

# PureLink™ Microbiome DNA Purification Kit

Purification of high-quality microbial DNA from rectal or environmental swab samples

Catalog Number A29790

Pub. No. MAN0014333 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](http://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 0.1–1 µg from rectal or environmental swab samples.

## Procedure overview

This guide describes purification of microbial DNA from rectal or environmental swab samples. (For purification of DNA from buccal, vaginal, or skin swab samples, refer to Pub. no. MAN0014268.) In this procedure, the microorganisms are efficiently lysed by a combination of heat, chemical, and mechanical disruption with specialized beads. 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	15°C to 30°C
S2—Lysis Enhancer	5 mL	
S3—Cleanup Buffer	12.5 mL	
S4—Binding Buffer	45 mL	
S5—Wash Buffer Concentrate <sup>[1]</sup>	13 mL	
S6—Elution Buffer	5 mL	

Component	Quantity	Storage
PureLink™ Spin Columns with Collection Tubes	50	15°C to 30°C
PureLink™ Collection 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.

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

## Required materials

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

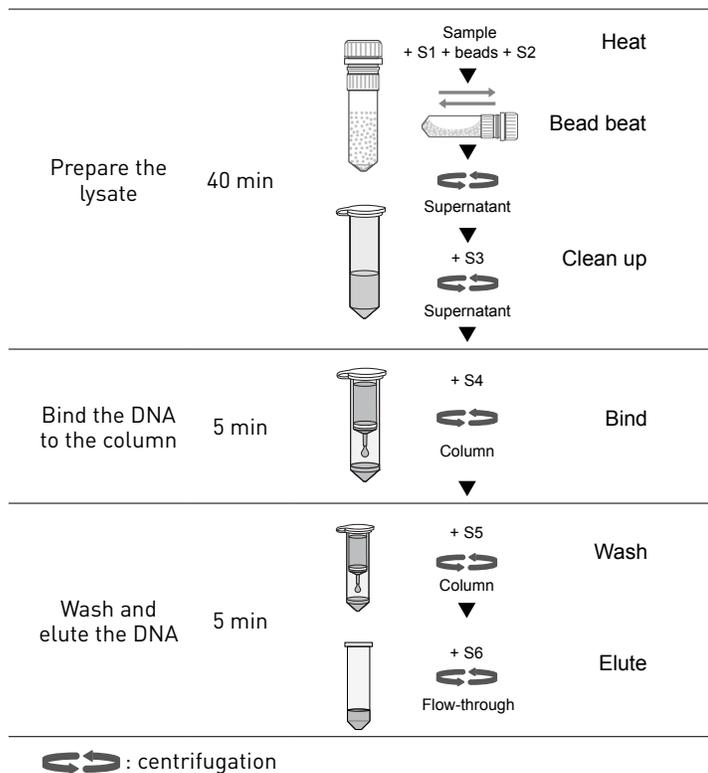
**Table 2** Required materials not included with the kit

Item	Source
Heat block, dry bath, or water bath, 65°C	MLS
<i>(Optional)</i> For dry bath, Lab Armor™ Beads	Cat. no. A12543
Microcentrifuge capable of 14,000 × 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>
<i>(Optional; alternative to vortex bead homogenization)</i> Bead mill homogenizer	Omni 19-040, or equivalent
Adjustable pipettors, 100–1000 µL	MLS
Microcentrifuge tubes, DNase-free, 1.5 mL or 2.0 mL	MLS
4N6FLOQSwabs™, Regular Tip, or equivalent	Cat. no. 4473979, or equivalent
Ethanol, 96–100%	MLS

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

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

## Workflow



## Important procedural guidelines

### Sample input requirements and handling

- The procedure was developed with 4N6FLOQSwabs™. Some testing was performed with Puritan™ PurFlock™ Ultra Flocked Swabs (Fisher Scientific Cat. no. 22-025-192).
- Collect swab samples according to your laboratory guidelines and experimental needs.
- Ensure that the swabs are broken to 1–3 cm in length, so that they fit inside the Bead Tube with the screw cap completely tightened.

### Alternatives to the optimized procedure

- This procedure is optimized for homogenization by bead beating on the vortex mixer with horizontal agitation. This is a cost-effective method for recovery of high-quality microbial DNA. Ensure that the vortex adapter enables horizontal agitation; adapters with a vertical tube orientation may not agitate adequately.

**Note:** Balance the vortex adapter to ensure proper movement of the adapter and optimal homogenization.

If you use a bead mill homogenizer, follow the manufacturer's instructions to optimize sample disruption.

- This procedure is optimized for centrifugations at  $14,000 \times g$ . The PureLink™ Spin Columns with Collection Tubes can withstand up to  $16,000 \times g$ .

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  $\mu\text{L}$  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  $\mu\text{L}$ , either:
  - Perform two sequential elution steps with 50  $\mu\text{L}$  of S6—Elution Buffer, or
  - Perform the first elution step with 100  $\mu\text{L}$  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  $37^\circ\text{C}$  for 5 minutes and shake well to dissolve the precipitate.

## Methods

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

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- 1 Prepare the lysate**
- Add 800  $\mu\text{L}$  of S1—Lysis Buffer to the Bead Tube, then add one swab.
  - Add 100  $\mu\text{L}$  of S2—Lysis Enhancer, cap securely, and vortex briefly.
  - Incubate at 65°C for 10 minutes.
  - Bead beat for 10 minutes at maximum speed on the vortex mixer.  
Use the hands-free adapter and horizontal agitation.
  - Centrifuge at 14,000  $\times g$  for 1 minute.
  - Transfer up to 400  $\mu\text{L}$  of the supernatant to a clean microcentrifuge tube.
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- IMPORTANT!** A layer of debris may be present on top of the bead pellet. Avoid transfer of this debris with the supernatant.
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- Add 250  $\mu\text{L}$  of S3—Cleanup Buffer, and vortex immediately.  
Vortex immediately to ensure even dispersion of S3—Cleanup Buffer and uniform precipitation of inhibitors.
  - Centrifuge at 14,000  $\times g$  for 2 minutes.
  - Transfer up to 500  $\mu\text{L}$  of the supernatant to a clean microcentrifuge tube, avoiding the pellet.
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- 2 Bind the DNA to the column**
- Add 900  $\mu\text{L}$  of S4—Binding Buffer, and vortex briefly.
  - Load 700  $\mu\text{L}$  of the sample mixture onto a spin column-tube assembly, and centrifuge at 14,000  $\times g$  for 1 minute.
  - 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.
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- 3 Wash and elute the DNA**
- Place the spin column in a clean collection tube, add 500  $\mu\text{L}$  of S5—Wash Buffer, then centrifuge the spin column-tube assembly at 14,000  $\times g$  for 1 minute.
  - 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.
  - Place the spin column in a clean tube, add 100  $\mu\text{L}$  of S6—Elution Buffer, then incubate at room temperature for 1 minute.
  - 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.
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## Troubleshooting

Observation	Possible cause	Recommended action	
Low yield	Inefficient lysis.	Heat samples at 95°C for 5–10 minutes instead of at 65°C for 10 minutes.	
		Heat at 95°C for 5–10 minutes, and bead beat for a longer time or using a higher power setting.	
	Low levels of DNA in the sample.	Repeat the purification with more starting material.	
Inhibition of PCR or other downstream reactions	For some challenging samples, too much starting material can result in low yield.	Repeat the purification with less starting material.	
		Presence of inhibitors in the recovered DNA.	Dilute the DNA 10- to 100-fold for PCR.
		After addition of S3—Cleanup Buffer, incubate the sample for 10 minutes on ice.	
		Repeat the purification with less starting material.	

## Documentation and support

### Revision history MAN0014333 (English)

Revision	Date	Description
A.0	September 2015	New document.

### Limited product warranty

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