

2025 NHSN MRSA Bacteremia LabID EXTERNAL VALIDATION TOOLKIT

V1.0 Updated March 2026 – for validating
2025 data

The 2025 MRSA Bacteremia LabID External Validation Toolkit is a HAI-specific supplement to be used in conjunction with the 2025 NHSN Patient Safety External Validation Toolkit (2025 PS EVT). It is intended to help guide the process of external validation specifically for MRSA Bacteremia LabID events with step-by-step instructions and screenshots from NHSN.



CDC VI | 3/26/26

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Section 1: Facility Selection

1.1 Steps Applicable to All Facility Selection Methods

Generate Datasets and Modify Report

1. Generate new datasets in NHSN to ensure any data updates are included for analysis. On the NHSN Landing Page, navigate to Patient Safety Component à [YOUR State/Jurisdiction Users' Group]. Select the "Analysis" tab and click "Generate Data Sets." For Beginning, enter 01/2025 and for Ending, 12/2025 (or other dates corresponding to the timeframe being validated) for the data set time period. Click the Generate New button. Allow the data set generation process to complete; you can leave NHSN during the generation process.

NHSN - National Healthcare Safety Network

NHSN Home

Dashboard

Reporting Plan

Event

Procedure

Summary Data

Hospital Respiratory Data

Surveys

Analysis

Users

Group

Generate Data Sets (Patient Safety)

Reporting Data Sets | Participation Alerts Data Set (Optional)

Include data for the following time period:

Beginning Ending



01/202X 1 mm/yyyy 1 Clear Time Period

Generate Reporting Data Sets

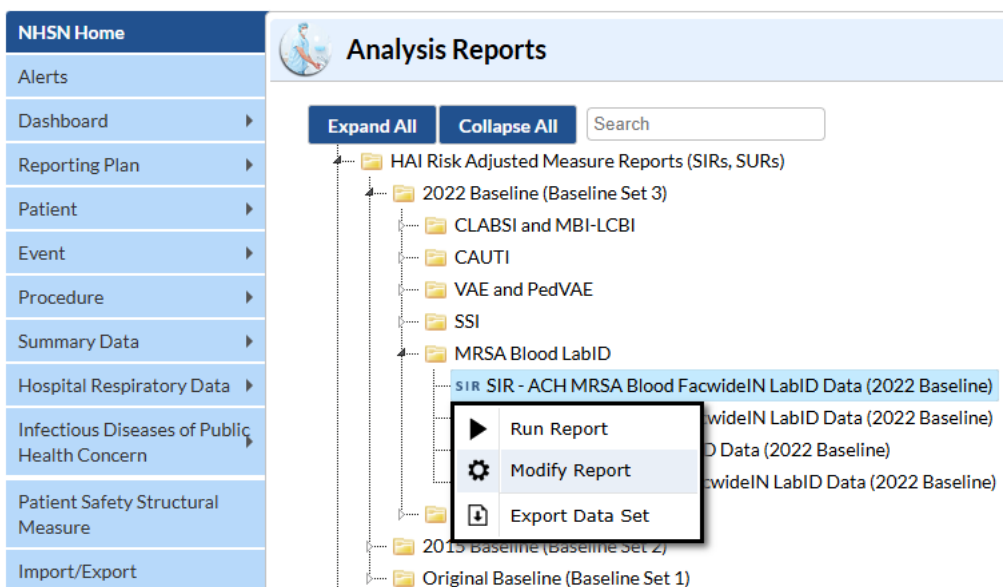
Last Generated: (UTC)
February 27, 2025 6:23 PM
to include data beginning 01/202X

2. After successful data set generation, navigate to Analysis → Reports to display the tree view list of all analysis reports available within NHSN's analysis tool.

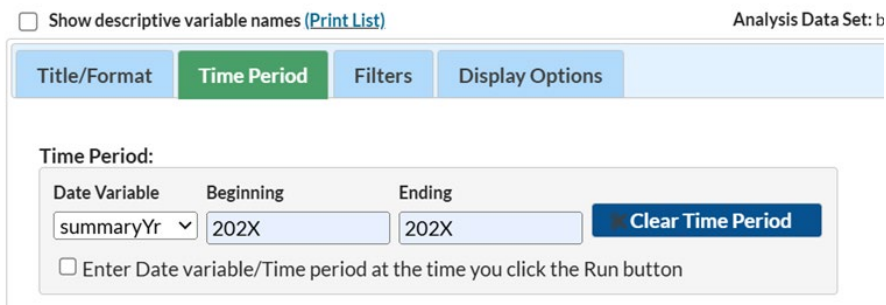
The screenshot shows the NHSN Patient Safety Component Home Page. On the left is a vertical navigation menu with the following items: NHSN Home, Dashboard, Reporting Plan, Event, Procedure, Summary Data, Hospital Respiratory Data, Surveys, Analysis, Users, Group, and Health Monitor. The 'Analysis' item is highlighted in a darker blue. To the right of the 'Analysis' item is a dropdown menu containing: Generate Data Sets, Reports (highlighted in a darker blue), Statistics Calculator, and Preferences. The main content area of the page has a light blue header with the NHSN logo and the title 'NHSN Patient Safety Component Home Page'. Below the header, there is a section titled 'Assurance of Confidentiality' with a paragraph of text and a link to 'Get Adobe Acrobat Reader for PDF files'. A small Adobe Reader icon is also visible.

| | |
|---------------------------|--|
| NHSN Home |  NHSN Patient Safety Component Home Page |
| Dashboard | |
| Reporting Plan | Assurance of Confidentiality: The voluntarily provided information obtained in this survey guarantee that it will be held in strict confidence, will be used only for the purposes stated, institution in accordance with Sections 304, 306 and 308(d) of the Public Health Service Act |
| Event |  Get Adobe Acrobat Reader for PDF files |
| Procedure | |
| Summary Data | |
| Hospital Respiratory Data | |
| Surveys | |
| Analysis | Generate Data Sets |
| Users | Reports |
| Group | Statistics Calculator |
| Health Monitor | Preferences |

- Expand the HAI Risk Adjusted Measure Reports (SIRs, SURs) folder, select 2022 Baseline (Baseline Set 3), MRSA Blood LabID, and then SIR ACH MRSA Blood FacWideIN LabID Data (2022 Baseline). If you are validating Critical Access Hospitals (CAHs), Inpatient Rehab Facilities (IRFs), or Long-term Acute Care Hospitals (LTACHs), select the SIR report that corresponds with that facility type. Click the Modify Report button to proceed to the modification window.



- In the modification window, there are two key areas to modify, one that controls the time interval of data that are analyzed and displayed and one that controls the level of aggregation of those data.
 - Under Title/Format tab, select xls format. Then navigate to the Time Period tab to define the time period of data that is included in the report to be exported. Set Date Variable to “summaryYr,” Beginning and Ending to 2025, or to the year of data being validated.



- Navigate to the “Filters” tab. In the row of drop-down boxes, select “mrsaLabIDbldPlan,” “equal,” and enter “Y.”

Show descriptive variable names ([Print List](#)) Analysis Data Set: bs LABID_RatesMRSA Type: SIR Last Generated (UTC) : February 27, 2025 6:21

Title/Format Time Period **Filters** Display Options

Additional Filters:

AND OR

AND OR

mrsaLabIDBldPlan equal Y - Yes

NOTE: Facilities that are conducting In-Plan MRSA all specimen surveillance are ALSO conducting in plan MRSA Bacteremia surveillance as a subset. NHSN includes these facilities under “mrsaLabIDBldPlan” = Yes. Any surveillance that is not in plan will be excluded. MRSA SIR will only calculate at FacWideIn level.

3) Under the Display Options section, use the Group by option to view the data at a particular level of aggregation. Change the Group by option to “summaryYr.”

Show descriptive variable names ([Print List](#))

Title/Format Time Period Filters **Display Options**

SIR Options:

Group by: summaryYH

- Cumulative
- summaryYH
- summaryYM
- summaryYQ
- summaryYr**

- After making the above modifications, scroll to the bottom of the modification window. Click the Export button to export the data selected by your modifications. This will open the “Export Analysis Data Set” window.
- Use the default file format (.csv) and select the bullet “Export Analysis Data Set using Modifications” to export the data. Click the Export button to begin the export process. NHSN will create a .zip file with your SIR data report in it and prompt you to specify a location to save the file on your computer.

Export Analysis Data Set

Analysis Data Set: bs3_LABID_RatesMRSA

Export Format: delimited file (comma-separated values) (*.csv) ▼

Export Entire Analysis Data Set
 Export Analysis Data Set using Modifications

Export
Cancel

- The exported SIR report will be displayed at several levels of aggregation. Select the orgID level, as illustrated in the screenshot below, to get an unduplicated list of facilities in your jurisdiction.

| location | summaryYr | MRSA_bldIncCount | numPred | numpatdays | SIR_pval | SIR | sir9Sci | SIR_pctl | orgID | |
|-----------|-----------|------------------|----------|------------|----------|-------|--------------|----------|-------|--|
| FACWIDEIN | 2021 | 9 | 5.627377 | 69905 | 0.1774 | 1.599 | 0.780, 2.935 | 77 | | <i>SIR for all facilities in group</i> |
| FACWIDEIN | 2021 | 6 | 3.025796 | 36000 | 0.1214 | 1.983 | 0.804, 4.124 | 87 | 10018 | <i>*THIS IS THE LEVEL TO EVALUATE*</i> |
| FACWIDEIN | 2021 | 3 | 1.940087 | 26000 | 0.4393 | 1.546 | 0.393, 4.208 | 76 | 10401 | <i>SIR for each facility in group</i> |
| FACWIDEIN | 2021 | 0 | 0.154561 | 2305 | | | | | 10541 | |
| FACWIDEIN | 2021 | 0 | 0.506932 | 5600 | | | | | 14461 | |

1.2 Calculate Ranking and Selection

Method 1: Prioritizing Facilities with Highest Likelihood of Event Occurrence

- Open the exported SIR report in Excel and select the aggregation level that provides a facility-specific SIR at the orgID level (shown in black in the above screenshot in Section 1.1 step 7). This will allow you to explore the level of exposure risk for MRSA Bacteremia LabID Event and measure performance at each facility. Once you see the list go through the highest orgID and start over at the smallest orgID, that is where the unduplicated facility list ends.
- Copy this information to a new spreadsheet. Arrange the facilities in descending rank order according to SIR, and create three new columns titled “Delta,” “Stratum,” and “Targeted Selection Number.”

3. Calculate Delta for each facility/row using the formula =ABS[row cell under InfCount]-[row cell under numPred]. Delta will be used only where an SIR is not calculated by NHSN.
4. Select the top tertile (33%) of facilities by predicted number of LabID events. This top tertile of facilities where MRSA Bacteremia LabID events are most expected and may have the greatest potential for surveillance and prevention impact.
5. Within the top tertile, sort by SIR in descending order, and identify the current median SIR for the top tertile. To sort just the top tertile, highlight the entire row for each facility in the top tertile, and click “Data,” “Sort”; Sort by “Column” (select SIR), “Sort On” (cell values), and “Order” (largest to smallest).
6. Within the top tertile, assign stratum A to facilities with SIR above the current median SIR, stratum B for remaining facilities with SIR less than or equal to the median and above zero, and stratum C for facilities with SIR = zero (but not missing). Note that some facilities will not have a calculated SIR; do not include these in the strata (see step 9 below).
7. Re-sort within each stratum A, B, and C, by numPred from highest to lowest. To sort just one stratum at a time, highlight the entire row for each facility in the first stratum, and click “Data,” “Sort”; Sort by “Column” (select numPred), “Sort On” (cell values), and “Order” (largest to smallest). Repeat this process for the next two strata, one-by-one.
8. Assign sequential Targeted Selection Numbers to facilities, by selecting the highest available numPred from each stratum, alternating through strata A, B, and C. For example, the facility with the highest numPred from stratum A would be Targeted Selection Number=1, the facility with the highest numPred from stratum B would be Targeted Selection Number=2, and the facility with the highest numPred from stratum C would be Targeted Selection Number=3. Return to stratum A and assign the facility with the next highest numPred as Targeted Selection Number=4. Continue alternating strata until no facilities remain or the target number of facilities is reached (typically 18 or 21; refer to the 2025 PS EVT for facility sample size recommendations). If additional facilities are needed, repeat steps 4-8 using the second and then third tertile based on risk level.
9. If additional facilities are needed to reach the targeted number after step 8 is complete, sort the remaining facilities without a calculated SIR by Delta in descending order, starting with the highest, and select facilities from the top of the list until targeted number is reached.
10. After the targeted selection is complete, randomly select additional 5% of remaining facilities from ALL tertiles. The targeted facilities along with the 5% randomly selected make up the total sample.

Method 2: Cumulative Attributable Difference (CAD) Approach

1. Open the exported SIR report in Excel and select the aggregation level that provides a facility-specific SIR at the orgID level (shown in black in the screenshot seen in Section 1.1 step 7). This level of aggregation will allow you to explore the level of exposure risk for MRSA bacteremia LabID events and measured performance at each facility. Once you see the list go through the highest orgID and start over at the smallest orgID, that is where the unduplicated facility list ends.

- If there are 30 or fewer facilities in your jurisdiction, [stop here](#) and validate them all. If there are more than 30 facilities, proceed through the following steps to create facility sampling frame.
- Select the rows for the aggregation level being evaluated and copy this information to a new spreadsheet. Insert a row above your data and copy the header row so you can identify the variables on the new spreadsheet. Next, sort the facilities by numPred (number of predicted events) in descending order (high to low).

| infCount | numPred | numclday | SIR_pval | SIR | sir95ci | locationTy | locCDC | orgID | facType |
|----------|----------|----------|----------|-------|--------------|------------|--------|--------|-----------|
| 13 | 18.51959 | 15267 | 0.1921 | 0.702 | 0.390, 1.170 | | | 100008 | HOSP-GEN |
| 22 | 15.32671 | 9910 | 0.1034 | 1.435 | 0.922, 2.138 | | | 100030 | HOSP-CHLD |
| 10 | 9.736101 | 8387 | 0.8926 | 1.027 | 0.522, 1.831 | | | 100014 | HOSP-GEN |
| 8 | 9.542312 | 7958 | 0.6509 | 0.838 | 0.389, 1.592 | | | 100046 | HOSP-GEN |
| 1 | 9.064373 | 7682 | 0.0013 | 0.11 | 0.006, 0.544 | | | 100001 | HOSP-GEN |
| 2 | 7.578169 | 6272 | 0.0235 | 0.264 | 0.044, 0.872 | | | 100002 | HOSP-GEN |
| 7 | 5.689505 | 4581 | 0.5585 | 1.23 | 0.538, 2.434 | | | 100022 | HOSP-GEN |
| 4 | 5.504663 | 4879 | 0.558 | 0.727 | 0.231, 1.753 | | | 100027 | HOSP-GEN |
| 2 | 3.159258 | 2784 | 0.5651 | 0.633 | 0.106, 2.092 | | | 100016 | HOSP-GEN |
| 2 | 2.437844 | 2304 | 0.8601 | 0.82 | 0.138, 2.710 | | | 100041 | HOSP-GEN |
| 0 | 1.945079 | 1724 | 0.143 | 0 | 1.540 | | | 100059 | HOSP-GEN |
| 3 | 1.572374 | 1812 | 0.2846 | 1.908 | 0.485, 5.193 | | | 100011 | HOSP-GEN |
| 1 | 1.527251 | 1760 | 0.7659 | 0.655 | 0.033, 3.229 | | | 100010 | HOSP-GEN |
| 2 | 1.329405 | 1357 | 0.5333 | 1.504 | 0.252, 4.970 | | | 100032 | HOSP-GEN |
| 0 | 1.242188 | 1101 | 0.2888 | 0 | 2.412 | | | 100049 | HOSP-GEN |
| 2 | 1.087298 | 1253 | 0.3934 | 1.839 | 0.308, 6.077 | | | 100005 | HOSP-GEN |
| 1 | 1.052644 | 933 | 1 | 0.95 | 0.048, 4.685 | | | 100007 | HOSP-GEN |
| 1 | 0.915007 | 934 | | | | | | 100040 | HOSP-GEN |
| 0 | 0.745198 | 989 | | | | | | 100026 | HOSP-GEN |
| 0 | 0.719899 | 823 | | | | | | 100004 | HOSP-GEN |
| 2 | 0.669096 | 888 | | | | | | 100023 | HOSP-GEN |

Sort the facilities in the descending order of number of predicted infections (numPred) and compute the 75th percentile value of the variable numPred

- Identify the 75th percentile of numPred for the validation period (minimum of two quarters of the data) using the Percentile.inc function in Excel by clicking on the function button (*fx*) to the left of the white text box and selecting “Percentile.inc.” A Function Arguments window will open and require an array and K values. For the “array” argument, select the column of your spreadsheet containing numPred values. For the “K” argument, enter the percentile value to be generated (0.75), making sure to use a decimal. Click OK and the cell where the function was entered will now show the 75th percentile value.

Function Arguments

PERCENTILE.INC

Array: C2:C50

K: 0.75

= PERCENTILE.INC(C2:C50,0.75)

Returns the k-th percentile of values in a range, where k is in the range 0..1, inclusive.

Array is the array or range of data that defines relative standing.

Formula result = PERCENTILE.INC(C2:C50,0.75)

[Help on this function](#) [OK] [Cancel]

- Use the numPred value corresponding to the 75th percentile as the minimum threshold value for selection of facilities eligible for validation. If this value is greater than 1, use the 75th percentile numPred value, otherwise use numPred=1 as the minimum threshold value.

| infCount | numPred | numclday | SIR_pval | SIR | sir95ci | locationTy | locCDC | orgID | facType |
|----------|----------|----------|----------|-------|--------------|------------|--------|--------|----------|
| 13 | 18.51959 | 15267 | 0.1921 | 0.702 | 0.390, 1.170 | | | 100008 | HOSP-GEN |
| 22 | 15.32671 | 9910 | 0.1034 | 1.435 | 0.922, 2.138 | | | 100030 | HOSP-CHI |
| 10 | 9.736101 | 8387 | 0.8926 | 1.027 | 0.522, 1.831 | | | 100014 | HOSP-GEN |
| 8 | 9.542312 | 7958 | 0.6509 | 0.838 | 0.389, 1.592 | | | 100046 | HOSP-GEN |
| 1 | 9.064373 | 7682 | 0.0013 | 0.11 | 0.006, 0.544 | | | 100001 | HOSP-GEN |
| 2 | 7.578169 | 6272 | 0.0235 | 0.264 | 0.044, 0.872 | | | 100002 | HOSP-GEN |
| 7 | 5.689505 | 4581 | 0.5585 | 1.23 | 0.538, 2.434 | | | 100022 | HOSP-GEN |
| 4 | 5.504663 | 4879 | 0.558 | 0.727 | 0.231, 1.753 | | | 100027 | HOSP-GEN |
| 2 | 3.159258 | 2784 | 0.5651 | 0.633 | 0.106, 2.092 | | | | |
| 2 | 2.437844 | 2304 | 0.8601 | 0.82 | 0.138, 2.710 | | | | |
| 0 | 1.945079 | 1724 | 0.143 | 0 | 1.540 | | | | |
| 3 | 1.572374 | 1812 | 0.2846 | 1.908 | 0.485, 5.193 | | | | |
| 1 | 1.527251 | 1760 | 0.7659 | 0.655 | 0.033, 3.229 | | | | |
| 2 | 1.329405 | 1357 | 0.5333 | 1.504 | 0.252, 4.970 | | | | |
| 0 | 1.242188 | 1101 | 0.2888 | 0 | 2.412 | | | | |
| 2 | 1.087298 | 1253 | 0.3934 | 1.839 | 0.308, 6.077 | | | 100005 | HOSP-GEN |

75th percentile value of numPred= 5.5. Select facilities with numPred >5.5. Only facilities in red box (numPred >5.5) are included in the sampling frame for targeted validation.

6. Create a subset of facilities that includes facilities with predicted number of MRSA Bacteremia LabID events greater than the threshold. In the example above, the 75% percentile value of the numPred variable was 5.5. All facilities with numPred value above 5.5 are selected for inclusion in validation sampling frame.
7. If the sampling frame derived from the 75th percentile of numPred consists of 30 or fewer facilities, select all facilities for validation, plus an additional random sample of 5% of facilities where numPred was less than the 75th percentile value. Refer to Table 1 below for 3 random number generation methods. In the example above, the number of facilities with numPred value >5.5 is fewer than 30, so all facilities with numPred value >5.5 are selected for validation and a 5% random sample is selected from the facilities with numPred value ≤5.5.
8. If sampling frame consists of greater than 30 facilities, select 30 facilities based on the criteria described in section B below.

A. Observed Events

- a) The Cumulative Attributable Difference (CAD) approach focuses on the difference between the predicted number of MRSA Bacteremia LabID events and actual observed LabID events (reported). The infCount is an aggregated count of observed LabID events.
- b) Create a column titled CAD next to numPred and compute the CAD values for each line by subtracting numPred value from infCount (observed – predicted).

B. Facility Selection: use this step if the sampling frame consists of greater than 30 facilities

- a) Divide the total facilities in the sampling frame into two strata:
 - Create a new column, “stratum,” and assign each facility to either Stratum 1 or Stratum 2:
 - » Stratum 1: Includes all facilities in the sampling frame that had zero infCount value, that is, zero reported pooled aggregate estimate of observed events for the validation time frame.

- » Stratum 2: includes all facilities in the sampling frame with non-zero infCount value, that is, non-zero reported pooled aggregate observed events for the validation time frame.

b) Stratum 1 (where facility reported zero events): Filter for Stratum 1 facilities (where infCount=0) and sort by ascending CAD value so Stratum 1 facilities with the lowest CAD value are at the top, shown in the green column below. Select the first 15 facilities from Stratum 1.

| infCount | numPred | CAD | numclDay | SIR_pval | SIR | sir95ci | SIR_pctl | locationTy | locCDC | orgID | facType |
|----------|----------|----------|----------|----------|-----|---------|----------|------------|--------|-------|----------|
| 0 | 15.11302 | -15.1130 | 150 | | | | | | | | HOSP-GEN |
| 0 | 12.12433 | -12.1243 | 165 | | | | | | | | HOSP-GEN |
| 0 | 11.03699 | -11.0370 | 68 | | | | | | | | HOSP-GEN |
| 0 | 10.03699 | -10.0370 | 68 | | | | | | | | HOSP-GEN |
| 0 | 9.113023 | -9.1130 | 150 | | | | | | | | HOSP-GEN |
| 0 | 8.124325 | -8.1243 | 165 | | | | | | | | HOSP-GEN |
| 0 | 8.113023 | -8.1130 | 150 | | | | | | | | HOSP-GEN |
| 0 | 8.011302 | -8.0113 | 15 | | | | | | | | HOSP-GEN |
| 0 | 5.011302 | -5.0113 | 15 | | | | | | | | HOSP-GEN |
| 0 | 4.036994 | -4.0370 | 68 | | | | | | | | HOSP-GEN |
| 0 | 3.036994 | -3.0370 | 68 | | | | | | | | HOSP-GEN |
| 0 | 3.011302 | -3.0113 | 15 | | | | | | | | HOSP-GEN |
| 0 | 2.036994 | -2.0370 | 68 | | | | | | | | HOSP-GEN |
| 0 | 1.011302 | -1.0113 | 15 | | | | | | | | HOSP-GEN |

Compute the CAD values for all facilities in the sampling frame. Filter for stratum 1 facilities, where infCount=0. Sort by ascending CAD values (lowest on the top). If the sampling frame has greater than 15 facilities, select the top 15 facilities.

c) Stratum 2 (facilities with non-zero events): Filter for Stratum 2 facilities (where infCount > 0). Sort the facilities by ascending CAD value so the facilities with the lowest CAD value are at the top, shown in the green column below. Select the first 15 facilities from Stratum 2.

| infCount | numPred | CAD | numclDay | SIR_pval | SIR | sir95ci | SIR_pctl | locationTy | locCDC | orgID | facType |
|----------|----------|----------|----------|----------|-------|--------------|----------|------------|--------|--------|-----------|
| 1 | 9.064373 | -8.06437 | 7682 | 0.0013 | | | | | | | HOSP-GEN |
| 2 | 7.578169 | -5.57817 | 6272 | 0.0235 | | | | | | | HOSP-GEN |
| 13 | 18.51959 | -5.51959 | 15267 | 0.1921 | | | | | | | HOSP-GEN |
| 8 | 9.542312 | -1.54231 | 7958 | 0.6509 | | | | | | | HOSP-GEN |
| 4 | 5.504663 | -1.50466 | 4879 | 0.558 | | | | | | | HOSP-GEN |
| 10 | 9.736101 | 0.263899 | 8387 | 0.8926 | | | | | | | HOSP-GEN |
| 7 | 5.689505 | 1.310495 | 4581 | 0.5585 | | | | | | | HOSP-GEN |
| 22 | 15.32671 | 6.673286 | 9910 | 0.1034 | 1.435 | 0.922, 2.138 | | | | 100030 | HOSP-CHLD |

Compute the CAD values for all facilities in the sampling frame. Filter for stratum 2 facilities, where infCount > 0. Sort by ascending CAD value (lowest values on the top). If the sampling frame has greater than 15 facilities, select the top 15 facilities.

d) If there are insufficient facilities in either of the strata, supplement the sample from other strata to reach the required number of facilities for the validation sample.

Note: Remember to randomly select 5% of the remaining facilities with a numPred less than the 75th percentile value.

Method 3: Stratified Random Sampling

1. Open the exported SIR report in Excel and select the aggregation level that provides a facility-specific SIR (shown in black in below screenshot seen in Section 1.1 step 7). This will allow you to explore the level of exposure risk for MRSA bacteremia LabID events and measured performance at each facility. Once you see the list go through the highest orgID and start over at the smallest orgID, that is where the unduplicated facility list ends.

2. Once you identify where the aggregation at orgID starts, click on the first orgID cell and drag until you reach the highest value (before it starts to repeat). Copy the selected cells and paste into a new Excel worksheet or a new sheet within the same worksheet. This is your final list of all unduplicated facilities reporting MRSA bacteremia LabID events during the timeframe you specified. You will use this list as your facility sampling frame.
3. Generate list of facilities that completed Annual Survey from NHSN:
 - 1) On the NHSN landing page, use the Analysis button in the navigation bar and select Reports.
 - 2) Use the tree view structure to select Supplemental Reports, Facility-Level Data, and Line Listing – Hospital Survey (2025 and later). If validating a type of facility other than Acute Care Hospitals, select the appropriate corresponding report.
 - 3) Select Modify Report and make the following modifications:
 - i. Under the Title/Format tab, select the xls format.
 - ii. Under the Time Period tab, select “completeddate” from the dropdown box, and enter 01/01/2025 for Beginning and 12/31/2025 for Ending. Modify dates as needed for the timeframe being validated.

Modify "Line Listing - Hospital Survey (2024 and later)"

Show descriptive variable names ([Print List](#)) Analysis Data Set: HospSurvey2024

Title/Format
Time Period
Filters
Display Variables
Sort Variables
Display Options

Time Period:

| | | | |
|-----------------|------------|------------|--|
| Date Variable | Beginning | Ending | |
| completeddate ▾ | 01/01/202X | 12/31/202X | Clear Time Period |

Enter Date variable/Time period at the time you click the Run button

Note: If a facility did not complete the Annual Survey during specified time period, they will not appear in this report.

- iii. Under the Sort Variables tab, double click “surveyYear” in the right-hand box to remove. Find “orgID” in the left-hand box, and double click to move it to the right-hand box.
 - iv. Click the Export button. In the Export Analysis Data Set window, keep the default file type (.csv) and click Export. This will generate a .zip file with a spreadsheet of all facilities that completed the NHSN Annual Survey in the time period designated above.
4. In the facility sampling frame spreadsheet, create a new column for the variable “bed size.”
 - 1) Ensure that facilities are sorted by orgID, in ascending order, in both the facility sampling frame and the Annual Survey line list. Confirm the orgIDs match up before proceeding.
 - 2) Copy the numBeds column from the Annual Survey line list and paste into the bed size column in the facility sampling frame spreadsheet. Ensure that the pasted bed size variable is matched to the correct facility.

5. Divide the total facilities in the sampling frame into two strata. Create a new column, "stratum," and assign each facility to either Stratum 1 or Stratum 2:
 - 1) Stratum 1: Includes all facilities in the sampling frame that have a bed size of <400.
 - 2) Stratum 2: Includes all facilities in the sampling frame that have a bed size of ≥ 400 .
6. Stratum 1:
 - 1) If there are 25 or fewer facilities within Stratum 1, select all facilities within Stratum 1 and proceed to Stratum 2.
 - 2) If there are more than 25 facilities within Stratum 1, assign a random number to each facility. Sort facilities by random number and select the first 25 facilities.
 - i. Refer to Table 1 below for three methods for random number assignment.
7. Stratum 2:
 - 1) If there are 5 or fewer facilities within Stratum 2, select all facilities within Stratum 2 then return to Stratum 1. Select additional facilities from Stratum 1 in descending order, starting with the first facility on the list that was not sampled during step 6, to reach a total of 30 facilities selected.
 - 2) If there are more than 5 facilities within Stratum 2, assign a random number to each facility. Select the first 5 facilities from the randomized facility list.
 - i. Refer to Table 1 below for three methods of random number assignment.
 - 3) If Stratum 1 has fewer than 25 facilities, return to Stratum 2.
8. Select additional facilities from Stratum 2 in descending order, starting with the first facility on the list not previously sampled, to reach a total of 30 facilities selected.

Table 1. Random number assignment methods

| Option | Description |
|---|--|
| <p>Option 1: Excel</p> | <ol style="list-style-type: none"> Using the facility list created above, or an HAI line list, insert the command =ROUND(RAND()*1000000,0) into column B and drag to paste this command for each row of the facility list. This will generate a random number for each orgID. Select and copy the values from column B and use the Paste Special (Paste Values) feature to paste the number values into column C. Note: any edit made to the Excel sheet will cause the numbers in column B to recalculate. This is normal and can be ignored if you have an iteration copied. Delete column B so the columns shift left and column C becomes column B. Sort by column B, making sure column A is included in the sort (click on “Expand selection” if a dialog box appears). This is your final list that has been assigned and sorted by a random number. |
| <p>Option 2: Random Number Generator Website + Excel</p> | <ol style="list-style-type: none"> Identify the total number of facilities from the list created above, or the number of records on HAI line list, Go to https://www.random.org/sequences/ Input 1 as the smallest value, and the total number of facilities/records as the largest value, and click “Get Sequence” Copy the sequence created and paste it into column B of your spreadsheet. Sort by column B, making sure column A is included in the sort (click on “Expand selection” if a dialog box appears). This is your final list that has been assigned and sorted by a random number. |
| <p>Option 3: SAS Codes</p> | <ol style="list-style-type: none"> Enter the appropriate file path where prompted in the code For medical record random number generation, determine if you need/want the program to create an ‘EoC’ number. If yes, run code as written. If no, delete the lines of code as specified in the program, then run code. The final list, assigned and sorted by a random number, will be exported to the same folder specified in step 1. |

Section 2: Download (“freeze”) the facility’s reported data from NHSN

Prior to selecting the medical records sample, use NHSN Analysis Reports and the modifications described below to “freeze” (take a snapshot of) the data and export the facility’s reported MRSA bacteremia LabID events. Freeze the data for each facility selected for validation. While in the NHSN application, this would be an opportune time to download each facility’s NHSN Annual Survey, which will be needed during the on-site, or virtual, visit. The Annual Survey will be used to review risk adjustment variables (teaching hospital affiliation, bed count, number of patient days, and number of admissions).

To “freeze” data, select the Analysis tab in the left-hand navigation bar, and then Reports. Select the HAI Detailed Reports (Line Lists, Rate Tables, etc.), MDRO/CDI Module – LabID Events, MRSA LabID Events, and then “Line Listing for All MRSA LabID Events,” and then click Modify Report.

Suggested Modifications:

- Under the Title/Format tab, select xls as the format. You may also change the title of the report (i.e. <Facility ID> <Freeze Date> NHSN MRSA Blood LabID Events Line List).
- Under the Time Period tab, go to the Date Variable and select “specDateYr.” For both Beginning and Ending, enter 2025, or the year of data to be validated.
- Under the Filters tab, verify the first row of drop-down boxes read “spcOrgType,” “equal,” and “MRSA - MRSA.”
- Click the Add Rule button and verify that “AND” is selected in blue. From the second row of drop-down boxes, select “specimenSource,” “equal,” and “BLDSPC - Blood specimen.”
- Click on the Add rule button to add another line, and select “orgID,” “equal,” and enter the facility’s orgID number.
 - Optional: Export single report with all facilities, sort by “orgID,” and copy/paste each facility’s data into its own spreadsheet. Save each line list in a secure location.
- Optional: Under the Sort Variables tab, select “specimenDate.”
- Click on the “Export” button. Keep the format as-is (.csv) and select the “Export Analysis Data Set using Modifications” radio button. This will generate the line listing in Excel.
- Save the line list to a secure location.

The screenshot shows the 'Filters' tab in the NHSN application. At the top, there are tabs for 'Title/Format', 'Time Period', 'Filters', 'Display Variables', 'Sort Variables', and 'Display Options'. Below these tabs, there are buttons for 'Additional Filters: Show' and 'Clear'. The main area displays a rule configuration with a tree structure. The root level has 'AND' selected in blue and 'OR' in grey, with an 'Add group' button. The first level has 'AND' selected in blue and 'OR' in grey, with an 'Add rule' button. The first rule consists of three conditions: 'spcOrgType' with a dropdown arrow, 'equal' with a dropdown arrow, and 'MRSA - MRSA' with a dropdown arrow, and a 'Delete' button. The second rule consists of two conditions: 'specimenSource' with a dropdown arrow, 'equal' with a dropdown arrow, and 'BLDSPC - Blood specimen' with a dropdown arrow, and a 'Delete' button.

To find a facility’s NHSN Annual Survey, log into NHSN and select Surveys in the navigation

bar, then click Find. In the Survey Type drop down menu, select the survey for the type of facility you are validating (for example, FACSRV-PS – Hospital Survey Data, for validation of Acute Care Hospitals). Then, select the survey year for which you are validating. Finally, click on the Find button, and a list of facilities and their Annual Surveys will be generated.

NOTE: Use the **Analysis** button on the navigation bar and select Reports to export the data. For more information about how to make modifications to these output options, read “How to Modify a Report” found in the Analysis Quick Reference Guide library at: <http://www.cdc.gov/nhsn/PS-Analysis-resources/reference-guides.html>

Section 3: Notify facilities of the planned validation and request necessary information

Suggestions on what information should be included in any outreach to facilities notifying them of their selection can be found in section 2.4 of the 2025 PS EVT. Template letters with suggested format of line listings are located in Appendix 1.

Section 4: Develop the medical record sampling frame for each selected facility

MRSA bacteremia LabID Event, facility-wide inpatient (FacWideIN)

For MRSA Bacteremia LabID Event, the sampling frame is derived from positive laboratory (blood specimen) line listings. From each selected facility, obtain a complete list of blood specimens positive for methicillin-resistant *Staphylococcus aureus*. MRSA includes *S. aureus* isolated from any specimen that tests oxacillin-, ceftazidime-, or methicillin-resistant by standard susceptibility testing methods or by a laboratory test that is FDA-approved for MRSA detection. Include those collected in 2025 for inpatient location/emergency department (ED)/24-hour observation locations facility-wide to select the patient admissions/episodes of care for which review is planned. These laboratory line lists should include patient location at the time of specimen collection. NHSN encourages facilities to develop capacity to generate these lists electronically because recurring need for this capability is expected and creation of manual line listings presents an excessive burden.

For positive MRSA bacteremia LabID Event (FacWideIN), the MRN, facility admission date, laboratory specimen number, blood specimen collection date, identified organism’s genus and species, methicillin susceptibility information (organism ID may be shortened to MRSA, covering genus, species, and methicillin susceptibility requirements), specific inpatient or ED location/24-hour observation location, and patient date of birth are required. Additional patient identifiers such as patient name may be helpful. See example of line list template in Appendix 1.2 of the 2025 PS EVT.

Section 5: Medical Record Selection

Use the securely transmitted line listing of positive MRSA blood specimens (PBS) obtained from each selected facility in the following medical record selection process.

1. For each facility, assign a random number to every PBS, following steps outlined in Table 1.
2. Sort the list of PBSs by MRN, admission date, and specimen date to generate clusters of PBSs with the same MRN and admission date, called unique “Episodes of Care” (EoC). Create an EoC column where the first EoC = 1. All PBSs in an episode should have the same EoC number.
3. Identify the first PBS for each EoC and randomly select 20:
 - 1) Create a new column, “stratum,” and assign the first PBS from each unique EoC to stratum 1.
 - 2) Filter to where stratum = 1.
 - 3) Sort by random number and select the first 20 PBSs with a unique EoC.
4. Identify and randomly select 20 non-first positive specimens:
 - 1) Filter to where stratum does not equal 1.
 - 2) Sort by random number and select the first 20 PBSs with a unique EoC number.
5. If there are any duplicate EoC numbers, keep the record with the smallest random number and substitute out the others with the next PBS on the list with a unique EoC number.
6. The final screening sample should contain 40 PBSs with unique EoC numbers. If the total number of sampled specimens does not equal 40, supplement the difference with the remaining specimens, as possible.
7. Request the selected medical records prior to the facility site visit using the template letter found in Appendix 1.3 in the 2025 PS EVT.

Section 6: Site Visit Activities

6.1 Structured Medical Record Review

Validator blinding and consultation at the facility site-visit

Validator blinding as to HAI status is recommended, when feasible. This can be accomplished by mixing and reviewing the selected medical records before determining which have been reported to NHSN with HAIs.

Medical records should be reviewed in a blinded manner using 2025 Medical Records Abstraction Tool (MRAT), which can be found at [2025 PSC Data Validation Resources | NHSN | CDC, Resources by HAI, MRSA Bacteremia LabID Event](#). This tool includes algorithms and logic designed to establish presence or absence of required criteria for case definitions and to provide support to avoid common errors.

6.2 Review risk adjustment variables

Have a copy of the facility NHSN Annual Survey available and review location mapping facility-wide if this has not been done to the jurisdiction's satisfaction in the past 3 years. Otherwise, review changes since the last facility-wide review.

Review the location mapping and bed size information with the IP. A list of CDC locations and descriptions can be found in the NHSN Patient Safety Manual Chapter 15. If there is insufficient time to complete this onsite, consider arranging a conference call to review location mapping when data are readily accessible.

Review NHSN definitions for teaching hospital types (under Key Terms, Patient Safety Manual Chapter 16) and ensure that facility teaching hospital status is accurate in the NHSN Annual Survey.

6.3 Review denominator collection methods and documentation

Electronically collected MRSA bacteremia facility-wide inpatient (FacWideIN) denominators

"FacWideIN" surveillance data includes all patient days counted at the same time each day for all inpatient locations, including any patients housed for the day in inpatient locations, whether the facility considers them "admitted patients" or "observation" patients, but excluding any patients housed for the day in outpatient "observation" locations. This information is often collected electronically. Because the task of validating "FacWideIN" patient days and admissions is daunting, denominator data validation can be accomplished using manual counting of patient days and admissions in three specified location types for one month each: one ICU, one Labor/Delivery/Recovery/Post-Partum (LDRP) location (if available), and one or more wards where "observation" patients are frequently located. Manual counts should be within 5% of the referent (usual) electronic counts, or an evaluation of why they differ should be conducted. This can be documented using the template in Section 6.6. One consideration is the facility's ability to capture "observation" patients within inpatient locations electronically. Electronic admissions, discharge, and transfer (ADT) data often are found to be more accurate than electronic billing data in this regard. This internal validation process can be conducted by facilities when requested or required.

6.4 (Optional) Template for Methicillin-resistant *Staphylococcus aureus* (MRSA) Bacteremia LabID Event Validation Discrepancies Discussion with Facilities

Please feel free to adapt these templates to meet your jurisdiction's needs to discuss discordant outcomes and request changes

Instructions: For each MRSA Bacteremia LabID Event with discordant outcome between facility reporters and validators, record the following (first row-enter hospital report; second row-enter recommended changes). Use the Comment area to document reasons for discrepancy, for example: overlooked candidate specimen; confusion regarding common commensals; did not meet alternative primary definition, not a uropathogen, etc. Many jurisdictions have examined this type of data to identify common errors and direct future education and training. Keep a copy for your records and leave a copy with the facility. F=facility; V=validator

| Pt. ID | | Admission Date | Date of first reportable LabID Event during this encounter | NHSN location of LabID Event | Positive MRSA blood specimen on date of admission? Y/N | Prior MRSA blood from same location within prior 14 days? Y/N | Other reason for error |
|-----------------|---|----------------|--|------------------------------|--|---|------------------------|
| | F | | | | | | |
| | V | | | | | | |
| Comment: | | | | | | | |
| | F | | | | | | |
| | V | | | | | | |
| Comment: | | | | | | | |
| | F | | | | | | |
| | V | | | | | | |
| Comment: | | | | | | | |
| | F | | | | | | |
| | V | | | | | | |
| Comment: | | | | | | | |
| | F | | | | | | |
| | V | | | | | | |
| Comment: | | | | | | | |

6.5 MRSA bacteremia LabID event surveillance methods survey (with key)

OrgID/Name of Hospital: _____ Date of Survey: _____

| LabID Event Surveillance Methods Survey | | | | |
|--|-----------|---------------------------|---|--|
| <i>Instructions: Administer this survey to the person who oversees NHSN LabID Event reporting</i> | | | | |
| Denominator Data Collection Questions | | | | |
| Name of individual interviewed: | Position: | FacWideIN MRSA bacteremia | Interviewer initials: | Date of survey: |
| 1) For FacWideIN reporting, denominator data are entered into NHSN once a month at the facility-wide level | | | <input type="checkbox"/> True <input type="checkbox"/> False | T |
| 2) Patient days include only admitted patients on inpatient wards; observation patients located on inpatient wards are excluded | | | <input type="checkbox"/> True <input type="checkbox"/> False | F (all patients housed in inpatient locations) |
| 3) For MRSA bacteremia reporting baby locations (NICU, newborn nursery, etc.) should be excluded from the denominator | | | <input type="checkbox"/> True <input type="checkbox"/> False | F (no location exclusions for MRSA) |
| LabID Event (Numerator) Data Collection Questions | | | | |
| Name of individual interviewed: | Position: | FacWideIN MRSA bacteremia | Interviewer initials: | Date of survey: |
| 4) For FacWideIN reporting, one monthly numerator for Events is reported at the facility-wide level | | | <input type="checkbox"/> True <input type="checkbox"/> False | F (events are reported by location) |
| 5) A second event is always reported if >14 days have passed from the most recent positive MRSA bacteremia | | | <input type="checkbox"/> True <input type="checkbox"/> False | T |
| 6) A second event is only reported if >14 days have passed from the most recently reported LabID event | | | <input type="checkbox"/> True <input type="checkbox"/> False | F (If the patient changes location, a second event is reported even within 14 days of prior event) |
| 7) A second event is only reported if the patient changes location OR >14 days have passed since the most recent positive MRSA bacteremia in the same location | | | <input type="checkbox"/> True <input type="checkbox"/> False | T |

Section 6.6 LabID Event facility-wide inpatient (FacWideIN) denominator validation template

Please feel free to adapt this template to meet your jurisdiction's needs

Electronically collected MRSA bacteremia denominators

“FacWideIN” includes all patient days counted at the same time each day for all inpatient locations, including any patients located for the day in inpatient locations, whether or not the facility considers them admitted patients or observation patients, but excluding any patients located for the day in outpatient observation locations. This information is typically collected electronically.

Because the task of validating electronic patient days and admissions facility-wide is daunting, denominator validation can be accomplished using manual counting of patient days and admissions in three specified location types for three months each: one ICU, one Labor/Delivery/Recovery/Post-Partum (LDRP) location (if available), and one or more inpatient wards where observation patients are frequently located. Facilities with inpatient rehabilitation facility (IRF) and/or inpatient psychiatric facility (IPF) locations with separate CCNs and facilities with baby-based locations (for example, NICU, well baby nursery, etc.) should also validate these locations.

Electronic counts should be within 5% of manual counts or an evaluation of why they differ should be conducted

| MRSA Bacteremia LabID Event Denominator Validation | | | | | | | |
|--|----------------------------------|-------------|------------------------|--------------|--------------|------------------------|--------------|
| Location of Validation* | Month of Validation (specify) | Admissions | | | Patient Days | | |
| | | Usual Count | 5% Tolerance interval† | Manual Count | Usual Count | 5% Tolerance interval† | Manual Count |
| | 1 | | | | | | |
| | 2 | | | | | | |
| | 3 | | | | | | |
| | 1 | | | | | | |
| | 2 | | | | | | |
| | 3 | | | | | | |
| | 1 | | | | | | |
| | 2 | | | | | | |
| | 3 | | | | | | |

*Select one ICU, one Labor/Delivery/Recovery/Post-Partum (LDRP) location if available, and one or more inpatient ward location where observation patients are frequently located and conduct manual (patient level) validation of admissions and patients days for three consecutive months, according to NHSN definitions. (https://www.cdc.gov/nhsn/pdfs/pscmanual/pscmanual_current.pdf and http://www.cdc.gov/nhsn/forms/instr/57_127.pdf).

Remember that for MRSA bacteremia **both mothers and babies** are counted in LDRP locations.

†Equation for 5% tolerance interval: Usual Count ± (Usual Count * 0.05).
 Example calculations where Usual Count = 164 and Manual Count = 178:
 Eligible 5% tolerance interval = [164±(164*0.05)]=155.8 to 172.2
 Manual Count 178 falls outside the tolerance interval, suggesting that Usual Count is inaccurate and should be investigated.

6.7 (Optional) 2025 MRSA Bacteremia LabID Validation Summary

*required **conditionally required

| Facility Validation Overview | |
|------------------------------|---|
| *Facility ID: | |
| *Facility Type: | <input type="checkbox"/> Acute care hospital <input type="checkbox"/> Long term acute care hospital (LTAC/LTACH) <input type="checkbox"/> Oncology hospital <input type="checkbox"/> Inpatient rehabilitation facility (IRF) |
| *Facility sampling method: | <input type="checkbox"/> CDC Method 1 (Targeted Sampling) <input type="checkbox"/> CDC Method 2 (Cumulative attributable difference) <input type="checkbox"/> CDC Method 3 (Stratified Random Sampling) |
| Reason Facility was Sampled: | <input type="checkbox"/> All facilities were validated <input type="checkbox"/> Targeted facility (Methods 1 or 2) <input type="checkbox"/> Randomly selected facility |

| Numerator Validation | | | | |
|---|---|--|---|---|
| *Sampling information for numerator validation at this facility: | | | | |
| | Event | Sampling Frame Elements | # episodes or procedures eligible for review for timeframe) | Total # events from facility reported to NHSN for timeframe (before validation) |
| | MRSA bacteremia LabID event | Inpatient [^] blood specimens positive for MRSA | _____ | _____ |
| *MRSA bacteremia LabID Event Validation Results: | | | | |
| | Event Determination | Validation: Yes - MRSA bacteremia LabID event | Validation: No – Not MRSA bacteremia reportable LabID event | |
| | Facility: Yes - Date-matched MRSA blood specimen reported as LabID event | a. _____ | b. _____ | |
| | Facility: No - Date-matched MRSA blood specimen NOT reported as LabID event | c. _____ | d. _____ | |

^Inpatient includes specimens, outpatient emergency department (adult and pediatric) and 24-hr Observation location(s)

Denominator Validation: MRSA bacteremia LabID event

**Has this facility completed any internal validation of LabID event denominator data counting? Yes No

Note: Validation of denominator data counting requires concurrent patient level denominator counting (reference) vs. standard electronic data for three specified location types [one ICU, one LDRP if available, and one or more wards where observation patients are frequently housed] for ≥1 month; validated data should fall within 5% of the reference standard.

**If yes, provide the following information for all months validated:

| Location of validation | Month of validation | Admissions | | Patient Days | |
|------------------------|---------------------|-------------|--------------|--------------|--------------|
| | | Usual count | Manual count | Usual count | Manual count |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |

NHSN Inpatient Location Validation: MAPPING

**Do any inpatient locations require mapping or re-mapping within NHSN? Yes No

**If yes, indicate which locations need to be mapped/re-mapped and recommendations:

| Location | Current CDC location code designation | Current bed count | Recommended CDC location code designation | Recommended bed count |
|----------|---------------------------------------|-------------------|---|-----------------------|
| | | | | |
| | | | | |
| | | | | |

Add rows as needed.

| | |
|---|---|
| <p>**How does this facility obtain inpatient admissions data?</p> | <input type="checkbox"/> Electronic from billing <input type="checkbox"/> Electronic from vendor system <input type="checkbox"/> Electronic from ADT <input type="checkbox"/> Other (specify): _____ |
| <p>**How does this facility obtain inpatient patient days data?</p> | <input type="checkbox"/> Electronic from billing <input type="checkbox"/> Electronic from vendor system <input type="checkbox"/> Electronic from ADT <input type="checkbox"/> Other (specify): _____ |

Risk Adjustment Variable Validation

*Teaching hospital affiliation

| | |
|---|--|
| <p>Facility teaching hospital affiliation reported on 2025 NHSN annual facility survey:</p> | <input type="checkbox"/> Non-teaching <input type="checkbox"/> Major <input type="checkbox"/> Graduate <input type="checkbox"/> Undergraduate <input type="checkbox"/> N/A (IRF & LTACH) |
|---|--|

| | |
|---|---|
| <p>Is facility teaching hospital affiliation correct?</p> | <input type="checkbox"/> Yes <input type="checkbox"/> No |
|---|---|

*Facility bed size (all inpatient locations, including 'baby locations')

| | |
|--|--|
| <p>Facility bed size reported on 2025 NHSN Annual Facility Survey:</p> | |
| <p>Validated bed size:</p> | |

Comments

| |
|----------|
| <p> </p> |
|----------|