

Setup for the rhAmpSeq™ CRISPR Analysis Tool

INTRODUCTION

One of the discerning features of the analysis platform is its security and flexibility when it comes to uploading sample data to the platform as well as downloading results from the platform.

The basic setup is straightforward; and includes more options for advanced users. This guide will explain both scenarios in the transfer of data. Read the instructions describing the basic setup and if you have any unresolved questions, refer to [Appendix A: Troubleshooting](#) for resolution. If you are experiencing any difficulty using this tool, [contact us](#).

REQUEST A CONNECTOR

IDT Service Connector

The IDT Service Connector software enables the streaming of data from an on-premise data storage location to the [rhAmpSeq CRISPR Analysis Tool](#). You will need to install this software on a machine that also has access to your sample data. With the IDT Service Connector, you can securely:

- Upload your sample data to the rhAmpSeq CRISPR Analysis Tool
- Download results from the rhAmpSeq CRISPR Analysis Tool

This software can be installed on a server, a personal computer (PC), or a laptop that has access to your sample data.

The IDT Service Connector makes two connections to the rhAmpSeq CRISPR Analysis Tool ([Figure 1](#)):

1. **A control connection.** The Service Connector uses this connection to get its configuration information from the rhAmpSeq CRISPR Analysis Tool.
2. **A connection to a storage node.** This connection is used to upload sample data to the rhAmpSeq CRISPR Analysis Tool, or download the results files.



Note: The IDT Service Connector runs in the background while its configuration setup occurs in the rhAmpSeq CRISPR Analysis Tool. The next several sections in this guide cover how to configure the connector and its different setup options.

> SEE WHAT MORE WE CAN DO FOR YOU AT WWW.IDTDNA.COM.

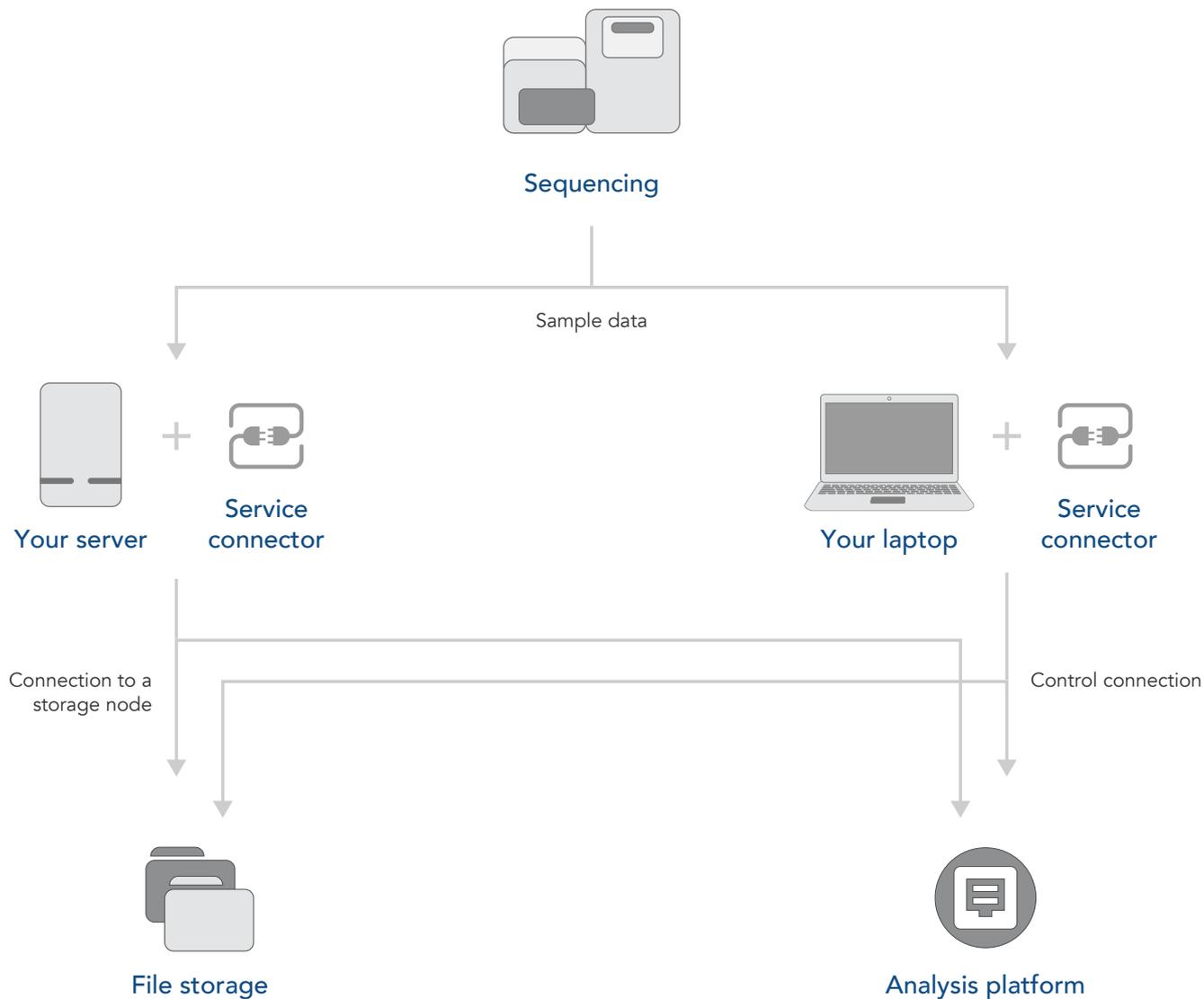


Figure 1. The two-pronged IDT Service Connector configuration.

Connector request

First, request a connector in the rhAmpSeq CRISPR Analysis Tool.

Go to Settings → Local Connector Settings.

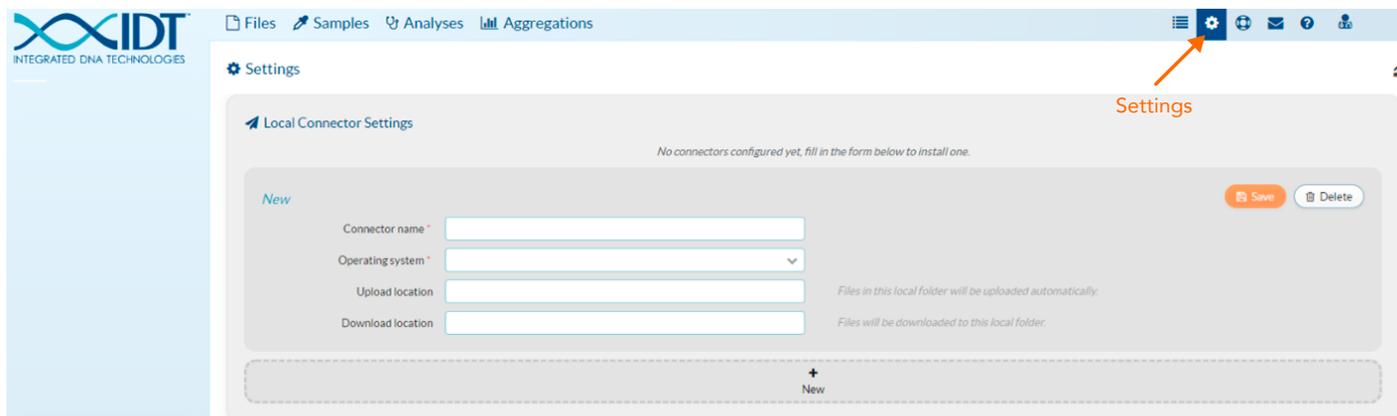


Figure 2. The Settings menu location in the rhAmpSeq CRISPR Analysis Tool.

Fill out the mandatory fields:

- **Connector name.** Choose a name for your connector (e.g., MyConnector).
- **Operating System (OS).** Select the OS of the server, PC, or laptop where you will be installing the connector.
- **Upload location.** Enter the full path to a local folder. Files from this folder will automatically upload to the rhAmpSeq CRISPR Analysis Tool (e.g., C:\Users\test\Documents\CRISPR\FASTQ\). See [Import data](#) for more information.
- **Download location.** Enter the full path to a local folder. Files from the rhAmpSeq CRISPR Analysis Tool will download directly to this folder.



Note: A secure file transfer protocol (SFTP) is used for transferring, accessing, and managing files between your local machine and the rhAmpSeq CRISPR Analysis Tool over an encrypted connection.

After all fields are defined, click **Save**. An initialization key will appear; this key will be used later when installing the IDT Service Connector. Record this alphanumeric key for later.

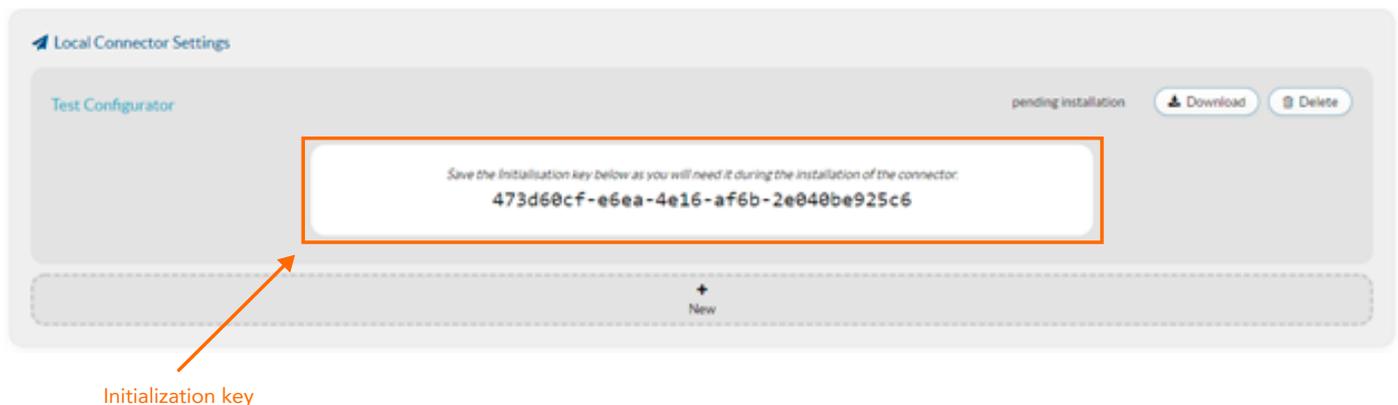


Figure 3. Initialization key to use when installing the IDT Service Connector.

Shared drives

When your data files are located on a shared drive, first create a folder on your local drive. Transfer one of the sample files to the folder, and then complete the connector setup to that folder. The connector will be correctly configured once you have verified the file is successfully uploaded to the rhAmpSeq CRISPR Analysis Tool.

However, be aware that the transfer process to and from a shared drive can be somewhat slow due to the integrity check that the connector conducts on each file before it starts the upload. Ultimately, this can result in the entire process taking up to 30 minutes after you configure a shared drive, and before uploads start.

- **Important:** The IDT Service Connector can upload or download to a shared drive if:
 - The shared drive is mounted locally.
 - For example: X:\idtupload or /Volumes/shareddrive/idtupload works, while \\shareddrive\idtupload or smb://shareddrive/idtupload will not work.
 - The IDT Service Connector user must have access to the shared drive without a password being required.

For Linux OS, the user needs to have read, write, and execute permissions for the installation folder.

MANAGE A CONNECTOR

Install and start a connector

When you have configured your connector in the rhAmpSeq CRISPR Analysis Tool platform, select **Download** in the upper right-hand selector.



Figure 4. The Download button is in the upper right-hand corner.

An installer automatically downloads a compatible connector for the OS that you have indicated. Follow the instructions below.

Windows

1. Double-click to run the downloaded .exe file. During the installation, the installer asks for the initialization key provided earlier. Fill in the alphanumeric key that is provided in the rhAmpSeq CRISPR Analysis Tool.
2. The installer will create the IDT Service Connector. Register it as a Windows service and start the service.
3. After a full minute, refresh the screen in the rhAmpSeq CRISPR Analysis Tool and make sure that the connector displays as connected.

! Important:

- Windows allows you to install only one connector. If you need to install a new one, you must first uninstall the current connector.
- For upgrades to a connector, do not uninstall the previous version. Upgrades are designed to recognize the installed version.

Mac OS X

1. Double-click to run the downloaded `.dmg` file.
2. Double-click the IDT Service Connector in the window that opens. Provide the installation key when prompted.
3. Once the connector is installed, open the app. (You can find the app at the local file location where you designated in the configuration step). When the connector starts, the connector icon appears in your dock.
4. To check if your local connector has been connected to the platform, go to the rhAmpSeq CRISPR Analysis Tool on the Settings page. Wait a full minute once you have started your connector locally, then refresh the Settings page to see the current status of your connector.



Important: To shut down your computer, close the connector app from your dock.

Linux

1. If using a Linux OS, make sure that Java SE 8 is installed. The connector will use the default Java version on the OS. Confirm the Java version present on your system with the command `'java -version'`.
2. Run the installer. Depending on whether or not you have an X server running, it will either display a user interface (UI), or have you follow a command line installation procedure. To force a command line installation, add a `'-c flag'`.
3. Start the connector from within the IDT home directory with the command `'./idtserviceconnector start.'`

Network requirements

Firewall considerations

To establish the network requirements for the rhAmpSeq CRISPR Analysis Tool, start with the control connection—it is always a TCP connection on port 443 to `platform.bluebee.com`. If you need additional IP addresses for whitelisting the service within your firewall, [contact us](#). Restart the connector after any changes.

The data transfer connection uses the SFTP protocol. [Table 1](#) lists the correct port to open for the transfer protocol.

Table 1. Ports for opening the transfer protocol.

Transfer protocol	Port
SFTP	TCP port 22

Proxy configuration

If you have a corporate proxy, you must configure the connector to use that proxy for its connections. If you would like extra guidance, [contact us](#) for assistance.

1. In the folder where you installed the application, locate the **config** folder containing the **init.properties** file. Open this file in a pure text editor (such as Notepad on Windows, or TextEdit on OS X—do not use Microsoft Word for this purpose).
2. In the **init.properties** file, add the following proxy configuration parameters:
 - `http.proxy.type=***`
 - `http.proxy.host=***`
 - `http.proxy.port=***`
 - `sftp.proxy.type=***`
 - `sftp.proxy.host=***`
 - `sftp.proxy.port=***`

The valid values for `xxxx.proxy.type` for both sftp and http are: "HTTP," "SOCKS4," and "SOCKS5." Check with your IT department to obtain the IP of the proxy server, the port where it is located, and which type of proxy you have, then enter those values. Save and close the **init.properties** file, and then restart the connector.

To check for any issues between the connector and the rhAmpSeq CRISPR Analysis Tool, locate the log file, **BSC.out**, found inside the installation directory for the connector. This file will update after any restart. It contains many of connector's technical details and also displays when the connector has problems connecting to the rhAmpSeq CRISPR Analysis Tool, making it is a useful file to refer to after any restart. For more information see the section, [Log files](#).

Update an existing installation

From time to time, new versions of the IDT Service Connector will be released with improvements and bug fixes. You can simply download a new version of the IDT Service Connector by clicking **Update to latest version** (Settings) in the rhAmpSeq CRISPR Analysis Tool.

After downloading and running the new version, choose the option '**Yes, update the existing installation.**'

Uninstall a connector

Windows

Go to the directory where you installed the IDT Service Connector, then run the uninstaller. Typically the path would be: `C:\Program Files(x86)\idt\uninstall.exe`.

Mac OS X

Open Launchpad, then drag the IDT Service Connector towards your garbage can.

Linux

Go to the directory where you installed the IDT Service Connector and locate the uninstall script. Execute this script to uninstall the connector.

CLOUD CONNECTORS

Supported cloud providers

You can import data to the rhAmpSeq CRISPR Analysis Tool from the following cloud providers:

- BaseSpace® (Illumina)
- Google
- Amazon

Request and configure a new cloud connector

A new Cloud Connector can only be requested from within the rhAmpSeq CRISPR Analysis Tool. In the project, go to the Settings page, then navigate to the Cloud Connectors Settings page. Request a new Cloud Connector by clicking the + button for your desired cloud provider.

 **Note:** It is possible to have multiple Cloud Connectors. For each Cloud Connector, provide a unique name, then select the provider you want to use to import data to the rhAmpSeq CRISPR Analysis Tool.

Specific information is required to make a connection between the bucket (or project) located at the cloud provider and the rhAmpSeq Analysis Tool. Instructions on how to find this information is listed by each cloud provider.

BaseSpace

 **Important:** Follow these instructions if you have already created a project that contains data. If you still need to create a project and upload data, see this [BaseSpace tutorial](#).

To connect the cloud connector in the rhAmpSeq CRISPR Analysis Tool with BaseSpace, define the following:

- **URL.** Keep the predefined URL.
- **Access Token.** BaseSpace provides [instructions online](#) on how to request your token (go to 'Steps for developing your first App') or follow these steps:
 1. Go to the **My Apps** page within the BaseSpace Developers environment.
 2. If you have not yet created an application, follow these additional steps:
 - a. Click **Steps** for developing your first App.
 - b. Click **Register**.
 - c. Click the Accept the Terms and Conditions **checkbox**.
 3. Click **Create a new Application**.
 - a. **Name.** Provide a unique name, e.g., your company name + 'IDT connector.'
 - b. **Organization.** Provide your company or organization name.
 - c. **App Type.** Select '**Web/Desktop = Other**.'
 - d. **Short Description.** Enter '**IDT connector**.'
 - e. Click **Create Application**.
 - f. Fill in the **Release Notes** and **Long Description**, as needed.

- g. Select a **Category**, if desired.
 - h. **Application Permission Settings**. Select **'read.'**
 - i. Click **Save**.
4. Scroll up to locate the **Credentials** tab, copy the **Access Token**, then paste it into the corresponding field in the Cloud Connector in the rhAmpSeq CRISPR Analysis Tool.

Google

To connect with Google, you will need a JSON file.

1. On the Google Cloud Platform, navigate to the **'Service accounts'** page under the AIM & Admin section.
2. Follow these steps for creating a new service account:
 - a. Make sure the service account permissions contain the role **'Storage Object Viewer'** for Storage.
 - b. Create a key for the service account in the type of JSON.
 - c. Download the JSON file, then upload it into the Cloud Connector for Google in the rhAmpSeq CRISPR Analysis Tool.

Amazon

Amazon provides information on how to obtain your access token in their [online documentation](#). Follow their instructions to create an IAM user (Console), then apply these characteristics when setting up the user:

1. **Type of access**. Select **'Programmatic access.'**
2. **Minimal permission for user group**. Select **'ListBucket'** and **'GetObject.'**
3. Lastly, to finish creating a user, either copy the **Access Key ID** and the **secret Access key**, or download the **CSV file** containing this information.



Important: Providing the key information requested is necessary to complete your configuration of the Cloud Connector to the platform.

More about importing

Depending on which cloud provider you want to import from, other necessary fields may need to be filled out in the import rule:

- **Automatic import**. If checked, files uploaded to this cloud project or bucket will immediately be imported to the rhAmpSeq CRISPR Analysis Tool. To import files manually, uncheck this box and check **List** instead.
- **Bucket** (Amazon, Google). Name of the bucket containing data that you want to import.
- **BaseSpace project** (BaseSpace). Name of the project containing data that you want to import from BaseSpace.
- **Object prefix** (Amazon, Google). Only files that match the prefix will be imported into the rhAmpSeq Analysis Tool and only one prefix can be configured.
- **File extensions** (BaseSpace). Only files that match the extensions listed here will be imported. Multiple file extensions can be listed as long as they are separated by a comma.

IMPORT DATA

Automatic import of data

Enable automatic import by checking the appropriate box in the import rule.

After uploading files into your cloud project, or bucket, the files will immediately import into the rhAmpSeq CRISPR Analysis Tool.

Manual import of data

Manual import can be used if you want to control when data is sent to the rhAmpSeq CRISPR Analysis Tool.

For manual data import, make sure automatic import is disabled by unchecking the appropriate box.

By default, all files will be listed that match your import rule and have not yet been imported. To view files that have previously been imported and match the import rule, enable the corresponding checkboxes.

APPENDIX A: TROUBLESHOOTING

Issue	Operating System	Solution
IDT Service Connector does not connect	Windows	<p>First, try restarting your computer. If that does not correct the problem, open the Services application (Click the Windows icon in the lower left-hand menu, then type 'services'). In the Services folder locate a service called 'IDT Service Connector.'</p> <ul style="list-style-type: none"> • If its status does <i>not</i> say 'Running,' try starting it by right-clicking the mouse, then select Start. • If its status <i>is</i> 'Running,' but it still does not connect, more than likely you have a corporate proxy. Refer to the section Proxy Configuration for more information. • If you do not have a corporate proxy, and your connector still does not connect, contact us to open a support ticket and include your connector log files for assistance.
	Mac OS X	<p>Check whether the connector is running. A simple check is to see if there is an IDT icon in your dock.</p> <ul style="list-style-type: none"> • First, try logging out and then log back in to the connector. An IDT Service Connector icon should appear in your dock. • Next, try starting the connector manually from the Launchpad menu. • If it still does not connect, you more than likely have a corporate proxy. Refer to the section Proxy Configuration for more information. • If you do not have a corporate proxy, and your connector still does not connect, contact us to open a support ticket and include your connector log files for assistance.
	Linux	<p>Confirm if the connector is running '<code>ps aux grep bluebee</code>.'</p> <ul style="list-style-type: none"> • First, try starting the service '<code>sudo service idtserviceconnector start</code>.' • If it is running but still does not connect, you more than likely have a corporate proxy. Refer to Proxy Configuration for more information. • If you do not have a corporate proxy, and your connector still does not connect, contact us to open a support ticket and include your connector log files for assistance.

Issue	Operating System	Solution
Connector is connected, but uploads will not start	General	<p>Create a new folder on your local disk, add a small file to it, then configure this folder as an upload folder.</p> <ul style="list-style-type: none"> • If this works and your sample files are on a shared drive, go to the Shared Drives section for more information. • If this works and your sample files are on your local disk, check for any of these possible issues: <ul style="list-style-type: none"> • There is an error in the upload folder's name and how it is configured in the platform. • For large files, or files on slow disk drives, the connector needs time to start the transfer because it calculates a hash while making sure there are no transfer errors. Wait for 30 minutes without changing anything on your connector configuration. • If these measures do not work, it is often because of a corporate proxy. Refer to Proxy Configuration for more information.
Upload from shared drive does not work	General	<p>Follow the guidelines in Shared Drives.</p> <p>Look in the connector's log file for an error about the directory not being present. [The log file, BSC.out, is found inside the installation directory for the connector.]</p> <ul style="list-style-type: none"> • If there is such an error, you have two ways to resolve: either correct the error in the folder name, or you will need to correct a permission problem. In the latter case, make sure the user running the connector has access <i>without</i> a password being requested to the network share. • If no error about the directory is in the connector's log file, then it is possible a consistency check could be occurring. This check can take an extended time on slow disks. Wait 30 mins to see if this resolves the issue.

Log files

The IDT Service Connector has a log file that contains technical details and clues to problems with the connector and the rhAmpSeq CRISPR Analysis Tool. If you have trouble interpreting this log file, [contact us](#) to help troubleshoot your issue. Attach the log file to your service ticket. Find this log file at the following location:

Issue	Solution
Windows	<p><BSC Installation Directory>\logs\BSC.out</p> <p>Often: C:\Program Files\bsc\logs\BSC.out</p>
Mac OS X	<p><BSC Installation Directory>/BlueBee Service Connector.app/Contents/java/app/logs/BSC.out</p> <p>Often: /Applications/BlueBee Service Connector.app/Contents/java/app/logs/BSC.out</p>
Linux	<BSC Installation Directory>/logs/BSC.out

REVISION HISTORY

Version	Release date	Description of changes
2	November 2022	Update to contact information
1	March 2021	Initial release

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Technical support: www.idtdna.com/pages/about/contact-us

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