BIO-RAD

Bio-Rad
Laboratories, Inc.

Release Notes for CFX Opus Instruments and the BR.io Cloud Platform

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Contents

Introduction

Using the BR.io Cloud Platform with CFX Opus instruments you can set up, run, monitor, and analyze your real-time PCR experiments on connected CFX Opus instruments. This document summarizes the main features, and also provides a short list of known issues.

Note: For detailed information regarding CFX Opus Real-Time PCR Systems, refer to the corresponding user guides available at www.bio-rad.com.

Supported Browsers

BR.io is supported on

- Chrome desktop browser v63 or later

- Safari desktop browser v11 or later

Summary of New Features

Support for the CFX Opus Deepwell System

The BR.io Cloud Platform now supports the CFX Opus Deepwell System, as follows:

- To create a run for a CFX Opus Deepwell System, set the Plate Size to 96 Wells. You can use all CFX protocols created in BR.io with a CFX Opus Deepwell System.

- When adding a gradient step to a CFX protocol, select the 96D button to display the gradient for a CFX Opus Deepwell System.

Fixed Issues

- A maximum number of 500 BR.io users can be linked to a CFX Opus instrument (previously 20).

- Exported .pcrd files that used a protocol containing a gradient step and were opened in CFX Maestro Software displayed the incorrect gradient.

Known Issues

- You must close the Run successfully uploaded to your BR.io account dialog box soon after the run is completed, or BR.io incorrectly displays the CFX Opus status as Offline.

- If you navigate from the CFX run workflow while uploading a file, BR.io does not warn you about unsaved changes to your CFX run.

- You must create CFX Opus run templates from an existing completed CFX run file.

- You cannot open, view, or edit CFX Opus run templates independently.

- After saving the run file created from a template, you cannot directly edit the sample list.

- If the sample list contains fewer samples than the plate layout accepts, you must open the run file after it has been saved, and manually clear the unused wells from the plate.

- If you change the Scan Mode for a pending CFX run in BR.io after loading it on the instrument the run will be performed using the original scan mode.

    - Workaround: Exit out of the run on the instrument, refresh the file browser on the instrument, then reload the run before starting it.

- BR.io does not currently support

    - Analysis of .pcrd or .zpcr files that contain legacy or user-calibrated fluorophores

        Note: You can upload the files, but working with them in the Analysis module can produce errors.

    - Application-based analysis, such as standard curve/absolute quantification, gene expression/relative quantification, and allelic discrimination
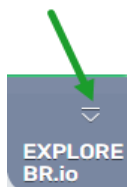
Documentation

Click the following URL, and then click the ⊘ icon to access the online Help Center.

https://br.io

For main BR.io pages, you can select Help for This Page.

You can also click the down arrow above EXPLORE BR.io to access videos that describe BR.io processes.

Contacting Technical Support

The Bio-Rad Technical Support department in the U.S. is open Monday through Friday, 5:00 AM to 5:00 PM, Pacific Time.

Phone: 1-800-424-6723, option 2
Email: Support@bio-rad.com (U.S./Canada Only)

For technical assistance outside the U.S. and Canada, contact your local technical support office or click the Contact Us link at www.bio-rad.com.

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