Bio-Rad Laboratories, Inc.

**Release Notes for the BR.io Cloud Platform**

**Version 1.2**

May 2021

# 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.

# Supported Browsers

BR.io is supported on

- Chrome desktop browser v63 or later
- Safari desktop browser v11 or later

# Summary of New Features

## FRET Scan Mode

You can create and execute CFX Opus runs using the FRET scan mode, and you can open and analyze completed CFX runs that use the FRET scan mode.

**Note:** This applies to CFX runs set up in BR.io and CFX runs manually uploaded as a .pcrd or .zpcr file.

## Baseline Cycle Range

You can now adjust the cycle range that is used to determine the baseline for baseline subtraction.

## Run Templates

You can now create run templates that enable you to quickly set up CFX Opus runs using predefined protocol, plate layout, and analysis settings. Templates also provide a streamlined workflow for entering the sample list for the run.

## Early Access Program Sign-Up

You can now express interest in joining the BR.io Early Access Program.

▶ From the Explore BR.io panel on the Home page, click Join the Early Access Program.

## 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.
- CFX protocols that are restored from the archive may not appear in the Select Protocol dropdown menu when creating a CFX run until the page is refreshed.
- CFX Opus run templates must be created from an existing completed CFX run file.
- CFX Opus run templates cannot be opened, viewed, or edited 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.
- 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.
  - Fluorescence drift correction analysis settings
  - Application-based analysis, such as standard curve/absolute quantification, gene expression/relative quantification, and allelic discrimination

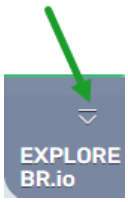
## Documentation

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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