AMPINEXT™ DNA Size Selection Kit

A complete set of optimized reagents for quick removal of DNA fragments of <150 bps for library preparation in next generation sequencing applications.

The AMPINEXT™ DNA Size Selection Kit is a complete set of optimized reagents for quick removal of DNA fragments of <150 bps for library preparation in next generation sequencing applications. The kit utilizes magnetic bead technology and is suitable for Illumina, Life Technologies (SOLiD), Ion Torrent, and Roche/454 platforms. It can also be used for removing undesired larger DNA fragments by optimizing the bead to DNA volume ratio accordingly. The indicated number of reactions can be performed for a standard 50 µl solution input DNA sample.

Ordering Information

Order Online »

ENZ-GEN506-0048	48Reactions
ENZ-GEN506-0096	96Reactions

Manuals, SDS & CofA

View Online »

- **Optimized fragment selection chemistries:** Complete separation of DNA fragments according to size.
- **Fast and straightforward:** Finished within 30 mins with no gels, columns or centrifugation are needed.
- **Efficient removal of primer-dimers:** No need for further clean-up steps.
- **High recovery of targeted DNA fragments**: Higher than 85% recovery of input DNA fragments.
- **Manual and automation friendly:** Scalable for use in single tube or 96-well plate format.

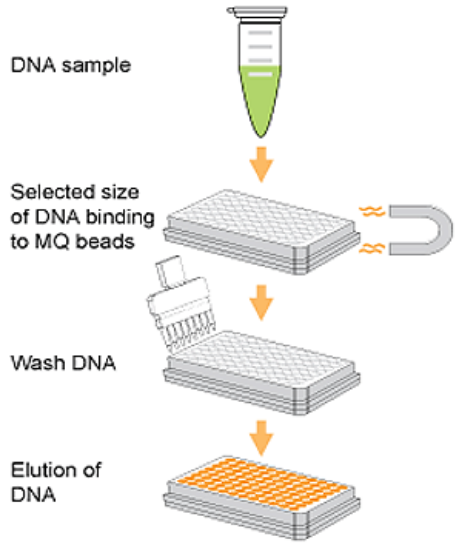

Figure 1. Schematic Procedure for using the AMPINEXT DNA Size Selection Kit

Handling & Storage

Use/Stability Upon receipt: Store the following components at 4°C: MQ Binding Beads, Elution Solution. Store all other components at room temperature. The kit is stable for at least 6 months from the shipment date, when stored properly.

Shipping Blue Ice

Regulatory Status

RUO - Research Use Only

Product Details

Application Notes

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Assay Time

30 minutes

Contents

MQ Binding Beads
Elution Solution
96-well plate

Technical Info / Product Notes

DNA size selection is necessary after DNA shearing as part of the library construction process for next generation sequencing, regardless of the platform used. Obtaining high recovery of selected DNA fragments is critical for the reduction of sequencing bias.

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