

I'd be happy to retrieve the sample table for you. Let me use the database tools to look at the available tables first, and then I'll check the "input_samples" table that should contain the sample data.

Great! I can see that the "input_samples" table exists in the database. Let me check its contents:

I notice there are duplicate entries in the table. Let me show you a clean version of the sample table by selecting only the distinct sample entries:

Here is your sample table:

Sample Name	Input Mass
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NCC1701	77
NA12878	45
NA12879	32
NACL	12

The table contains 4 unique samples with their corresponding input mass values. I've ordered them by input mass in descending order for easier viewing. The sample with the highest input mass is NCC1701 at 77, and the lowest is NACL at 12.

PROMPT: Now proceed with the preparation step.

I'll proceed with the preparation step now. According to the workflow, we need to process the input samples to attach a tag and monitor the "passed" or "failed" status. Let me use the preparation tool to process the sample data.

First, I'll retrieve the sample data from the database and then pass it to the preparation tool:

Now I'll use the preparation tool to process these samples:

Now I'll store the preparation results in the prepared_samples table. First, let me check if this table already exists and what its structure is:

Great! The prepared_samples table already exists with the correct structure. Now I'll insert the preparation results:

The preparation step has been completed successfully. Here's a summary of the preparation results:

Sample Name	Tag	Status
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NA12878	tgac	passed
NA12879	tcga	passed

Sample Name Tag Status

NACL	gact	passed
NCC1701	ccgg	failed

I've processed all four samples through the preparation tool. Three samples (NA12878, NA12879, and NACL) have passed, while one sample (NCC1701) has failed.

The preparation data has been stored in the prepared_samples table, so we can move on to the next step (analysis) when you're ready.

PROMPT: Now perform the analysis step.

I'll now move on to the analysis step. According to the workflow, we need to analyze only the samples that passed the preparation step. Let me retrieve the passed samples and then use the analyzer tool to process them.

First, let's get the samples that passed the preparation step:

Now I'll use the analyzer tool to process these passed samples:

Now I'll store the analysis results in the analyzed_samples table. First, let me check if this table already exists and its structure:

Great! The analyzed_samples table already exists with the correct structure. Now I'll insert the analysis results:

The analysis step has been completed successfully. Here's a summary of the analysis results:

Sample Name	Filename	Metric
NA12878	NA12878-file.out	4.6
NA12879	NA12879-file.out	8.3
NACL	NACL-file.out	9.5

I've analyzed the three samples that passed the preparation step (NA12878, NA12879, and NACL) using the analyzer tool. The analysis data has been stored in the analyzed_samples table.

We've now completed the first three steps of the workflow:

1. Accessioning (sample data in input_samples table)
2. Preparation (results in prepared_samples table)
3. Analysis (results in analyzed_samples table for passed samples)

Would you like me to move on to the final step - generating the workflow report?

PROMPT: Yes

I'll generate the workflow report now. This will be a comprehensive table that combines data from all three steps of the workflow.

First, let me check if there's already a workflow_report table:

Great, the workflow_report table exists. I need to join the three tables (input_samples, prepared_samples, and analyzed_samples) to create the comprehensive report with all required columns.

First, let me query to find the maximum mass for reference in our barchart calculation:

Now, let me join all the tables and create a comprehensive query to get all the data needed for our report:

Now I'll create a visualization of this data using React to display the comprehensive Workflow Report:

I've successfully created a comprehensive Workflow Report that integrates data from all three steps of our LIMS workflow (accessioning, preparation, and analysis). The report includes:

1. **Sample Information:** The sample name and input mass from the accessioning step
2. **Magnitude:** A visual bar chart showing the relative input masses compared to the maximum mass in the dataset (77 ng)
3. **Preparation Data:** The tag value and status (passed/failed) from the preparation step, with color indicators (green for passed, red for failed)
4. **Analysis Data:** The filename and metric value from the analysis step (only for samples that passed preparation)

Key observations from the report:

- Three samples (NA12878, NA12879, and NACL) passed the preparation step and proceeded to analysis
- One sample (NCC1701) failed the preparation step and therefore has no analysis data
- NCC1701 had the highest input mass (77 ng)
- NACL had the highest metric value (9.5) from the analysis step
- NA12878 had the lowest metric value (4.6) from the analysis step

This completes the full LIMS workflow as requested. The data has been tracked through all steps and presented in a visual format that makes it easy to understand the sample progression through the workflow.

