

Annual Report of Method Tracking

1. Jurisdiction
2. Date of entry
3. Which organisms are you performing identification on?
4. Please list which "other" organism(s) ID is performed on
5. Which organisms are you performing antimicrobial susceptibility testing (AST) on?
6. Please list which "other" organism(s) AST is performed on
7. Which organisms are you performing phenotypic testing on?
8. Please list which "other" organism(s) phenotypic testing is performed on
9. Which organisms are you performing molecular mechanism testing on?
10. Please list which "other" organism(s) molecular mechanism testing is being performed on
11. Which AR Lab Network methods are CLIA validated and reported for patient treatment?
12. Organism identification method (select all that apply)
13. If other, please specify
14. If using a MALDI-TOF, which system?
15. Which MALDI-TOF databases are utilized? Please list.
16. Antimicrobial susceptibility testing (AST) method (select all that apply)
17. If other AST method, please specify
18. Please explain why your laboratory is not performing AST on HAI isolates.
19. If BMD, which platform(s) do you use?
20. If other BMD platform, please specify
21. Which Sensititre panel(s) do you test?
22. If custom, please share which drugs are tested on your panel
23. If other, please share which panel you use and what drugs are included
24. If performing BMD with Sensititre, what transfer inoculum do you use?
25. If other Sensititre transfer inoculum used, please specify
26. If performing BMD with Sensititre, what incubation method do you use?
27. If performing BMD with Sensititre, what read method do you use?
28. If ATI, which instrument(s) do you use?
29. If ATI, which panel(s) do you test?
30. If using Microscan, what inoculation method do you use?
31. If other Microscan inoculation method, please specify
32. If using Microscan, what read method do you use?
33. If using Microscan, what incubation method do you use?
34. Are all drugs on the panel(s) tested validated?
35. If not all drugs on a panel are validated, please list which drugs are NOT currently validated on your panel(s)
36. List of drugs (and the manufacturer) tested and reported by your laboratory
37. Phenotypic carbapenemase production testing method (select all that apply)
38. ATI instrument brand used for phenotypic carbapenemase testing (select all that apply)

Public reporting burden of this collection of information is estimated to average 120 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. An agency may not conduct or sponsor, and a person is not required to respond to a collection of information unless it displays a currently valid OMB Control Number. Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to CDC/ATSDR Reports Clearance Officer, 1600 Clifton Road NE, MS H21-8, Atlanta, Georgia 30333; ATTN: PRA 0920-1310

39. If other carbapenemase detection method, please specify
40. If using more than one method for phenotypic carbapenemase detection, please describe workflow. (Example, CarbaNP is performed on isolates testing intermediate via mCIM.)
41. Carbapenemase gene identification method (select all that apply)
42. If other, please specify
43. Please select all activities for which your GeneXpert detection is utilized
44. What extraction method do you use?
45. If other, please specify
46. What PCR equipment do you use for rt-PCR?
47. If other, please specify
48. What Master Mix (catalog number) do you use?
49. If other, please specify
50. Which mechanisms do you have molecular detection validated/verified?
51. If other was selected, what other mechanisms do you perform molecular detection for?
52. Is your PCR multiplex or singleplex?
53. If multiplex, which targets are multiplexed?
54. If other, please specify
55. Please list any "new" instrumentation or assays undergoing evaluation or validation/verification in your laboratory
56. What laboratory information management system (LIMS) is your laboratory using?
57. Are instruments used for testing ARLN isolates integrated to report results in your Laboratory Information Management System (LIMS)?
58. If yes, please describe which instruments are integrated to report results in your Laboratory Information Management System (LIMS)
59. Please describe the CURRENT "life of an isolate" within your lab--from receipt to reporting of results (i.e. Day 1 subculture, Day 2 mCIM/CP production, Day 3 PCR/AST, etc).
60. Alternatively, please upload any SOP or visual workflow of an isolate in your lab--from receipt to reporting of results
61. Are you performing whole genome sequencing (WGS)?
62. Are your WGS (wet-lab) protocols validated and verified under CLIA standards?
63. If yes, please describe which WGS (wet-lab) protocols are validated and verified under CLIA standards (e.g., DNA extraction, library preparation, MiSeq sequencing)?
64. Are your bioinformatic protocols validated and verified under CLIA standards?
65. If yes, please describe which bioinformatic tools and/or pipelines are validated and verified under CLIA standards?
66. Is this WGS work currently funded, at least in part, by CDC?
67. If yes, by which mechanisms? (select all that apply)
68. If other, please specify

69. Is HAI/AR WGS conducted via a sequencing core facility that also supports WGS for other programs/pathogens?
70. What short-read sequencing platform do you use? (select all that apply)
71. If other, please specify.
72. Number of iSeq instruments available for use
73. Number of MiniSeq instruments available for use
74. Number of MiSeq DX instruments available for use
75. Number of MiSeq instruments available for use
76. Number of HiSeq instruments available for use
77. Number of NextSeq instruments available for use
78. Number of NovaSeq instruments available for use
79. Number of ClearLabs instruments available for use
80. Please specify other short-read platforms you are using and the number of each
81. What long-read sequencing platform do you use? (select all that apply)
82. If other, please specify.
83. Number of MinION instruments available for use
84. Number of GridION instruments available for use
85. Number of PromethION instruments available for use
86. Number of PacBio RSII instruments available for use
87. Number of PacBio Sequel instruments available for use
88. Please specify other long-read platforms you are using and the number of each
89. What type of DNA extraction does your lab perform?
90. What kit(s) and/or instrument(s) are used for DNA extraction?
91. What type of DNA library preparation does your lab perform?
92. What kit(s) and/or instrument(s) are used for DNA library preparation?
93. What kit(s) and instrument(s) are used to assess DNA quantity, quality and/or fragment size?
94. Are your bioinformatics supported through a contracted vendor/partner?
95. What type of platform do you use to run your bioinformatic analysis?" (check all that apply). If you send isolates to a regional lab for analysis, please select "other" and report which state samples are sent to.
96. If other, please specify.
97. Report which state WGS samples are sent to for bioinformatic analysis.
98. What bioinformatic pipeline(s) do you use for taxa ID and AR gene detection? (Check all that apply). If you send isolates to a regional lab for analysis, please select "other" and report which state samples are sent to.
99. If other, please specify.
100. What barriers are keeping your lab from analyzing your own WGS data? (Check all that apply).
101. Describe "other" barriers keeping your lab from analyzing your own WGS data.
102. Are you performing culture-based colonization screenings?

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103. If yes, please share which anatomical sites are validated and which are RUO (and if organism specific, please specify)
104. If yes, please upload your culture-based screening methods
105. Alternatively, if you don't want to upload methods, please describe your culture-based screening methods
106. Have you validated gram-positive organism colonization screening methods?
107. Please list which Gram positive organisms your lab performs screening for
108. If yes, please upload your gram-positive colonization screening methods
109. Who within your jurisdiction does the reporting for CPOs? (Select all that apply)
110. Which antibiotic resistance organisms are reportable within your jurisdiction? (Check all that apply)
111. Please list "other" reportable antibiotic resistant organisms within your jurisdiction.
112. Does your jurisdiction restrict reporting requirement to specific organisms (e.g., E. coli, K. pneumoniae, E. cloacae, etc.)?
113. List the specific organism your jurisdiction restricts reporting to.
114. How are isolates submitted to the PHL in your jurisdiction?
115. Which organisms are required or requested to be submitted within your jurisdiction? (Select all that apply).
116. POC(s) for G2 project (please provide names and email addresses for any staff that should be involved in communications and meeting invites)