



# Quick Guide to mtDetect™ Web App

## Access and use of mtDetect™ web app

1. Send mail to [ngs@revvity.com](mailto:ngs@revvity.com) requesting access to the app.
2. Within 2 business days you will receive your username and password.
3. Go to [Revvity | mtDetect](#) and Sign In.
4. Click on **New Analysis** button.
5. Introduce the Name (or ID) and press **Save Analysis**.
6. Drop or browse files to be analysed.
7. Press **Upload**. Do not refresh browser while data is being uploaded.
8. Press **Begin Analysis** and then **OK**.
9. 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](mailto:ngs@revvity.com)

For research use only. Not for use in diagnostic applications

