

Full-Length 16S Sequencing



Studying Microbial Communities Using Long-Read Sequencing

The 16S ribosomal RNA (rRNA) gene is approximately 1.5 kb long and contains several conserved and hypervariable regions (V1-V9) that vary between different bacteria. These hypervariable sequences can be used to identify and characterize microbial diversity. Therefore, the 16S rRNA gene is a common marker to characterize microbial communities in various specimens.

Using the PacBio single molecule real-time (SMRT) technology, we accurately sequence the full-length 16S rRNA gene, covering all variable regions with an average HiFi read length of about 1.5 kb. The extraordinary accuracy and length of PacBio HiFi reads generated using circular consensus sequencing (CCS) mode allows microbial taxa detection at high resolution.

Applications of full-length 16S sequencing are diverse and include:

- ✕ Characterization of different microbial communities
- ✕ Microbial biomarker detection
- ✕ Disease monitoring
- ✕ Drug development



Explore Our Product for Full-Length 16S Sequencing

	Full-Length 16S Sequencing
Species	Bacteria
Sample types	Isolated DNA & various other sample types upon request
Target	Complete 16S rRNA gene (V1-V9 regions)
Read length	Approx. 1.5 kb
Sequencing platform	PacBio
Output	15,000 HiFi reads per sample
Included deliverables	Project report & FASTQ files

Want to Discover More?

We invite you to take a look at our website.
www.cebata.com/full-length-16s-sequencing





About Us

CeGaT was founded in 2009 in Tübingen, Germany. Our scientists are specialized in next-generation sequencing (NGS) for genetic diagnostics, and we also provide a variety of sequencing services for research purposes and pharma solutions. Our sequencing service portfolio is complemented by analyses suited for microbiome, immunology, and translational oncology studies.

Our dedicated project management team of scientists and bio-informaticians works closely with you to develop the best strategy to realize your project. Depending on its scope, we select the most suitable library preparation and conditions on our sequencing platforms.

**We would be pleased to provide you with our excellent service.
Contact us today to start planning your next project.**



Accredited by DAKKS according to
DIN EN ISO/IEC 17025:2018



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