## PureLink™ Microbiome DNA Purification Kit

Purification of high-quality host DNA from stool samples

Catalog Number A29790

Pub. No. MAN0014334 Rev. A.0



**WARNING!** Read the Safety Data Sheets (SDSs) and follow the handling instructions. Wear appropriate protective eyewear, clothing, and gloves. Safety Data Sheets (SDSs) are available from **thermofisher.com/support**.

## Product description

The Invitrogen™ PureLink™ Microbiome DNA Purification Kit enables fast purification of high-quality microbial and host DNA from a wide variety of sample types. The kit uses proven PureLink™ spin-column technology for robust yields of purified DNA that is ready for downstream PCR, sequencing, or other applications.

Typical DNA recovery is  $3-15~\mu g$  from 0.2~g of human stool. Host DNA comprises up to 20% of the recovered DNA; the balance is microbial DNA.

#### Procedure overview

This guide describes purification of DNA from stool samples with a rapid procedure that is optimized for recovery of host DNA. (For purification of microbial and host DNA from stool samples, refer to Pub. no. MAN0014266.)

Host cells are easier to lyse than the microorganisms present in stool, therefore this procedure takes less time and omits the heat lysis step required for recovery of microbial DNA. A combination of chemical and brief mechanical disruption with specialized beads efficiently lyses host cells (and a small portion of easier-to-lyse microorganisms). Inhibitors are eliminated by precipitation using a proprietary cleanup buffer. The sample is then applied to a PureLink™ spin column, and the DNA that is bound to the column undergoes a single wash step before elution.

#### Kit contents

**Table 1** PureLink™ Microbiome DNA Purification Kit (Cat. no. A29790, 50 reactions)

Component	Quantity	Storage
S1—Lysis Buffer	40 mL	
S2—Lysis Enhancer	5 mL	15°C to 30°C
S3—Cleanup Buffer	12.5 mL	15-0 10 30-0
S4—Binding Buffer	45 mL	

Component	Quantity	Storage	
S5—Wash Buffer Concentrate <sup>[1]</sup>	13 mL		
S6—Elution Buffer	5 mL		
PureLink™ Spin Columns with Collection Tubes	50	15°C to 30°C	
PureLink™ Collection Tubes	ction Tubes 100		
Bead Tubes <sup>[2]</sup>	50		

<sup>[1]</sup> Add 13 mL of 96–100% ethanol before use. See "Before you begin" on page 2.

## Required materials

Unless otherwise indicated, all materials are available through thermofisher.com. MLS: Fisher Scientific (www.fisherscientific.com) or other major laboratory supplier.

Table 2 Required materials not included with the kit

Item	Source
Microcentrifuge capable of 14,000 $ imes g$	MLS
Vortex mixers, 2 <sup>[1]</sup>	MLS
For vortex bead homogenization: hands-free adapter for vortex mixer, with horizontal tube orientation	Fisher Scientific NC0070788 <sup>[2]</sup>
Adjustable pipettors, 100–1000 μL	MLS
Microcentrifuge tubes, DNase-free, 1.5 mL or 2.0 mL	MLS
Ethanol, 96–100%	MLS

<sup>[1]</sup> For vortex bead homogenization: we recommend using two mixers, one dedicated to the hands-free adapter.

 Table 3
 Additional materials required for stool samples

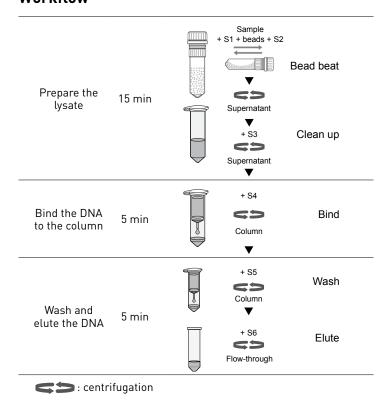
Item	Source
Corning™ Microspatula #3013	Fisher Scientific 14-245-102, or equivalent
Laboratory scale	MLS



<sup>[2]</sup> Ships separately.

<sup>[2]</sup> Cat. no. AM10024 (not available for sale) can also be used.

## Workflow



## Important procedural guidelines

## Sample input requirements and handling

- Collect stool samples according to your laboratory guidelines and experimental needs.
- Depending on the size of the feces, mix stool samples thoroughly to create a homogenous sample before weighing and transferring a portion to the Bead Tube.

The Corning $^{\text{\tiny{M}}}$  Microspatula is recommended because it is sturdy enough for sample mixing, and it fits the opening of the Bead Tube.

• Recommended input amount:

Source	Amount <sup>[1]</sup>
Human or other medium to large animals	0.2±0.05 g
Rodent or other small animals	0.1±0.05 g

<sup>[1]</sup> Do not exceed 0.25 g.

 Ensure that samples are mixed thoroughly with S1—Lysis Buffer and S2—Lysis Enhancer to create a homogenous sample.

One way to ensure thorough mixing is to vortex the tube with the cap down.

## Alternatives to the optimized procedure

 Horizontal bead-beating is most efficient for recovery of microbial DNA, but it is optional for recovery of host DNA (this procedure). **Note:** If a hands-free vortex adapter is used, balance the adapter to ensure proper movement of the adapter and optimal homogenization. Vortexing without the adapter is an option for low-throughput needs.

• This procedure is optimized for centrifugations at 14,000 × *g*. The PureLink™ Spin Columns with Collection Tubes can withstand up to 16,000 × *g*.

If your microcentrifuge is not capable of  $14,000 \times g$ , adjust the centrifugation times to ensure that all of the sample passes through the column.

#### Options for elution

- The DNA can be eluted from the column with 50–200 µL of S6—Elution Buffer, to optimize the concentration of the recovered DNA.
- Two sequential elution steps with S6—Elution Buffer might increase the yield slightly. For example, for a total elution volume of 100  $\mu$ L, either:
  - Perform two sequential elution steps with 50  $\mu L$  of S6–Elution Buffer, or
  - Perform the first elution step with 100  $\mu$ L of S6—Elution Buffer, then apply the flow-through (containing the eluted DNA) to the same column and repeat for a second elution.
- If desired, perform the final elution spin into nuclease-free 1.5-mL microcentrifuge tubes, instead of the collection tubes supplied with the kit, which do not have caps. Position the cap of the microcentrifuge tubes opposite the direction of rotation.

## Before you begin

#### Before first use of the kit: prepare S5—Wash Buffer

Add 13 mL of 96–100% ethanol to S5–Wash Buffer Concentrate , mix well, and store at room temperature.

#### Before each use of the kit

If precipitate is visible in S1—Lysis Buffer or S4—Binding Buffer, warm the buffers at 37°C for 5 minutes and shake well to dissolve the precipitate.

#### **Methods**

Perform the procedure at room temperature (20–25°C), unless otherwise indicated.

#### Prepare the lysate

a. Add sample and S1—Lysis Buffer to the Bead Tube, according to the sample source.

Source	Sample	S1—Lysis Buffer <sup>[1]</sup>
Human or other medium to large animals	0.2±0.05 g	600 μL
Rodent or other small animal	0.1±0.05 g	700 μL

 $<sup>^{[1]}</sup>$  Adjust the volume of S1—Lysis Buffer to bring the total mixture to ~800  $\mu L$ 

**b.** Cap securely, then vortex.

Ensure that the sample is thoroughly dispersed in the liquid.

- c. Add 100 μL of S2—Lysis Enhancer, cap securely, and vortex briefly.
- **d.** Homogenize by bead beating for 1 minute at maximum speed on the vortex mixer.
- **e.** Centrifuge at  $14,000 \times g$  for 5 minutes.
- f. Transfer up to 400 μL of the supernatant to a clean microcentrifuge tube.

**IMPORTANT!** A layer of debris may be present on top of the bead pellet. Avoid transfer of this debris with the supernatant.

g. Add 250 µL of S3—Cleanup Buffer, and vortex immediately.

Vortex immediately to ensure even dispersion of S3—Cleanup Buffer and uniform precipitation of inhibitors.

- **h.** Centrifuge at  $14,000 \times g$  for 2 minutes.
- i. Transfer up to 500 μL of the supernatant to a clean microcentrifuge tube, avoiding the pellet.

# 2 Bind the DNA to the column

- **a.** Add 900 μL of S4—Binding Buffer, and vortex briefly.
- **b.** Load 700  $\mu$ L of the sample mixture onto a spin column-tube assembly, and centrifuge at 14,000 × *g* for 1 minute.
- c. Discard the flow-through, and repeat step 2b with the remaining sample mixture.

Ensure that the entire sample mixture has passed into the collection tube by inspecting the column. If sample remains in the column, centrifuge again at  $14,000 \times g$  for 1 minute.

#### Wash and elute the DNA

- a. Place the spin column in a clean collection tube, add 500  $\mu$ L of S5—Wash Buffer, then centrifuge the spin column-tube assembly at 14,000  $\times$  g for 1 minute.
- **b.** Discard the flow-through, then centrifuge the spin column-tube assembly at  $14,000 \times g$  for 30 seconds.

The second centrifugation optimizes removal of S5—Wash Buffer, which could interfere with downstream applications.

- c. Place the spin column in a clean tube, add 100  $\mu L$  of S6—Elution Buffer, then incubate at room temperature for 1 minute.
- **d.** Centrifuge the spin column-tube assembly at  $14,000 \times g$  for 1 minute, then discard the column. The purified DNA is in the tube.

The DNA is ready for immediate use. Alternatively, store the purified DNA:

- At 4°C for up to 1 week.
- At –20°C for long-term storage.

## **Troubleshooting**

Observation	Possible cause	Recommended action
There is less than 400 µL of supernatant after lysis	For some samples, it can be difficult to withdraw 400 µL of supernatant at step 1f, while avoiding debris.	If <250 $\mu L$ of supernatant is transferred, add S1—Lysis Buffer to the transferred supernatant to bring the volume to 400 $\mu L$
	Stools from some grass-eating animals (for example, horse) may have a larger debris field over the bead pellet.	It is acceptable to penetrate the debris layer in these cases, to maximize lysate recovery. If <250 $\mu L$ of supernatant is transferred, add S1—Lysis Buffer to the transferred supernatant to bring the volume to 400 $\mu L$ .
Low yield	Inefficient lysis.	After step 1c, heat samples at 65°C for 10 minutes.
	Low levels of DNA in the sample.	Repeat the purification with more starting material.
	The recovered DNA is a mixture of host and microbial DNA; the host DNA typically comprises up to 20% of the total recovered DNA.	Do not exceed 0.25 g.
	For some challenging samples, too much starting material can result in low yield.	Repeat the purification with less starting material, and increase the volume of S1—Lysis Buffer so that the total volume of sample/S1—Lysis Buffer is 800 µL.
Inhibition of PCR or other Presence of inhibitors in the		Dilute the DNA 10- to 100-fold for PCR.
downstream reactions	recovered DNA.	After addition of S3—Cleanup Buffer, incubate the sample for 10 minutes on ice.
		Repeat the purification with less starting material. Increase the volume of S1—Lysis Buffer so that the total volume of sample/S1—Lysis Buffer is 800 µL.

## **Documentation and support**

## Revision history MAN0014334 (English)

R	evision	Date	Description
	A.0	September 2015	New document.

## Limited product warranty

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