Quick Guide to MitoID™ Web App

Access and use of MitoID™ web app

1. Go to Revvity | MitoID.

2. Register in the system and Sign In

3. Click on **New Analysis** button.

4. Introduce the Name (or ID) and press **Save Analysis.**

5. Drop or browse files to be analysed.

6. Press **Upload.** Do not refresh browser while data is being uploaded.

7. Press **Begin Analysis** and then **OK.**

8. When finished, status will be marked as Complete and result files can be downloaded.

Data Requirements

- The application accepts single and paired-ended sequencing data.

- Sequencing data files should contain a minimum of 250,000 reads per sample.

- Sequencing data files should have a **fastq.gz** format.

- Filenames should contain **_L001_R1_001.fastq.gz** structure.

- Filenames should not have any spaces and special characters in them.

- A minimum of 2 samples from the same sequencing run must be uploaded for batch analysis.

If you have any questions, please reach out at ngs@revvity.com

For research use only. Not for use in diagnostic applications