

DNA Purification Magnetic Beads

Cat. No. G950, G951

Store at 4°C.

Name	Quantity	Cat. No.
DNA Purification Magnetic Beads (5 ml)	4 x 1.25 ml (100 – 500 rxns)	G950
DNA Purification Magnetic Beads (25 ml)	25 ml (1000 – 5000 rxns)	G951

Product Description

abm's **DNA Purification Magnetic Beads** are magnetic particles coated with carboxyl groups that can reversibly bind to DNA and are formulated to specifically bind to DNA and purify out unwanted excess primers, adapter dimers, and salts and enzymes from a wide variety of reactions. It can be used for PCR purification, NGS library prep cleanup, or even DNA concentration. An important feature of the magnetic beads is its flexibility for fine-tuning DNA-Bead ratios for specific size selection of DNA fragments.

Key Features

- A cost effective alternative to other commercially available bead products, such as Ampure XP, NucleoMag, PCRClean DX, Pure Beads, etc.
- Replaces labour intensive and time consuming PCR purification
- Can be seamlessly integrated into NGS Library Prep workflows
- No centrifugation or filtration required
- No salt carryover

Protocol

This is a standard protocol for PCR purification using a bead:DNA ratio of 1.8X, but can be adapted for different bead:DNA ratios for size selection or different sample volumes. For larger sample volumes (eg. >100 μ), we recommend splitting the sample into 2 or more wells in a PCR plate or performing the purification in a 1.5 ml microcentrifuge tube with a suitable magnetic separation rack.

Additional Materials Required (not included)

- Freshly prepared 70% ethanol
- Nuclease-free water, Tris-Acetate (10 mM pH 8.0) or TE Buffer (10 mM Tris-Acetate
- pH 8.0, 1mM EDTA) for DNA elution
- Magnetic separation rack (for microcentrifuge tubes or 96-well plate format)

Before starting, ensure that the DNA Purification Beads have been warmed up to room temperature for 30 minutes, and prepare fresh 70% ethanol for the wash step.

- For a bead:DNA ratio of 1.8X, add 1.8 µl DNA Purification Beads per 1.0 µl of sample (eg. 90 µl beads per 50 µl sample) and pipette the entire volume 10 times to mix thoroughly. Allow the mixed samples to incubate at room temperature for 3-5 minutes for optimal binding.
- 2. Place the reaction plate or microfuge tube onto the magnetic separation rack for 5 minutes to allow for the solution to clear and the beads to collect on the magnet.
- 3. Keeping the plate or tube on the magnet for the entire wash step, carefully aspirate and discard the cleared solution. Avoid disturbing the beads.
- 4. Dispense 200 µl of 70% ethanol to the side of the tube or well opposite to where the beads are to avoid disturbing them and incubate for 30 seconds at room temperature. Aspirate and discard all of the ethanol from the well. Repeat for a total of 2 washes.
- 5. Allow the plate to air-dry for 2-5 minutes to remove residual ethanol. Air-dry the beads until they no longer appear shiny, but before they start to crack. If the beads are not dried enough, residual ethanol may affect downstream reactions. If the beads are overdried, it may be more difficult to elute the DNA from the beads completely.
- 6. Remove the plate or tube from the magnet and add 15-50 μl of the desired elution buffer (water, Tris or TE) to resuspend the beads. Pipette the entire volume 10 times to thoroughly resuspend the beads and ensure there are no clumps. Incubate at room temperature for 1 minute, then place the tube or plate on the magnet for 2-5 minutes.
- 7. Once the beads collect on the magnet, carefully transfer the eluant to a new tube. If there are beads carried over, place the eluant tube on the magnet to remove the residual beads and transfer the eluant into another new tube.
- 8. The purified DNA is ready for downstream applications or storage at -20°C.

General Notes

- Beads appear brown and may settle during storage. Vortex mix thoroughly for at least 30 seconds before use. It should appear homogenous and consistent in colour.
- Store tightly sealed at 4°C upon arrival. Freezing may reduce the binding efficiency of the beads and result in lower yield.