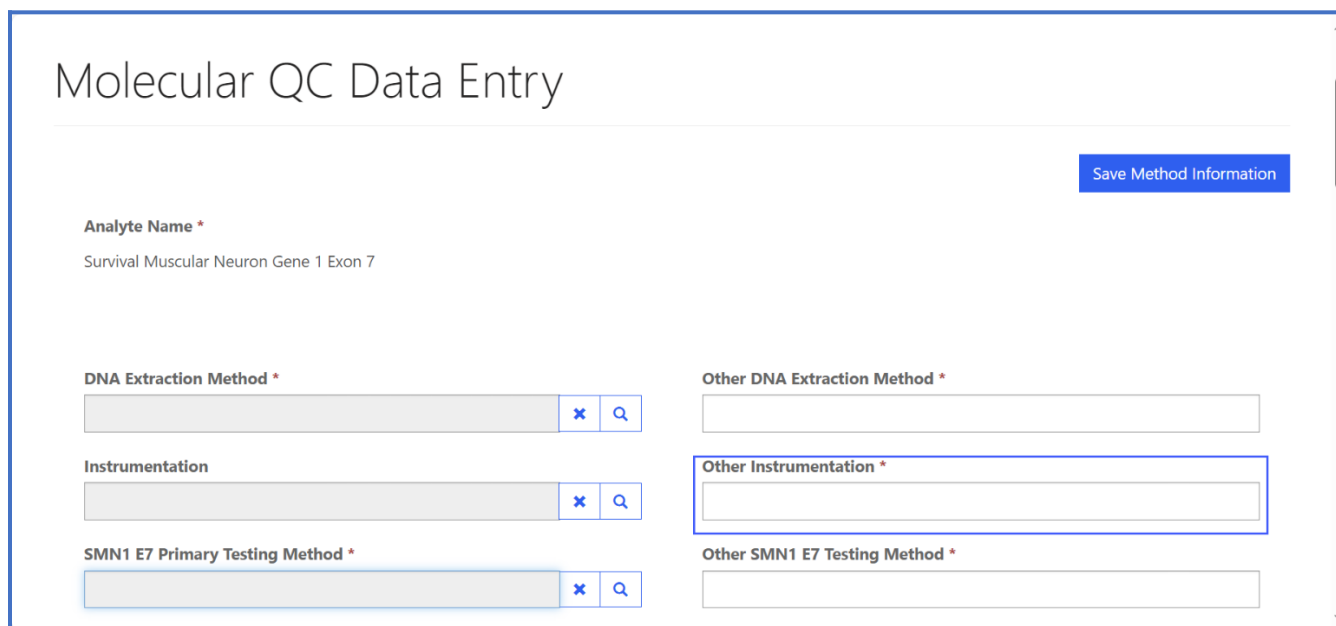
Search [Magnifying Glass Icon]

Choose one record and click Select to continue

✓ Name	Created On
☐ Viaa7	1/23/2024 7:49 AM
☐ QS5	1/23/2024 7:49 AM
☐ QS5-DX	1/23/2024 7:49 AM
☐ QS6	1/23/2024 7:49 AM
☐ QS7	1/23/2024 7:50 AM
☐ QS12	1/23/2024 7:50 AM
☐ QS7-Dx	1/23/2024 7:50 AM

Select Cancel Remove value

10. If **'Other'** was chosen, enter the name of the other instrumentation in the **'Other Instrumentation'** field that appears.



The screenshot shows the 'Molecular QC Data Entry' form. The 'Analyte Name' field is populated with 'Survival Muscular Neuron Gene 1 Exon 7'. The 'DNA Extraction Method' and 'Instrumentation' fields are empty. The 'SMN1 E7 Primary Testing Method' field is empty. The 'Other DNA Extraction Method', 'Other Instrumentation', and 'Other SMN1 E7 Testing Method' fields are also empty. The 'Other Instrumentation' field is highlighted with a blue border, indicating it is the focus of the instruction.

Molecular QC Data Entry

Save Method Information

Analyte Name *

Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *

Other DNA Extraction Method *

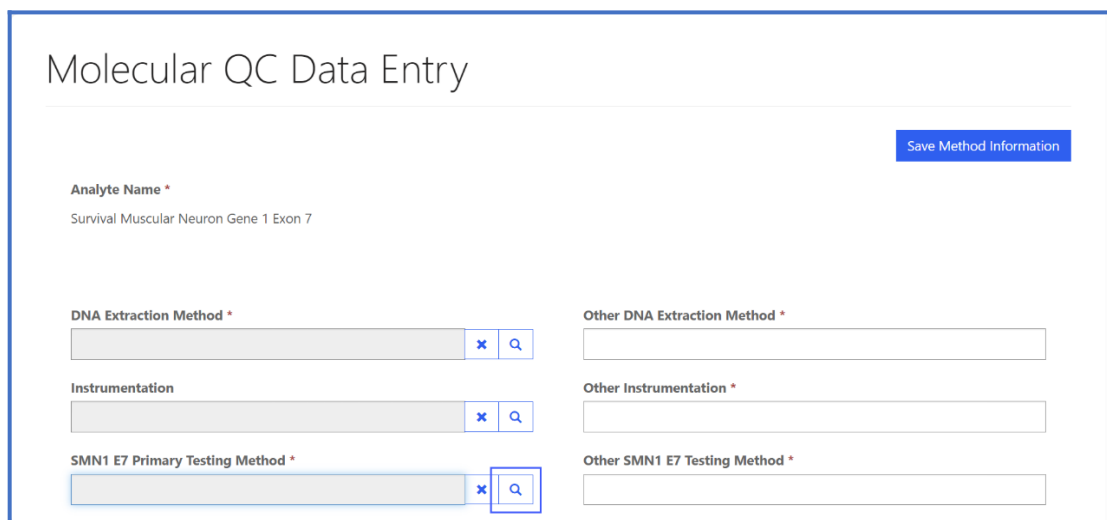
Instrumentation

Other Instrumentation *

SMN1 E7 Primary Testing Method *

Other SMN1 E7 Testing Method *

11. Select the **'Magnifying Glass'** icon on the **'SMN1 E7 Primary Testing Method'** field.



The screenshot shows the 'Molecular QC Data Entry' form. The 'Analyte Name' field is populated with 'Survival Muscular Neuron Gene 1 Exon 7'. The 'DNA Extraction Method' and 'Instrumentation' fields are empty. The 'SMN1 E7 Primary Testing Method' field is empty. The 'Other DNA Extraction Method', 'Other Instrumentation', and 'Other SMN1 E7 Testing Method' fields are also empty. The magnifying glass icon on the 'SMN1 E7 Primary Testing Method' field is highlighted with a blue border, indicating it is the focus of the instruction.

Molecular QC Data Entry

Save Method Information

Analyte Name *

Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *

Other DNA Extraction Method *

Instrumentation

Other Instrumentation *

SMN1 E7 Primary Testing Method *

Other SMN1 E7 Testing Method *

12. A new window will appear listing SMN1 E7 Primary Testing Methods for the analyte. Click on the record, and the row will highlight with a check mark on the left side. Click the **'Select'** button at the bottom of the window to choose the SMN1 E7 Primary Testing Method and close the window.

The 'Lookup records' window displays a list of testing methods. The 'Select' button at the bottom is highlighted with a blue border.

✓	Name ↑
☐	ImmunoIVD SPOT-it™ TREC & SMN1 Screening Kit
☐	LDT Real Time PCR - SMN1 AND Reference Gene run in a single tube
☐	LDT Real Time PCR - SMN1/TREC AND Reference Gene run in a single tube
☐	MRC Holland SALSA MC002 SMA Newborn Screen
☐	Other
☐	Perkin Elmer Eonis™ SCID-SMA kit
☐	Perkin Elmer NeoMDx RUO

Buttons: Select, Cancel, Remove value

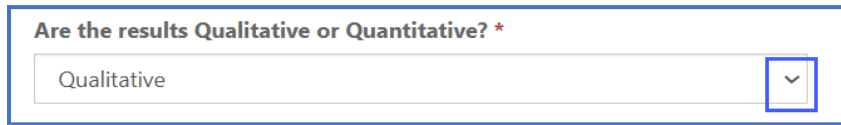
13. If **'Other'** was chosen, enter the other primary testing method into the **'Other SMN1 E7 Testing Method'** field that appears.

The 'Molecular QC Data Entry' form contains the following fields:

- Analyte Name ***: Survival Muscular Neuron Gene 1 Exon 7
- DNA Extraction Method ***: [Field with clear and search icons]
- Other DNA Extraction Method ***: [Field]
- Instrumentation**: [Field with clear and search icons]
- Other Instrumentation ***: [Field]
- SMN1 E7 Primary Testing Method ***: [Field with clear and search icons]
- Other SMN1 E7 Testing Method ***: [Field, highlighted with a blue border]

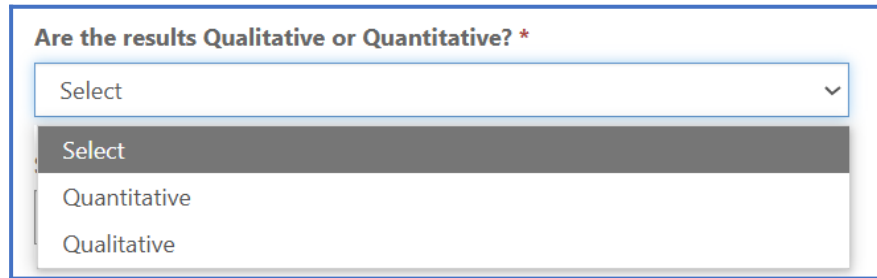
Buttons: Save Method Information

14. Select the ^ icon on the 'Are the results Qualitative or Quantitative?' field.



A screenshot of a form field titled "Are the results Qualitative or Quantitative? *". The field contains the text "Qualitative" and a small downward-pointing arrow icon on the right side, which is highlighted with a blue box.

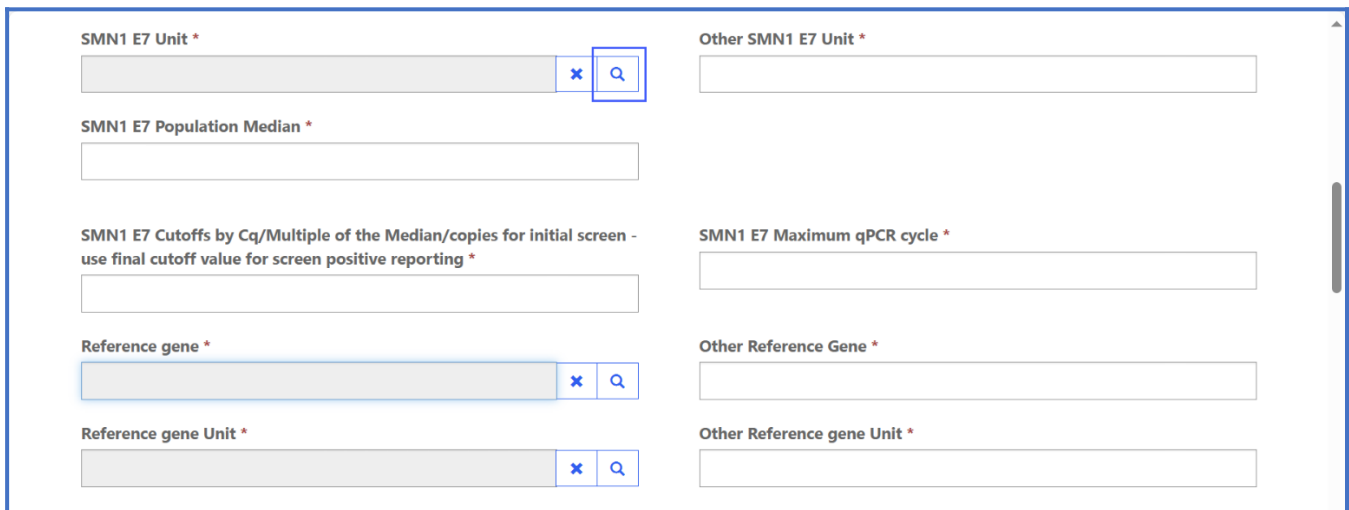
15. A dropdown menu will display with options for Qualitative and Quantitative. Click on Qualitative or Quantitative to select one.



A screenshot of the dropdown menu for the field "Are the results Qualitative or Quantitative? *". The menu is open, showing a "Select" option at the top, followed by "Quantitative" and "Qualitative". The "Qualitative" option is highlighted with a blue box.

16. When selecting Qualitative the 'SMN1 E7 Unit,' 'SMN1 E7 Maximum qPCR cycle,' 'SMN1 E7 Population Median,' 'SMN1 E7 Cutoff,' 'Reference Gene Unit,' 'Reference Gene Population Median,' and 'Reference Gene Cutoff' fields will not be displayed. *Skip to step 29.*

17. Select the 'Magnifying Glass' icon on the 'SMN1 E7 Unit' field.



A screenshot of a form with several input fields. The fields are arranged in two columns. The left column contains: "SMN1 E7 Unit *", "SMN1 E7 Population Median *", "SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *", "Reference gene *", and "Reference gene Unit *". The right column contains: "Other SMN1 E7 Unit *", "SMN1 E7 Maximum qPCR cycle *", "Other Reference Gene *", and "Other Reference gene Unit *". The "SMN1 E7 Unit *" field has a magnifying glass icon highlighted with a blue box.

18. A new window will appear with other SMN1 E7 units for the analyte. Click on the record, and the row will highlight with a check mark on the left side. Click the **‘Select’** button at the bottom of the window to choose the SMN1 E7 Unit and close the window.

Lookup records ×

Search Q

Choose one record and click Select to continue

✓

Name

Created On

☐	Other	1/12/2024 10:32 AM
☐	Cq	1/12/2024 10:33 AM
☐	Copies/ul	1/12/2024 10:33 AM
☐	MoM Cq	1/12/2024 10:34 AM
☐	MoM Copy	1/12/2024 10:34 AM
☐	Copies/mL	4/19/2024 10:07 AM

Select

Cancel

Remove value

19. If **'Other'** is selected, type in the other SMN1 E7 Unit.

SMN1 E7 Unit *

SMN1 E7 Population Median *

SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *

Reference gene *

Reference gene Unit *

Other SMN1 E7 Unit *

SMN1 E7 Maximum qPCR cycle *

Other Reference Gene *

Other Reference gene Unit *

20. Enter values for the **'SMN1 E7 Population Median,' 'SMN1 E7 Cutoffs'** and **'SMN1 E7 Maximum qPCR cycle'** fields.

SMN1 E7 Unit *

SMN1 E7 Population Median *

SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *

Reference gene *

Reference gene Unit *

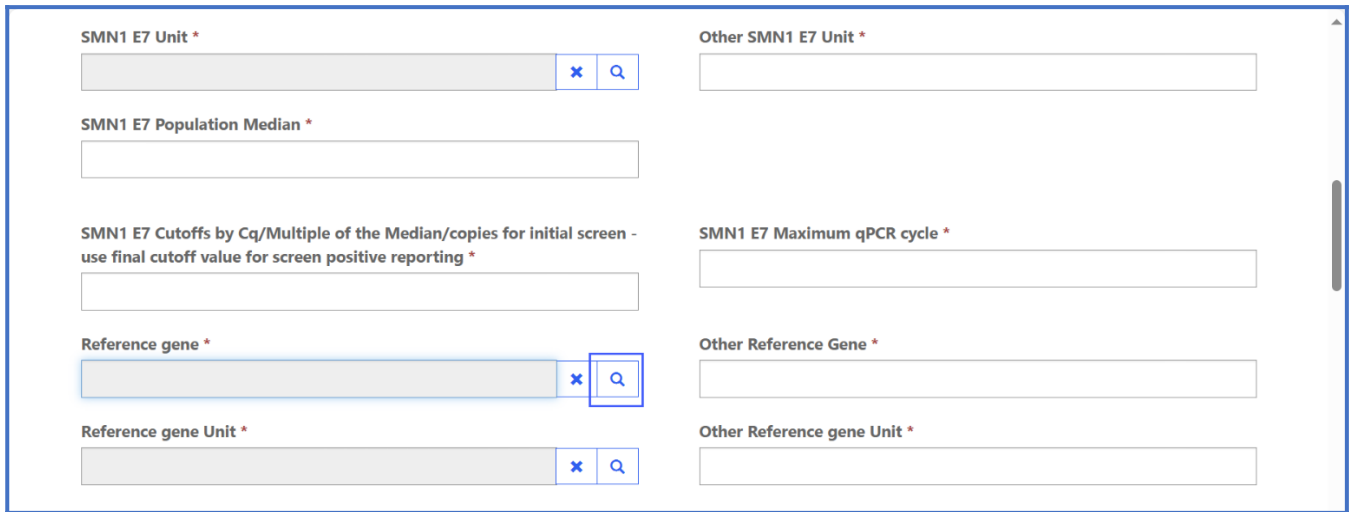
Other SMN1 E7 Unit *

SMN1 E7 Maximum qPCR cycle *

Other Reference Gene *

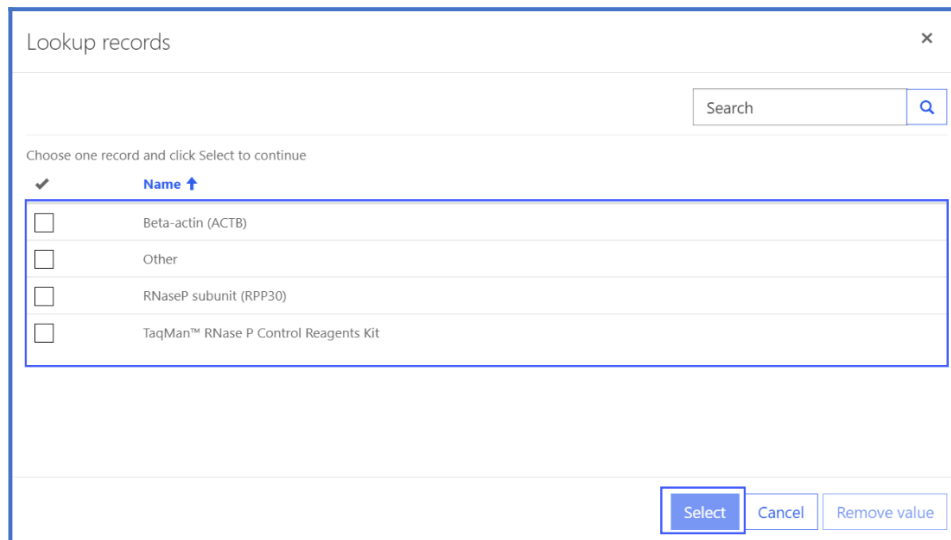
Other Reference gene Unit *

21. Select the **'Magnifying Glass'** icon on the 'Reference gene' field.



The screenshot shows a form with several input fields. The 'Reference gene' field is highlighted with a blue border, and a magnifying glass icon is also highlighted with a blue border. The form includes fields for 'SMN1 E7 Unit', 'Other SMN1 E7 Unit', 'SMN1 E7 Population Median', 'SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting', 'SMN1 E7 Maximum qPCR cycle', 'Reference gene', 'Other Reference Gene', 'Reference gene Unit', and 'Other Reference gene Unit'.

22. A new window will appear with other reference gene values for the analyte. Click on the record, and the row will highlight with a check mark on the left side. Click the **'Select'** button at the bottom of the window to choose the Reference gene and close the window.



The screenshot shows a 'Lookup records' window. It has a search bar at the top right. Below the search bar, there is a table with a checkmark column and a 'Name' column. The table lists four options: 'Beta-actin (ACTB)', 'Other', 'RNaseP subunit (RPP30)', and 'TaqMan™ RNase P Control Reagents Kit'. The 'Select' button at the bottom right is highlighted with a blue border.

	Name ↑
☐	Beta-actin (ACTB)
☐	Other
☐	RNaseP subunit (RPP30)
☐	TaqMan™ RNase P Control Reagents Kit

23. If 'Other' is selected, type in the other SMN1 E7 Unit.

The screenshot shows a form with two columns of input fields. The left column contains: 'SMN1 E7 Unit *' (highlighted with a blue box), 'SMN1 E7 Population Median *', 'SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *', 'Reference gene *' (highlighted with a blue box), and 'Reference gene Unit *' (highlighted with a blue box). The right column contains: 'Other SMN1 E7 Unit *', 'SMN1 E7 Maximum qPCR cycle *', 'Other Reference Gene *' (highlighted with a blue box), and 'Other Reference gene Unit *'. The 'Other SMN1 E7 Unit *' field is highlighted with a blue box.

24. Select the 'Magnifying Glass' icon on the 'Reference gene Unit' field.

The screenshot shows the same form as above. The 'Reference gene Unit *' field is highlighted with a blue box, and the 'Magnifying Glass' icon (a small square with a magnifying glass) is also highlighted with a blue box. The 'Other SMN1 E7 Unit *' field is also highlighted with a blue box.

25. A new window will appear with other reference gene unit values for the analyte. Click on the record, and the row will highlight with a check mark on the left side. Click the **'Select'** button at the bottom of the window to choose the Reference gene unit and close the window.

Lookup records

Search

Choose one record and click Select to continue

✓ Name	Created On
☐ Other	1/12/2024 10:32 AM
☐ Cq	1/12/2024 10:33 AM
☐ Copies/ul	1/12/2024 10:33 AM
☐ MoM Cq	1/12/2024 10:34 AM
☐ MoM Copy	1/12/2024 10:34 AM
☐ Copies/mL	4/19/2024 10:07 AM

Select Cancel Remove value

26. If **'Other'** is selected, type in the Other Reference gene Unit.

SMN1 E7 Unit *

Other SMN1 E7 Unit *

SMN1 E7 Population Median *

SMN1 E7 Cutoffs by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *

SMN1 E7 Maximum qPCR cycle *

Reference gene *

Other Reference Gene *

Reference gene Unit *

Other Reference gene Unit *

27. Enter a value for the Reference Gene Population Median.

Reference Gene *	Other Reference Gene *
Reference Gene Unit *	Other Reference Gene Unit *
Reference Gene Population Median *	
Reference Gene Cutoff by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *	

28. Enter a value for the Reference Gene Cutoff.

Reference Gene *	Other Reference Gene *
Reference Gene Unit *	Other Reference Gene Unit *
Reference Gene Population Median *	
Reference Gene Cutoff by Cq/Multiple of the Median/copies for initial screen - use final cutoff value for screen positive reporting *	

29. Select the 'Save Method Information' button to save the method for the analyte.

Molecular QC Data Entry

Save Method Information

Analyte Name *

Survival Muscular Neuron Gene 1 Exon 7

DNA Extraction Method *	Other DNA Extraction Method *
Instrumentation	Other Instrumentation *
SMN1 E7 Primary Testing Method *	Other SMN1 E7 Testing Method *

30. To add Molecular QC data, select the Run hyperlink in the **'Runs'** summary table.

Runs

[Download](#)

RUNS ↑	Analyte	Method	DNA Extraction Method	Units	Lot_A	Replicate_1A	Replicate_2A	Reference Gene_1A	Reference Gene_2A	Lot_B	Replicate_1B	Replicate_2B	Re Ge
1	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run in a single tube	Extracta™ DBS with one wash	Cq	LOT#1	23.500	24.212	1.000	1.000	LOT#2	23.548	23.548	1.0
2	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run	Extracta™ DBS with one wash	Cq	LOT#1	24.500	23.200			LOT#2	21.300		

31. A data entry window will appear.

- If qualitative was selected in step 14, qualitative data entry fields will display. Select a value of Present or Absent for both replicates per lot, select a reference gene value for both replicates per lot, then select the **'SAVE RUN DATA'** button.

View details ×

Analyte: Survival Muscular Neuron Gene 1
Exon 7

Run: 1

[SAVE RUN DATA](#)

NSQAP will interpret the data reported based on the method which is selected.

Values

Lot#1

Replicate_1A *

Select

Replicate_2A *

Select

Reference
Gene_1A *

Select

Reference
Gene_2A *

Select

Lot#2

- b. If quantitative was selected in step 14, quantitative data entry fields will display. Enter a quantitative value or select '**No signal detected**' for both replicates per lot, enter a reference gene value for both replicates per lot, then select the '**SAVE RUN DATA**' button.

View details

Analyte: Survival Muscular Neuron Gene 1
Exon 7

Run: 1

SAVE RUN DATA

NSQAP will interpret the data reported based on the method which is selected.

Values

LOT#1

Replicate_1A *

☐ No signal detected

Replicate_2A *

☐ No signal detected

Reference Gene_1A *

Reference Gene_2A *

LOT#2

Replicate_1B *

☐ No signal detected

Replicate_2B *

☐ No signal detected

Reference Gene_1B *

Reference Gene_2B *

LOT#3

NOTE: To save run data, each value must have data or 'No signal detected' selected.

32. Data will appear in the summary table when the run is saved.

Runs

Download

RUNS	Analyte	Method	DNA Extraction Method	Units	Lot_A	Replicate_1A	Replicate_2A	Reference Gene_1A	Reference Gene_2A	Lot_B	Replicate_1B	Replicate_2B	Re Ge
1	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run in a single tube	Extracta™ DBS with one wash	Cq	LOT#1	23.500	24.212	1.000	1.000	LOT#2	23.548	23.548	1.0
2	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run	Extracta™ DBS with one wash	Cq	LOT#1	24.500	23.200			LOT#2	21.300		

33. Analyte specific data can be entered, reviewed, and edited on this page.

NOTE: Export results to an Excel spreadsheet by selecting the ‘Download Summary’ button.
(Optional)

Runs

Download

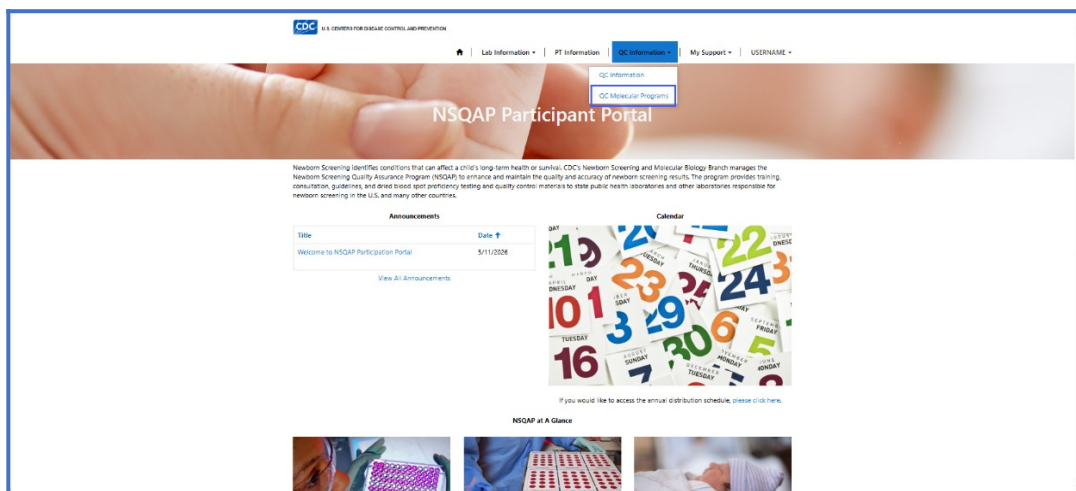
RUNS	Analyte	Method	DNA Extraction Method	Units	Lot_A	Replicate_1A	Replicate_2A	Reference Gene_1A	Reference Gene_2A	Lot_B	Replicate_1B	Replicate_2B	Re Ge
1	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run in a single tube	Extracta™ DBS with one wash	Cq	LOT#1	23.500	24.212	1.000	1.000	LOT#2	23.548	23.548	1.0
2	SMN1 E7	LDT Real Time PCR - SMN1 AND Reference Gene run	Extracta™ DBS with one wash	Cq	LOT#1	24.500	23.200			LOT#2	21.300		

34. Repeat this process for each analyte.

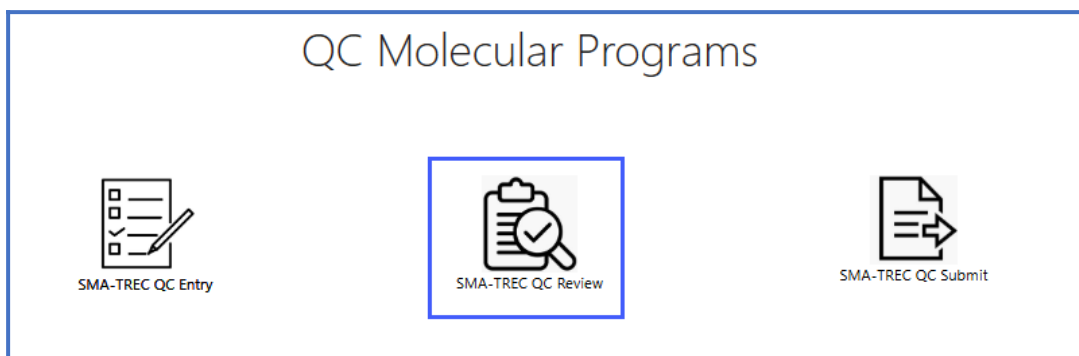
2.2 Review Manually Entered Data

All manually entered SMA & TREC QC data can be reviewed by accessing the **'SMA & TREC QC Review'** option page on **'QC Molecular Programs'** from the **'QC Information'** dropdown on the toolbar.

1. Select the **'QC Information'** button at the top of the page on the toolbar and select the **'QC Molecular Programs'** option.



2. Select the **'SMA-TREC QC Review'** button.



3. On the 'SMA-TREC QC Review' page, results can be reviewed, edited, and filtered by Analyte.

Home > QC Molecular Review

QC Molecular Review

To filter the data by program, select the check box(es) next to the program and click the "Apply" button on the left hand side.

Filter by Analyte

☐ Spinal Muscular Atrophy (SMA)

☐ T-Cell Receptor Excision Circle (TREC)

Apply

Download

RUNS ↑	Analyte	Method	DNA Extraction Method	Cutoffs	Units	Polulation Median	Replicate_1A	Replicate_2A	Replicate_1B	Rep
1	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
1	TREC			2.00	Other	4.00	100.000	100.000	100.000	
2	SMA	Other	Other	34.00	Other	3.00	1.000	2.000	1.000	2.00

4. To review Molecular QC data, navigate through the results table using the navigation features located on the right side and the bottom of the table.

Filter by Analyte

☐ Spinal Muscular Atrophy (SMA)

☐ T-Cell Receptor Excision Circle (TREC)

Apply

RUNS ↑	Analyte	Method	DNA Extraction Method	Cutoffs	Units	Polulation Median	Replicate_1A	Replicate_2A	Replicate_1B	Rep
1	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
1	TREC			2.00	Other	4.00	100.000	100.000	100.000	
2	SMA	Other	Other	34.00	Other	3.00	1.000	2.000	1.000	2.00
2	TREC			2.00	Other	4.00				
3	SMA	Other	Other	34.00	Other	3.00	111.000	1,111.000	222.000	222.000
3	TREC			2.00	Other	4.00				
4	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
4	TREC			2.00	Other	4.00				
5	SMA	Other	Other	34.00	Other	3.00	2.000	2.000	3.000	2.00
5	TREC			2.00	Other	4.00				

5. To edit data, select the hyperlinked run number on the row of interest.

Filter by Analyte

☐ Spinal Muscular Atrophy (SMA)

☐ T-Cell Receptor Excision Circle (TREC)

[Apply](#)

RUNS ↑	Analyte	Method	DNA Extraction Method	Cutoffs	Units	Polulation Median	Replicate_1A	Replicate_2A	Replicate_1B	Rep
1	SMA	Other	Other	34.00	Other	3.00	1,000	1,000	2,000	2.00
1	TREC			2.00	Other	4.00	100,000	100,000	100,000	
2	SMA	Other	Other	34.00	Other	3.00	1,000	2,000	1,000	2.00
2	TREC			2.00	Other	4.00				
3	SMA	Other	Other	34.00	Other	3.00	111,000	1,111,000	222,000	222.
3	TREC			2.00	Other	4.00				
4	SMA	Other	Other	34.00	Other	3.00	1,000	1,000	2,000	2.00
4	TREC			2.00	Other	4.00				
5	SMA	Other	Other	34.00	Other	3.00	2,000	2,000	3,000	2.00
5	TREC			2.00	Other	4.00				

6. The analyte data entry page will appear where the data can be edited and saved.

View details
×

Analyte: Survival Muscular Neuron Gene 1 Exon 7

Run: 1

SAVE RUN DATA

NSQAP will interpret the data reported based on the method which is selected.

Values

LOT#1

Replicate_1A *

☐ No signal detected

Reference Gene_1A *

Replicate_2A *

☐ No signal detected

LOT#2

Replicate_1B *

☐ No signal detected

Reference Gene_1B *

Replicate_2B *

☐ No signal detected

7. After selecting **'Save Run Data'**, the User will be directed back to the **'QC Molecular Review'** page to continue reviewing the data.

Filter by Analyte
☐ Spinal Muscular Atrophy (SMA)
☐ T-Cell Receptor Excision Circle (TREC)

RUNS ↑	Analyte	Method	DNA Extraction Method	Cutoffs	Units	Polulation Median	Replicate_1A	Replicate_2A	Replicate_1B	Rep
1	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
1	TREC			2.00	Other	4.00	100.000	100.000	100.000	
2	SMA	Other	Other	34.00	Other	3.00	1.000	2.000	1.000	2.00
2	TREC			2.00	Other	4.00				
3	SMA	Other	Other	34.00	Other	3.00	111.000	1,111.000	222.000	222.
3	TREC			2.00	Other	4.00				
4	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
4	TREC			2.00	Other	4.00				
5	SMA	Other	Other	34.00	Other	3.00	2.000	2.000	3.000	2.00
5	TREC			2.00	Other	4.00				

8. Review QC data offline by selecting **'Download'** to generate an Excel spreadsheet of the data entered.

Home > QC Molecular Review

QC Molecular Review

To filter the data by program, select the check box(es) next to the program and click the "Apply" button on the left hand side.

Filter by Analyte
☐ Spinal Muscular Atrophy (SMA)
☐ T-Cell Receptor Excision Circle (TREC)

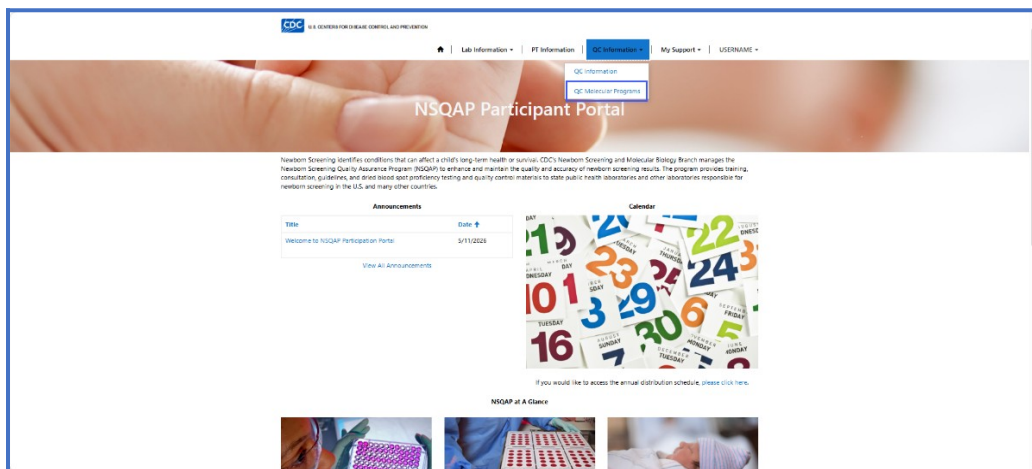
RUNS ↑	Analyte	Method	DNA Extraction Method	Cutoffs	Units	Polulation Median	Replicate_1A	Replicate_2A	Replicate_1B	Rep
1	SMA	Other	Other	34.00	Other	3.00	1.000	1.000	2.000	2.00
1	TREC			2.00	Other	4.00	100.000	100.000	100.000	
2	SMA	Other	Other	34.00	Other	3.00	1.000	2.000	1.000	2.00

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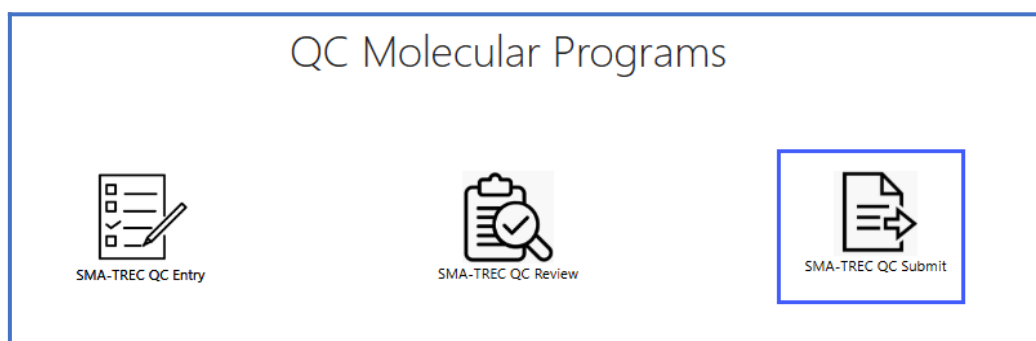
22

2.3 Submit Manually Entered Data

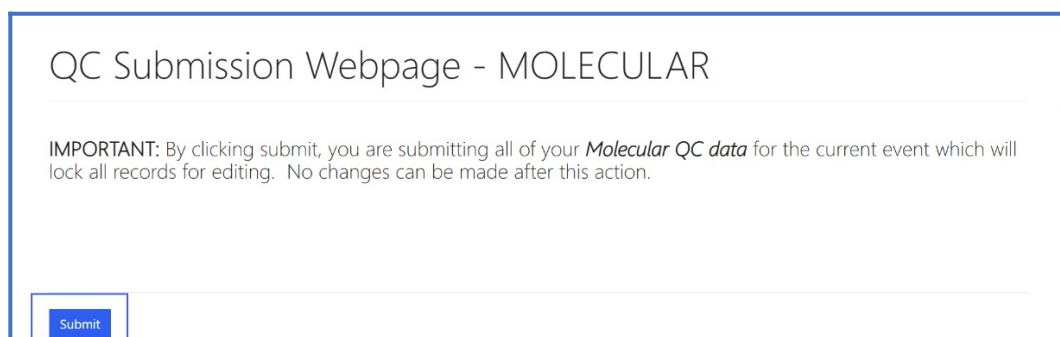
1. After reviewing data, navigate to the '**SMA & TREC QC Submit**' page by selecting the '**QC Information**' dropdown at the top of the page on the toolbar and select the '**QC Molecular Programs**' option.



2. Select the '**SMA-TREC QC Submit**' option.



3. Select '**Submit**'.



4. A confirmation page will appear once the submission is complete.

