



revvity

COSMOSID-HUB[®]
Microbiome

Quick Guide to CosmosID-HUB 16S Data Upload

Redeeming your CosmosID-HUB Credits

1. Go to <https://cosmosidhub.com/revvity/>
2. Complete the form, including your unique Kit ID* (you may enter multiple).
3. A member of the CosmosID-HUB team will reach out to complete your onboarding.
4. Once onboarding is completed, HUB credits will be issued to your account.
5. Upload your 16S data and run your microbiome study for up to 60 days.

16S Data Upload Requirements

- Amplicon 16S profiling workflow accepts *paired-end* sequencing data exclusively.
- Sequencing data files should not exceed a size of 100 MB in fastq.gz format.
- For each sample ID, two paired-end fastq files must be uploaded with "R1_001 " or "R2_001 " followed by the sequencing suffix (e.g., *Sample0123_R1_001.fastq.gz* + *Sample0123_R2_001.fastq.gz*)
- File names should not have any spaces and special characters in them.
- Maintaining an average base quality score >PHRED 20 is expected across all individual reads inside a fastq file.
- A minimum of 10 samples from the same sequencing run must be uploaded for batch analysis through Amplicon 16S profiling workflow, which uses DADA2's denoising and taxonomic classification framework for amplicon 16S analysis.
- The forward and reverse reads must overlap by at least 15 identical bases.

*If you have any questions and to receive your unique Kit ID, please reach out at ngs@revvity.com