

APHL Sequencing Support Help Desk



As public health laboratories rapidly build sequencing capacity to respond to COVID-19 surveillance needs, it's essential to have access to timely and appropriate assistance. To support this, APHL is launching the **APHL Sequencing Support Help Desk!**

Through this help desk, APHL member laboratories can connect with subject matter experts or other technical resources. APHL will track support requests for common trends so we can facilitate more efficient and timely responses and identify opportunities for new resources and trainings that address common challenges.

Send your genomic sequencing issues and questions to
sequencing.support@aphl.org

for timely and personalized assistance!

How do I get support?

Send an email to sequencing.support@aphl.org with as much detail as possible about the issue and any specific requests. Once received, APHL will assign your ticket to an appropriate resource, usually within two business days.

Who will help me?

Depending on the specific request, it will likely be assigned to a specific CDC team—such as the COVID-19 Technical Outreach and Assistance for States Team (TOAST)—subject matter expert or bioinformatics regional resource (BRR). In most cases, you will be matched with your normal BRR, but if they do not have the capacity to respond, we will find someone who can help.

How does it work?

Once your ticket is assigned, progress will be tracked through the ticketing system and the person assigned to help you can pull in other resources as needed or escalate urgent issues. APHL will track tickets and make sure you get a response.

What types of requests can I submit?

The Help Desk will be able to field a variety of questions or issues, such as (but not limited to):

- Where can I find a protocol to sequence samples on a MinION?
- Can you connect me with another lab that has experience with the ARTIC protocol?
- Can you connect me with another lab that has experience with automation instruments?
- I've hit a wall troubleshooting [issue], can someone please help me?
- What quality control metrics should be used to identify a SARS-CoV-2 specimen as a variant of concern?
- How can we create sequencing data visualizations for our epidemiologists?
- I keep having samples rejected during submission to GISAID, how can I get my samples accepted?
- What bioinformatics pipeline should I use?
- How do I get started in building cloud computing infrastructure?
- I'm hiring a bioinformatician—what criteria should I look for on applications?
- We are just starting to sequence and need help getting set up. Who can we talk with about everything from wet lab to bioinformatics and LIMS support?

If we can't help you address your question, we will let you know and work to point you in the right direction.

