## Simplify your 16S library prep and analysis.



Revvity now brings flexibility to your microbial community profiling projects with three 16S library prep kits, each covering different regions in the 16S rRNA gene. These kits are available alone or bundled with the CosmosID-Hub® analysis solution, delivering user-friendly access to version-controlled 16S pipelines.

- Robust, fast and easy library prep protocol
- Low input - Only 1 ng of input required
- Options now available with the CosmosID-Hub ${ }^{\circ}$ solution to simplify analysis
- Multiplex up to 384 libraries
- Automation protocols available for the Sciclone ${ }^{\text {m" }}$ NGS and NGSx workstations


## NEXTFLEX ${ }^{\text {T }}$ - 16 S V4 Amplicon-Seq kit 2.0

Researchers often choose the V4 region because of the availability of reference databases (e.g., SILVA). it provides sufficient diversity to allow discrimination of genus and sometimes bacterial species while avoiding excessive noise from hyper-variable regions. Additionally, it is relative short, making it an effective for choice Illumina ${ }^{\oplus}$ sequencing platforms.

## NEXTFLEX 16S V3-V4 Amplicon-Seq kit

This kit offer comparable benefits. Widely used and well established, V3-V4 data has contributed to community diversity metrics such as UniFrac and Faith's phylogenetic diversity.

## NEXTFLEX 16 S V1-V3 Amplicon-Seq kit

The V1-V3 region provides higher taxomic precision for specific microbial taxa. Researchers planning to use this region must weigh the trade-offs between taxonomic precision and comprehensive community profiling.


