Benzonase Nuclease

Degrading DNA and RNA of any form

Benzonase Nuclease is an endonuclease that can degrade nucleic acid into 5'-monophosphate nucleotides of 2-5 bases. Because of its high efficiency in degrading DNA and RNA of any form (double-stranded, single-stranded, linear, cyclic), it is also called omnipotent nuclease. It has no protein cleavage activity.

Specifications

- Benzonase Nuclease
- Endotoxin-free Benzonase Nuclease
- Strep tagII Benzonase Nuclease
- Endotoxin-free Strep tagII Benzonase Nuclease

Quality Assurance (General)

QC Items	Specifications
Activity	More than 250kU/ml
Purity of protein	More than 99%
Activity of protein	More than 10^6 U/mg
Appearance	Colorless
Bacteria colony count	Less than 25 CFU/ml (250kU)
Endotoxin Level	Less than 50 EU/ml (250kU)

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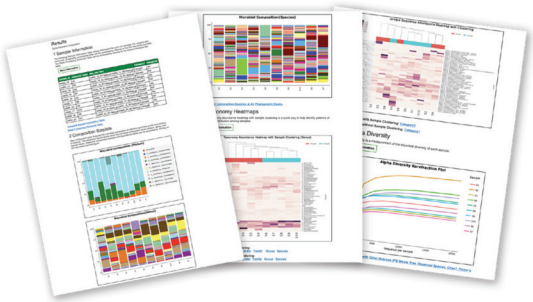
Microbiomics Services

Celebrate Your Discoveries

A Complete Microbiomics Solution

Get data worth celebrating! Zymo Research is proud to offer unbiased microbiome profiling services, from DNA extraction to sequencing and bioinformatics analysis. ZymoBIOMICS® microbiomics services achieve species-level resolution with 16S sequencing and strain-level resolution with shotgun sequencing. All services include publication-ready data.

End-to-End Microbiomics Services, Including Bioinformatics Analysis.



Comprehensive and User-Friendly Report Includes:

- Composition Bar Plots
- Taxonomy Heatmaps
- Alpha-Diversity
- Beta-Diversity
- Absolute Abundance for 16S/ITS
- Biomarker Discovery (LEfSe)

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NET-CAGE : Native Elongating Transcript Cap Analysis of Gene Expression

A novel solution for Genome-wide Enhancer / Promoter Annotation

NET-CAGE is a new NGS library preparation method using “cap-trapping” technology which enables you to detect **transcription start site** and **instantaneous transcriptional activity** of RNA pol II transcripts including **short-lived transcripts** such as **eRNAs** and **uaRNAs**.

- **Genome-wide High-resolution detection of active enhancers**—identify precise position of active enhancers by detection of bidirectional enhancer RNAs (eRNAs).
- **Detection of instantaneous gene expression**—detect accurate transcriptional activity at a given moment by quantifying nascent RNA pol II transcripts.
- **Accurate quantification of gene expression**—PCR-free library preparation process without fragmentation allows for more reliable quantification of gene expression than RNA-seq.
- **Applicable for cryopreserved cells and tissue samples**—The protocol does not contain any incorporation process for labeling.

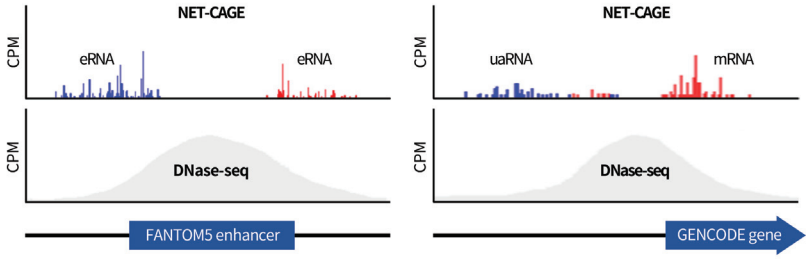

Fig.1. NET-CAGE signals around a region of FANTOM5 enhancer (left) and GENCODE gene (right).

NET-CAGE library preparation /analysis services	
NET-RNA extraction	100 USD/sample
CAGE library preparation for Illumina sequencers	500 USD/sample
Sequencing (Illumina HiSeq/ NextSeq)	250 USD/sample
CAGE bioinformatics analysis	250 USD/sample

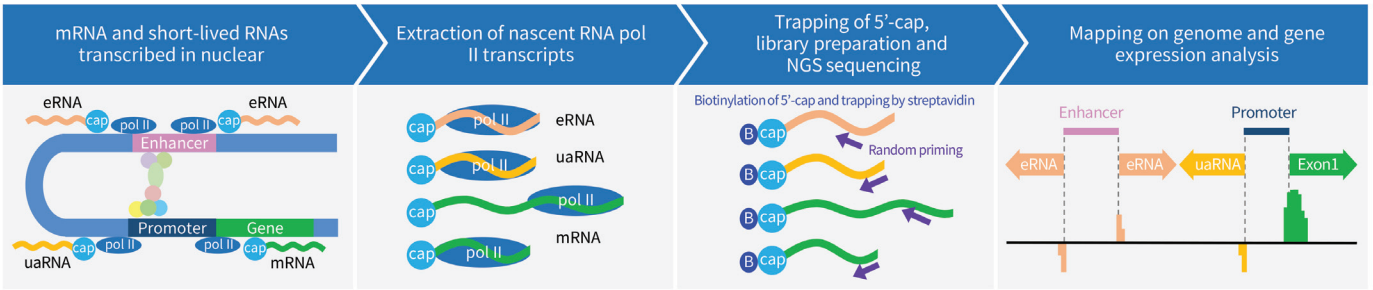

Fig.2. Workflow of the NET-CAGE. NET-CAGE is a unique NGS library preparation method using “cap-trapping” technology.

More than 250 papers using CAGE have been published!
Learn more about CAGE at **cage-seq.com**

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  Co-purify mRNA and small RNAs in the same purification run
- **Higher Yield**
  Get more RNA and miRNA than with conventional technologies
- **Simple Lysis**
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