Anaerostipes hadrus Genomic DNA

Cat. No.: LBGF-0925-GF147

This product is for research use only and is not intended for diagnostic use.

PRODUCT INFORMATION

Product Overview	This product contains high-quality, intact genomic DNA isolated from *Anaerostipes hadrus* Genomic DNA. It is a purified and ready-to-use DNA sample, ideal for a wide range of molecular biology applications, including PCR, qPCR, and Next-Generation Sequencing.
Target	*Anaerostipes* DNA
Derived From	*Anaerostipes hadrus*
Format	Lyophilized powder
Product Type	Purified Microbial Genomic DNA
Size	5 µg
DNA Concentration	Lot-Specific Data. These actual results will be clearly detailed on the Certificate of Analysis (CoA) included with your shipment.
Purity (A260/A280)	Lot-Specific Data These actual results will be clearly detailed on the Certificate of Analysis (CoA) included with your shipment.
Biosafety Level	Purified genomic DNA is considered non-infectious and can be handled at BSL-1.
Storage	2-8°C
Shipping Conditions	Ambient temperature

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Shelf Life	12 Months
Applications	1. Genomic Research and Sequencing. 2. PCR-based Detection and Quantification. 3. Quality Control and Assay Validation. 4.Gene Cloning and Expression.
Handling Procedure (Reconstitution)	1. Centrifuge the product tube at 12,000 rpm for 1 min. 2. Carefully add the required volume of sterile , nuclease-free ultrapure water. 3. Vortex the tube to ensure the product is fully dissolved. 4. To prevent degradation from repeated freeze-thaw cycles and to ensure long-term integrity, we recommend creating multiple single-use aliquots immediately after reconstitution. Store aliquots at −20°C for long-term storage. For immediate use, an aliquot may be stored at 4°C for up to 4 weeks.
Key Features	1. High-quality genomic DNA from an authenticated microbial strain. 2. High purity and integrity, suitable for a range of applications. 3. Specific concentration and total amount.
Key Precautions	1. Avoid repeated freeze-thaw cycles. 2. Use nuclease-free water and labware. 3. For best long-term results, use a buffer.

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