

AR Lab Network Alert and Monthly Data Report Form for *Candida*

<u>Data element Name</u>	<u>Data element Definition</u>
<a href="#">arln_isolate_or_redcap_id</a>	ARLN isolate or REDCap ID. Unique ID for this record. Use an isolate ID if available. If not available or not applicable, use a specimen ID as long as no other REDCap records will use the same ID. Please include your lab's two- or three-letter jurisdiction abbreviation as a prefix to the id. Please separate the prefix and the id with a hyphen (e.g., capitalized jurisdiction prefix-id).
<a href="#">arln_specimen_id</a>	ARLN specimen id. The id assigned to the specimen by the testing lab.
<a href="#">performingorgstate</a>	ARLN PHL State. The testing lab's state, territory, or jurisdiction.
<a href="#">performing_facility</a>	Public health laboratory name. Name of your public health laboratory.
<a href="#">redcap_reporting_date</a>	REDCap reporting date. Date this form was created and the data was initially reported in REDCap. Format: YYYY-MM-DD
<a href="#">alert_type</a>	Alert type. Only create one alert record per isolate. You may change an existing <i>C. auris</i> alert to be a <i>C. auris</i> resistance alert after AFST is completed, as needed. If an isolate meets the criteria for <i>C. auris</i> pan-resistance and <i>C. auris</i> echinocandin resistance and/or <i>C. auris</i> amphotericin B resistance with elevated MIC, only mark <i>C. auris</i> pan-resistance here. If an isolate meets the criteria for <i>C. auris</i> echinocandin resistance and <i>C. auris</i> amphotericin B resistance with elevated MIC, but is susceptible to azoles (i.e. is not pan-resistant), only mark <i>C. auris</i> echinocandin resistance here.
<a href="#">epi</a>	Please describe the epi that justified this alert.
<a href="#">alert_date</a>	Alert date. Date the alert was entered. Format: YYYY-MM-DD
<a href="#">new_case</a>	Has this patient had a previous <i>C. auris</i> case? Indicate whether the patient was already known to be positive for <i>C. auris</i> .
<a href="#">specimen_type</a>	Specimen type. Source of the specimen (e.g., blood). Use the SNOMED preferred concept name whenever possible.
<a href="#">specimen_collection_date</a>	Specimen collection date. Date when the specimen collection was completed. Format: YYYY-MM-DD
<a href="#">specimen_received_date</a>	Specimen received date. Date the specimen received for testing at your lab. Format: YYYY-MM-DD
<a href="#">clinical_sample_or_isolate</a>	Clinical sample or isolate. Indicate whether the specimen received was a clinical sample (e.g., swab) from colonization screening or an isolate.
<a href="#">facilitystate</a>	Healthcare facility of origin state or territory. State or territory of the healthcare facility where the specimen was collected. Do not enter commercial, reference, or public health laboratories. This should be the facility where the specimen was originally collected.

Public reporting burden of this collection of information is estimated to average 20 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

facilityzip	Healthcare facility of origin zip code. Zip code of the healthcare facility where the specimen was collected. Do not enter commercial, reference, or public health laboratories. This should be the facility where the specimen was originally collected.
facilityname	Healthcare facility of origin name. Name of the healthcare facility where the specimen was collected. Do not enter commercial, reference, or public health laboratories. This should be the facility where the specimen was originally collected.
facilityid	Healthcare facility of origin id. Healthcare facility ID where the specimen was collected. Do not enter commercial, reference, or public health laboratories. This should be the facility where the specimen was originally collected.
submitter_specimen_id	Submitter specimen id. Specimen ID assigned by the submitting entity (facility, laboratory, etc.).
submitter_facility_state	Submitter facility state or territory. State or territory of the facility that sent the specimen or isolate to your lab.
submitter_facility_zipcode	Submitter facility zip code. Zip code of the facility that sent the specimen or isolate to your lab.
submitter_facility_name	Submitter facility name. The name of the facility that sent the specimen or isolate to your lab.
submitter_facility_id	Submitter facility id. ID of the facility that sent the specimen or isolate to your lab.
patient_id	Patient ID. This information should be provided in the following order of preference:1) Unique patient ID assigned by the public health department.2) Unique patient ID assigned by the hospital/facility.3) Other unique patient ID. The patient ID should facilitate linking lab data to data provided from epidemiologists and other sources in public health. If you do not have a patient ID, put 'Not reported'.
patient_dob	Patient date of birth. Patient date of birth. Format: YYYY-MM-DD
patient_age	Patient's age. Patient's age at the specimen collection date (in the units specified in the question below).
patient_age_unit	Patient age unit. This could be years, months, or days.
patient_sex	Patient's sex. This is the administrative sex.
patient_race	Patient's race. Race of the patient.
race_other	Race Other.
patient_ethnicity	Patient ethnicity. Ethnicity of the patient.
patient_county_fips	Patient's county code of residence Federal Information Processing Standard (FIPS) county code. Format: This should be a 5-digit code.
patient_county	Patient's county of residence. Name of patient's county. Do not write the word "County" in the name (e.g. "Cook" instead of "Cook County").
patient_state	Patient's state or territory of residence. Patient's state or territory of residence.
patient_country	Patient's country of residence. Complete this field if the patient's location of residence is outside of the U.S.

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c_auris_pcr	For C. auris colonization testing only. The PCR result from the screening swab.
c_auris_pcr_dt	For C. auris colonization testing only. Date PCR testing was performed for the screening swab. Format: YYYY-MM-DD
c_auris_pcr_drr	For C. auris colonization testing only. Date C. auris PCR result was reported to the submitter. Format: YYYY-MM-DD
c_auris_culture	For C. auris colonization testing only. C. auris culture result.
c_auris_culture_dt	For C. auris colonization testing only. Date the culture was performed for the screening swab. Format: YYYY-MM-DD
c_auris_culture_drr	For C. auris colonization testing only. Date the C. auris culture result was reported to the submitter. Format: YYYY-MM-DD
candida_or_aspergillus_testing	Indicate the type of testing your lab is performing for isolate testing.
speciescl	For Candida testing only. The Candida species was identified by the clinical lab. Please spell out the genus for the species results.
organism_suspected	For Candida testing only. The suspected organism in the specimen when received by your lab. Please spell out the genus for the species results.
species_candida	For Candida testing only. The species identified by your lab. Please spell out the genus for the species results.
species_aspergillus	For azole-resistant Aspergillus fumigatus testing only. The species identified by your lab.
species_dt	Date the species identification was performed by your lab. Date the species identification was performed by your lab. Format: YYYY-MM-DD
species_drr	Date the species identified by your lab was reported to the submitter. Date the species identified by your lab was reported to the submitter. Format: YYYY-MM-DD
itraconazole_screen	Itraconazole screen. For Aspergillus testing only. Screening results for itraconazole.
posaconazole_screen	Posaconazole screen. For Aspergillus testing only. Screening results for posaconazole.
voriconazole_screen	Voriconazole screen. For Aspergillus testing only. Screening results for voriconazole.
test_date_screen	Date azole screening testing finalized. For Aspergillus testing only. Date azole screening testing finalized. Format: YYYY-MM-DD
amphotericin_b_mic	Amphotericin b MIC. Amphotericin b MIC.
amphotericin_b_mic_other	Other amphotericin b MIC. Other amphotericin b MIC.
amphotericin_b_mic_dt	Date of amphotericin b MIC. Date isolate underwent AFST for amphotericin b. Format: YYYY-MM-DD
amphotericin_b_mic_drr	Date amphotericin b MIC results reported Date amphotericin b MIC results were reported to the submitter. Format: YYYY-MM-DD
anidulafungin_mic	Anidulafungin MIC. Anidulafungin MIC.

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anidulafungin_mic_other	Other anidulafungin MIC. Other anidulafungin MIC.
anidulafungin_mic_dt	Date of anidulafungin MIC. Date of anidulafungin MIC results were reported to the submitter. Format: YYYY-MM-DD
anidulafungin_mic_drr	Date of anidulafungin MIC results reported. Date isolate underwent AFST for anidulafungin. Format: YYYY-MM-DD
casprofungin_mic	Casprofungin MIC. Casprofungin MIC.
casprofungin_mic_other	Other casprofungin MIC. Other casprofungin MIC.
casprofungin_mic_dt	Date of casprofungin AFST. Date isolate underwent AFST for casprofungin. Format: YYYY-MM-DD
casprofungin_mic_drr	Date casprofungin MIC results reported. Date casprofungin MIC results were reported to the submitter. Format: YYYY-MM-DD
ibrexafungerp_mic	Ibrexafungerp MIC. Ibrexafungerp MIC.
ibrexafungerp_mic_other	Other ibrexafungerp MIC. Other ibrexafungerp MIC.
ibrexafungerp_mic_dt	Date of ibrexafungerp MIC. Date isolate underwent AFST for ibrexafungerp. Format: YYYY-MM-DD
ibrexafungerp_mic_drr	Date ibrexafungerp MIC reported Date ibrexafungerp MIC were reported to the submitter. Format: YYYY-MM-DD
fluconazole_mic	Fluconazole MIC. Fluconazole MIC.
fluconazole_mic_other	Other fluconazole MIC. Other fluconazole MIC.
fluconazole_mic_dt	Date of fluconazole MIC Date isolate underwent AFST for fluconazole. Format: YYYY-MM-DD
fluconazole_mic_drr	Date fluconazole MIC reported Date fluconazole MIC were reported to the submitter. Format: YYYY-MM-DD
isavuconazole_mic	Isavuconazole MIC. Isavuconazole MIC.
isavuconazole_mic_other	Other isavuconazole MIC. Other isavuconazole MIC.
isavuconazole_mic_dt	Date of isavuconazole MIC. Date isolate underwent AFST for isavuconazole. Format: YYYY-MM-DD
isavuconazole_mic_drr	Date isavuconazole MIC results reported. Date isavuconazole MIC results were reported to the submitter. Format: YYYY-MM-DD
itraconazole_mic	Itraconazole MIC. Itraconazole MIC.
itraconazole_mic_other	Other itraconazole MIC. Other itraconazole MIC.
itraconazole_mic_dt	Date of itraconazole MIC. Date isolate underwent AFST for itraconazole. Format: YYYY-MM-DD
itraconazole_mic_drr	Date itraconazole MIC results reported. Date itraconazole MIC results were reported to the submitter. Format: YYYY-MM-DD
micafungin_mic	Micafungin MIC. Micafungin MIC.
micafungin_mic_other	Other micafungin MIC. Other micafungin MIC.
micafungin_mic_dt	Date micafungin MIC Date isolate underwent AFST for micafungin. Format: YYYY-MM-DD

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<a href="#">micafungin_mic_drr</a>	Date micafungin MIC results reported. Date of micafungin MIC results were reported to the submitter. Format: YYYY-MM-DD
<a href="#">posaconazole_mic</a>	Posaconazole MIC. Posaconazole MIC.
<a href="#">posaconazole_mic_other</a>	Other posaconazole MIC. Other posaconazole MIC.
<a href="#">posaconazole_mic_dt</a>	Date of posaconazole MIC. Date isolate underwent AFST for posaconazole. Format: YYYY-MM-DD
<a href="#">posaconazole_mic_drr</a>	Date posaconazole results reported. Date posaconazole MIC results were reported to the submitter. Format: YYYY-MM-DD
<a href="#">voriconazole_mic</a>	Voriconazole MIC. Voriconazole MIC.
<a href="#">voriconazole_mic_other</a>	Other voriconazole MIC. Other voriconazole MIC.
<a href="#">voriconazole_mic_dt</a>	Date of voriconazole MIC. Date isolate underwent AFST for voriconazole. Format: YYYY-MM-DD
<a href="#">voriconazole_mic_drr</a>	Date voriconazole MIC results reported. Date voriconazole MIC results were reported to the submitter. Format: YYYY-MM-DD
<a href="#">isolate_forwarded</a>	Isolate forwarded? Indicate whether the isolate was forwarded to another lab for testing.
<a href="#">date_isolate_forwarded</a>	Date isolate forwarded. Date isolate was forwarded by your lab to another lab for further testing. Format: YYYY-DD-MM
<a href="#">performingorgstate_forwarded</a>	PHL where the isolate was forwarded. The state, territory, or jurisdiction of the testing lab where the isolate was forwarded. If you are a regional lab and the the isolate was forwarded to CDC, indicate CDC for this field.
<a href="#">phl_forwarded</a>	PHL name where the isolate was forwarded. Name of the public health lab where the isolate was forwarded. If you are a regional lab and the the isolate was forwarded to CDC, indicate CDC for this field.
<a href="#">wgs_performed</a>	Did your lab perform WGS on this isolate? Indicate whether WGS will be performed on this isolate by your lab.
<a href="#">wgs_dt</a>	The date the raw WGS data was generated by your lab. Format: YYYY-MM-DD
<a href="#">wgs_id</a>	WGS ID; The WGS ID assigned to the sample that is used for public posting to NCBI. Format: STATE-LAB-SPECIES-SAMPLE (i.e., ST-LLLLLL-CAU-#####).
<a href="#">srr_number</a>	SRR number. The run accession from the isolate's SRA submission (i.e., SRR#)
<a href="#">c_auris_wgs_clade</a>	For C. auris WGS only. The C. auris clade that the isolate belongs to as it appears in the visualized phylogenetic tree. This should be based on WGS data.
<a href="#">c_auris_clade_other</a>	For C. auris WGS only. If the C. auris isolate clusters to a clade other than I-V, indicate that here.
<a href="#">fks</a>	Genotype of FKS1 hotspot (HS) regions.
<a href="#">fks_other</a>	Other FKS mutation.
<a href="#">fks_method</a>	Method used for identifying the genotype of FKS1 hotspot (HS) regions.
<a href="#">fks_method_other</a>	Other method used for identifying the genotype of FKS1 hotspot (HS) regions.

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<a href="#">wgs_drr</a>	Date sequence results reported. The date the WGS results were disseminated to the health department. This includes the phylogenetic tree visualization, clade, and any inferences based on the epidemiologic information. Format: YYYY-MM-DD
<a href="#">wgs_comments</a>	WGS comments. Please share any additional comments related to WGS.
<a href="#">obs_comment</a>	Any comments from your lab? Any comments from the testing lab.
<a href="#">delete_record</a>	Do you want MDB to delete this record from your dataset?  Check 'yes' if this record should be deleted from your dataset.
<a href="#">close_out</a>	Is this a record update for a DAART record that cannot be resubmitted via HL7?

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