Part No.: H-020-000834-00

MGIEasy

Stool Microbiome DNA Extraction Kit II

Instructions for Use

Version: 3.0

Leading Life Science Innovation

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Research Use Only

Wuhan MGI Tech Co., Ltd.

About the instructions for use

This instructions for use is applicable to MGIEasy Stool Microbiome DNA Extraction Kit II. The version of the instructions for use is 3.0 and the kit version is 1.0.

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Revision history

Version	Date	Description
3.0	September 13, 2024	Added a warning about Buffer PC
2.0	December 5, 2023	Deleted wrong catalog number and corrected the kit name
1.0	November 9, 2023	Initial release

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Chapter 1 Introduction

1.1 Product name

MGIEasy Stool Microbiome DNA Extraction Kit II

1.2 Specifications

Kit name	Model	Cat. No.	Specification
MGIEasy Stool Microbiome DNA Extraction Kit II	SD03T-96	940-001247-00	96 Preps
MGIEasy Stool Microbiome DNA Extraction Kit II	SD03T-384	940-001246-00	384 Preps

1.3 Intended use

This set is used to extract, enrich and purify nucleic acids.

1.4 Working principle

This kit is used to extract or purify microbiome DNA from fresh or frozen human stool samples, which is mainly used in metagenome sequencing. By using this product, DNA is captured by the unique, high-binding, super-paramagnetic magnetic beads and washed by a specific wash buffer to remove impurities. After being dried, the DNA in magnetic beads is eluted by the elution buffer and high-purity as well as high-quality DNA is obtained. The extracted microbiome DNA can be used for various routine applications, including enzyme digestion, PCR, real-time PCR, library preparation, and high-throughput sequencing.

1.5 Main components

Table 1 MGIEasy Stool Microbiome DNA Extraction Kit II (SD03T-96)
Cat. No.: 940-001247-00

Name	Component	Specification	Storage condition	Validity period	Transportation condition
MGIEasy Stool Microbiome DNA Extraction Kit II Cat. No.: 940-001247-00	Buffer PC	35 mL/tube×1	2 ℃ to 30 ℃	12 months	2 ℃ to 30 ℃
	Buffer PL	25 mL/tube×1			
	Buffer PH	10 mL/tube×1			
	Buffer PF	20 mL/tube×1			
	Buffer W1	20 mL/tube×1			
	Buffer W2	24 mL/tube×1			
	Buffer PB	15 mL/tube×1			
	Magnetic beads-T	2 mL/tube×1			

Table 2 MGIEasy Stool Microbiome DNA Extraction Kit II (SD03T-384)
Cat. No.: 940-001246-00

Name	Component	Specification	Storage condition	Validity period	Transportation condition
MGIEasy Stool Microbiome DNA Extraction Kit II Cat. No.: 940-001246-00	Buffer PC	140 mL/tube×1	2 ℃ to 30 ℃	12 months	2 ℃ to 30 ℃
	Buffer PL	100 mL/tube×1			
	Buffer PH	40 mL/tube×1			
	Buffer PF	80 mL/tube×1			
	Buffer W1	80 mL/tube×1			
	Buffer W2	96 mL/tube×1			
	Buffer PB	60 mL/tube×1			
	Magnetic beads-T	8 mL/tube×1			

Chapter 2 Applicable device

- MGISP-960RS High-throughput Automated Sample Preparation System (Configuration 1/2/6/7/8/9/10)
- MGISP-NE384RS Automated Nucleic Acid Extractor

Chapter 3 Sample requirements

3.1 Applicable sample

This product is applicable to freshly extracted stool, saliva and swab samples.

3.2 Sample amount requirements

		Manual extraction	Extraction on MGISP-960RS	Extraction on MGISP-NE384RS
Stool	Solid or semi-solid stool	180 mg to 200 mg	180 mg to 200 mg	180 mg to 200 mg
	Stool with stool preservative	200 μL to 1000 μL	200 μL to 1000 μL	200 μL to 1000 μL
Saliva	Fresh saliva	500 μL	500 μL	500 μL
	Saliva with saliva preservative	1 mL	1 mL	1 mL
Swab	Swab	1 mL	1 mL	1 mL
	Swab with saliva preservative	1 mL	1 mL	1 mL

3.3 Sample storage

- Samples that are collected and placed in the tube with stool preservative within 2 hours can be stored for 7 days at room temperature and for 1 year at -80 ℃ .
- Samples that are collected and placed in the sampling cup within 2 hours can be stored for 1 year at -80 ℃ or in dry ice.

- If the freshly collected samples will be used in a short time, store them at 4 ℃ and extract them on the same day.
- To avoid frequent freeze-thaw cycles, when thawing the samples for the first time, add the stool preservative into the frozen stool samples in the ratio of 4:1. For example, for 2 g of frozen stool samples, you need to add 8 mL of stool preservative. Mix the tube until the color of samples changes completely. Use a wide-bore pipette tip to transfer 3 mL to 5 mL of sample suspension to a 5 mL centrifuge tube and store the tube at -80 ℃ .
- Do not freeze and thaw frozen samples frequently. Otherwise, the DNA quality may decrease.

3.4 Sample transportation

- For samples stored with stool preservative, transport them at room temperature for up to 7 days.
- For samples stored in a sampling cup, use the dry ice for transportation for up to 7 days.
- During transportation, avoid frequent freeze-thaw cycles.

3.5 Sample safety

All samples are regarded potentially infectious. All samples should be extracted after being inactivated according to relevant national regulations.

Chapter 4 Operation

4.1 Preparing materials

Prepare the following materials:

Table 3 User-supplied materials

Type	Item	Description
Equipment	Mini centrifuge	• 2.0 mL • With a speed no less than 12000 rpm
	Vortex mixer	With a speed no less than 2500 rpm

Type	Item	Description
Equipment	Thermomixer compact	None
	1.5 mL magnetic rack	None
	Pipette	1 mL/200 µL/20 µL
Reagent	Absolute ethanol	Analytically pure
	Isopropanol	Analytically pure
	MGI stool sample collection set	MGI，1000003702
	Proteinase K	• 20 mg/mL • Only used for extracting saliva samples and swab samples
	MGI stool preservative	MGI，940-000475-00
	MGIEasy tissue grinding beads	MGI，940-000136-00
Consumables	Pipette tips	1 mL/200 µL/20 µL
	Centrifuge tube	• 2 mL/1.5 mL • DNase-free and RNase-free

4.2 Pretreating samples

Pretreat samples according to the sample type.

Tips Before use, frozen samples need to be thawed and mixed thoroughly.

4.2.1 Stool sample

Perform the following steps:

1. Perform different steps according to the stool sample type:
   - Solid and semi-solid samples
     a. Add 180 mg to 220 mg of stool samples into a 2 mL centrifuge tube.
     b. Add 1 mL of stool preservative into the tube.
        Tips 1× PBS can replace the stool preservative.
     c. Vortex the tube at no less than 2500 rpm for 3 to 5 minutes until the color of sample changes and samples suspend evenly.
     d. Use a pipette tip to transfer 200 µL to 1000 µL of sample suspension to a new 2 mL centrifuge tube.

Tips To prevent the pipette tip from being blocked by impurities, you can cut a part of the tip.

- Samples with stool preservative

  a. Vortex the tube at no less than 2500 rpm for 3 to 5 minutes until the color of sample changes and samples suspend evenly.

  b. Use a pipette tip to transfer 200 µL to 1000 µL of sample suspension to a new 2 mL centrifuge tube.

  Tips
  - The recommended volume is 1000 µL.
  - To prevent the pipette tip from being blocked by impurities, you can cut a part of the tip.

2. Centrifuge the tube at 12000 rpm for 2 minutes. Use a pipette tip to slowly aspirate the supernatant avoiding aspirating the solid precipitation at the bottom of the tube.
3. Add 100 µL of grinding beads or 0.15 g of grinding beads into the 2 mL centrifuge tube.
4. Add 350 µL of Buffer PC and 250 µL of Buffer PL into the tube.
5. Vortex the tube at no less than 2500 rpm for 60 seconds.

   Tips
   - If samples remain at the bottom of the tube, use the pipette tip to help disperse the suspension.
   - If more G+ bacteria is needed, it is recommended to use grinding mill (Recommended brand: Mobio/QIAGEN) to grind the sample at 30 Hz at 1800 rpm for 5 minutes.
6. Place the tube at a thermomixer compact at 70 °C at 1000 rpm for 20 minutes.
7. Centrifuge the tube at 12000 rpm for 2 minutes.
8. Use a pipette tip to transfer 400 µL of supernatant to a new 1.5 mL centrifuge tube.

   Tips That the solution at the top is layered is normal. Go to the next step.
9. Add 100 µL of Buffer PH into the tube. Vortex the tube to mix it thoroughly and place it on ice or into a refrigerator at 4 °C for 10 minutes.
10. Centrifuge the tube at 12000 rpm for 2 minutes.
11. Use a pipette tip to transfer 400 µL of supernatant to a new 2 mL centrifuge tube and mark it for further use.

4.2.2 Saliva sample

Perform the following steps:

1. Perform different steps according to the sample type:

- Fresh saliva sample
  a. Add 500 µL of sample, and 500 µL of stool preservative into a new 2 mL centrifuge tube, and mix the tube.
  Tips 1× PBS can replace the stool preservative.
  b. Centrifuge the tube at 12000 rpm for 2 minutes.
  c. Use a pipette tip to remove 900 µL of supernatant.
- Saliva sample with saliva sample preservative
  a. Add 1 mL of sample into a new 2 mL centrifuge tube.
  b. Centrifuge the tube at 12000 rpm for 2 minutes.
  c. Use a pipette tip to remove 900 µL of supernatant.
- Fresh swab sample
  a. Add 1.5 mL of PBS or stool preservative into a new sampling tube.
  b. Insert the swab head into the oral cavity or use the swab to touch the tongue. After collection, immerse the swab head in the solution completely.
  c. Tighten the cap, vortex the tube to mix the tube thoroughly.
  d. Add 1 mL of sample into a new 2 mL centrifuge tube.
  e. Centrifuge the tube at 12000 rpm for 2 minutes.
  f. Use a pipette tip to remove 850 µL of supernatant and leave the swab head in the tube.
- Swab sample with stool preservative
  a. Add 1 mL of sample into a new 2 mL centrifuge tube.
  b. Centrifuge the tube at 12000 rpm for 2 minutes.
  c. Use a pipette tip to remove 850 µL of supernatant and leave the swab head in the tube.

2. Add 100 µL of grinding beads or 0.15 g of grinding beads into the 2 mL centrifuge tube.
3. Add 400 µL of Buffer PL and 10 µL of Proteinase K into the tube.
4. Vortex the tube at no less than 2500 rpm for 60 seconds.
   Tips If more G+ bacteria is needed, it is recommended to use grinding mill (Recommended brand: Mobio/QIAGEN) to grind the sample at 30 Hz at 1800 rpm for 5 minutes.
5. Place the tube at a thermomixer compact at 70 ℃ at 1000 rpm for 20 minutes.
6. Centrifuge the tube at 12000 rpm for 2 minutes.
7. Use a pipette tip to transfer 400 µL of supernatant to a new 2 mL centrifuge tube and mark it for further use.

4.2.3 Swab sample

Perform the following steps:

1. Perform different steps according to the sample type:
   - Fresh swab sample
     a. Add 1.5 mL of stool preservative into a new sampling tube.
     Tips 1× PBS can replace the stool preservative.
     b. Insert the swab head into the oral cavity or use the swab to touch the tongue. After collection, immerse the swab head in the solution completely.
     c. Tighten the cap, vortex the tube to mix the tube thoroughly.
     d. Add 1 mL of sample into a new 2 mL centrifuge tube.
     e. Centrifuge the tube at 12000 rpm for 2 minutes.
     f. Use a pipette tip to remove 850 µL of supernatant and leave the swab head in the tube.
   - Swab sample with stool preservative
     a. Add 1 mL of sample into a new 2 mL centrifuge tube.
     b. Centrifuge the tube at 12000 rpm for 2 minutes.
     c. Use a pipette tip to remove 850 µL of supernatant and leave the swab head in the tube.
2. Add 100 µL of grinding beads or 0.15 g of grinding beads into the 2 mL centrifuge tube.
3. Add 400 µL of Buffer PL and 10 µL of Proteinase K into the tube.
4. Vortex the tube at no less than 2500 rpm for 60 seconds.
   Tips If more G+ bacteria is needed, it is recommended to use grinding mill (Recommended brand: Mobio/QIAGEN) to grind the sample at 30 Hz at 1800 rpm for 5 minutes.
5. Place the tube at a thermomixer compact at 70 ℃ at 1000 rpm for 20 minutes.
6. Centrifuge the tube at 12000 rpm for 2 minutes.
7. Use a pipette tip to transfer 400 µL of supernatant to a new 2 mL centrifuge tube and mark it for further use.

4.3 Extracting the nucleic acids

Tips You can extract the nucleic acids manually or on automation devices. For automated nucleic acid extraction, ensure that you prepare applicable consumables.

4.3.1 Extracting the nucleic acids manually

Before extraction, add absolute ethanol into Buffer W1 and Buffer W2, and add isopropanol into Buffer PF according to the label.

Perform the following steps:

1. Take out the tube with pretreated samples and add 500 µL of Buffer PF and 20 µL of Magnetic beads-T into the tube. Vortex the tube and place it at room temperature for 10 minutes during which vortex the tube 3 to 5 times with 10 seconds for each time.

   Tips Place Magnetic beads-T at room temperature for 30 minutes in advance and mix it thoroughly before use.

2. Place the tube on the magnetic rack for 2 minutes. When Magnetic beads-T is adsorbed completely on the tube wall, use a pipette to remove the supernatant.
3. Remove the tube from the rack. Add 500 µL of Buffer W1 into the tube and vortex the tube for 2 minutes.

   Tips After adding Buffer W1, do mix the tube thoroughly. Otherwise, the purity of nucleic acid may decrease.

4. Place the tube on the magnetic rack for 1 minute. When Magnetic beads-T is adsorbed completely on the tube wall, use a pipette to remove the supernatant.
5. Remove the tube from the rack. Add 600 µL of Buffer W2 into the tube and vortex the tube for 1 minute.
6. Place the tube on the magnetic rack for 1 minute. When Magnetic beads-T is adsorbed completely on the tube wall, use a pipette to remove the supernatant.
7. Repeat steps 5 to 6 once. Remove the liquid in the tube as much as possible.
8. Place the tube on the magnetic rack. Decap and dry the tube for 5 minutes until no liquid remains on the tube.
9. Remove the tube from the rack. Add 50 µL to 150 µL of Buffer PB into the tube and vortex the tube to mix thoroughly.
10. Place the tube at a thermomixer compact at 56 ℃ at 1000 rpm for 5 minutes
11. Place the tube on the magnetic rack. When Magnetic beads-T is adsorbed completely on the tube wall, use a pipette to transfer the supernatant to a new 1.5 mL tube. Mark the tube and store it at -20 ℃ .

4.3.2 Extracting the nucleic acids automatically on MGISP-960RS

4.3.2.1 Preparing consumables

According to the following table, prepare consumables for a workflow of automated extraction on MGISP-960RS and place them at room temperature until use.

Name	Brand	Cat. No.	Number
250 µL automated filter tips	MGI	1000000723	6
1.3 mL U-bottom 96-well deep-well plate	MGI	1000004644	5
96 Well Half-skirt PCR Plate	MGI	1000000671	1
Adaptor for Half-Skirt PCR Plate	MGI	010-901739-00	1

Tips The combination of the adaptor for half-skirt PCR plate (MGI, 010-901739-00) and 96-well half-skirt PCR plate can be used as the hard-shell thin-wall 96-well skirted PCR plates (MGI, 1000012059). The adaptor for half-skirt PCR plate is needed for MGISP-960RS configuration 1/2/6/7/8/10 but not for MGISP-960RS configuration 9.

4.3.2.2 Preparing reagents

Perform the following steps:

1. Add absolute ethanol into Buffer W1 according to the label.
2. Add absolute ethanol into Buffer W2 according to the label.
3. Add isopropanol into Buffer PF according to the label.
4. Prepare the Mix with 300 µL of Buffer PF and 20 µL of Magnetic beads-T for each reaction and mix it.
5. Take out 4 96-well deep-well plates. Add sample and reagents according to the following table:

Reagent name	Adding volume (µL/well)	Plate
Mix+sample	320+240	1.3 mL U-bottom 96-well deep-well plate
Buffer W1	400	1.3 mL U-bottom 96-well deep-well plate
Buffer W2	800	1.3 mL U-bottom 96-well deep-well plate

Reagent name	Adding volume (μL/well)	Plate
Buffer PB	120	1.3 mL U-bottom 96-well deep-well plate

4.3.2.3 Preparing samples

You can extract 1 to 96 samples on MGISP-960RS.

Perform the following steps:

1. Pretreat samples according to *Pretreating samples on Page 5*.
2. Aspirate 240 μL of sample to the deep-well plate containing the Mix. Ensure that no bubble exists at the bottom of the plate and that no liquid exists on the wall of the well. Place the plate on ice until use.

4.3.2.4 Starting extraction

Perform the following steps:

1. Switch to the | position to power on the device.
2. Turn on the computer and the desktop appears. Double-click  to run the software.
3. Select **User** and **Real**. Enter the password.
4. Click **Login** to enter the main interface.
5. On the upper-right corner of the control software, click  and select **WDesigner**. The home interface is displayed.
6. Ensure that the application file in the *.wfex* format has been prepared.
7. Click  in the toolbar and find the file location in the pop-up window.
8. Select the file and click **Open**, fill in the **Application** and **Project**, and click **Confirm** to save the application file. Then this application file can be executed in the control software.
9. After the file is imported successfully, click  in the toolbar.
10. Click **Initialize** on the top of the interface to start initializing.

    You will be prompted after a successful initialization.
11. Click  on the left of the interface, and select **Clean** > **Pre-clean** > **Start**.
12. Follow the on-screen instructions to complete operations and click **Continue**. The UV lamp and air filter start working.

    CAUTION The ultraviolet radiation is harmful to the human body, so do not open the door after the pre-clean starts.

13. Import the application scripts according to *MGISP-100&MGISP-960 Application Script Installation Instructions*.
14. Tap ☰ >**Run Wizard** to enter the Run Wizard interface.
15. Click the drop-down list of **Solution** and select **JB-A09-149 MGIEasy Stool Microbiome DNA Extraction Kit II_RV1.0_SV1.0**. Click the drop-down list of **Script** and select **Microbiome Genomic DNA Extraction for Stool II_V1.0.py**. Place samples, reagents and consumables according to the following figure:

Name	Position
250 µL automated filter tips	Pos1 to Pos6
Waste plate	Pos15
Adaptor for half-skirt PCR plate and 96-well half-skirt PCR plate	Pos16
Buffer W1	Pos17
Buffer W2	Pos18
Mix+sample	Pos20
Buffer PB	Pos22

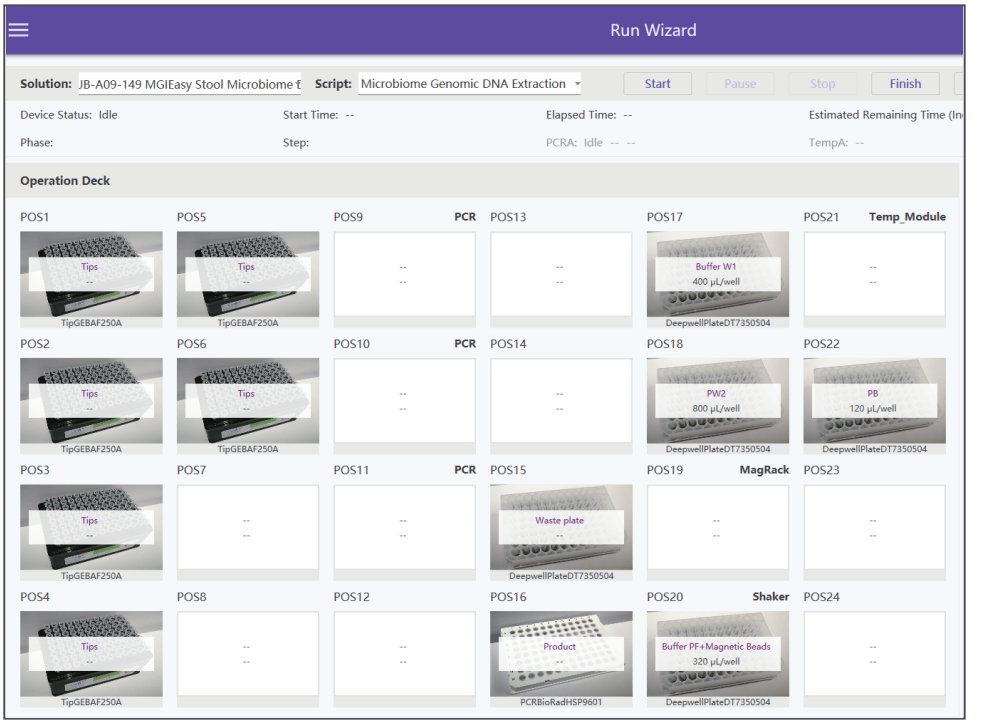

Figure 1 Plate position

16. Click **Start**. The extraction workflow starts. It takes about 1 hour.

    During the workflow, click **Pause** to pause and click **Resume** to resume the workflow if required.

17. At the end of the workflow, remove the DNA product from Pos16.

    If the product is not used immediately, seal and store it in a freezer at -80 ℃ .

18. Dispose of the used deep-well plates, PCR plates, and waste bag.

4.3.3 Extracting the nucleic acids automatically on MGISP-NE384RS

4.3.3.1 Preparing consumables

According to the following table, prepare consumables for a workflow of automated extraction on MGISP-NE384RS and place them at room temperature until use:

Name	Brand	Cat. No.	Number
2.2 mL V-bottom 96-well deep-well plate	MGI	1000008088	24
96-well tips comb	MGI	1000025661	4

4.3.3.2 Preparing reagents

Perform the following steps:

1. Add absolute ethanol into Buffer W1 according to the label.
2. Add absolute ethanol into Buffer W2 according to the label.
3. Add isopropanol into Buffer PF according to the label.
4. Use Milli-Q water or nuclease-free water to dilute the Magnetic beads-T at a ratio of 1 to 14 (Magnetic beads-T to Milli-Q water or nuclease-free water). Each sample needs 300 µL of Magnetic beads-T. Please prepare enough diluted magnetic beads according to the number of samples.
5. Take out 6 96-well deep-well plates. Add sample and reagents according to the following table:

Reagent name	Adding volume (µL/well)	Plate
Mix+sample	500 + 400	2.2 mL V-bottom 96-well deep-well plate
Diluted magnetic beads	300	2.2 mL V-bottom 96-well deep-well plate

Reagent name	Adding volume (μL/well)	Plate
Buffer W1	500	2.2 mL V-bottom 96-well deep-well plate
Buffer W2-1	600	2.2 mL V-bottom 96-well deep-well plate
Buffer W2-2	600	2.2 mL V-bottom 96-well deep-well plate
Buffer PB	150	2.2 mL V-bottom 96-well deep-well plate

4.3.3.3 Preparing samples

You can extract 1 to 384 samples on MGISP-NE384RS.

Perform the following steps:

1. Pretreat samples according to *Pretreating samples on Page 5*.
2. Aspirate 400 μL of sample to the deep-well plate containing Buffer PF. Ensure that no bubble exists at the bottom of the plate and that no liquid exists on the wall of the well. Place the plate on ice until use.

4.3.3.4 Starting extraction

Perform the following steps:

1. Switch to the | position to power on the device.
2. Turn on the computer and the desktop appears. Double-click the icon of MGISP-NE384RS to run the software.
3. Select **User** and **Real**, and enter the password. Click **Login** to enter the main interface.
4. Click **Initialize** on the top of the interface to start initializing.

   You will be prompted after a successful initialization.
5. Click **Process manage** >  to import the script.
6. Click  > **Workflow**. Click the drop-down list of **Script** and select **MGI Microbiome DNA Extraction for Stool**. Place samples, reagents and consumables according to the following table:

Reagent name	Position
Sample+Mix	Pos1
Diluted magnetic beads	Pos2

Reagent name	Position
Buffer W1	Pos3
Buffer W2-1	Pos4
Buffer W2-2	Pos5
Buffer PB	Pos6

7. Place 96-well tips comb according to the number of samples.
8. Click **Run**. Select the required lanes and tips comb in the pop-up window. Click **OK**. The device starts extraction according to the following table. The whole workflow takes about 30 minutes.

   During the workflow, click **Pause** to pause and click **Resume** to resume the workflow if required.

   Heating settings are as follows:

   Lysis temperature: 37 ℃ . Lysis heating ends at step 1.

   Elution temperature: 56 ℃ . Elution heating starts at step 5.

Step No.	1	2	3	4	5	6	7
Step name	Beads	Bind	Wash1	Wash2-1	Wash2-2	Elution	Release
Position	2	1	3	4	5	6	2
Volume (μL)	300	900	600	700	700	150	300
Delay time (s)	0	0	0	0	0	90	0
Mix	True	True	True	True	True	True	True
Mix type	Normal	Normal	Normal	Normal	Normal	Normal	Normal
Mix rate	High	Middle	High	High	High	High	High
Mix time (s)	15	300	100	90	90	180	10
Collect	True	True	True	True	True	True	False
Collect mode	Cycle	Cycle	Cycle	Cycle	Cycle	Cycle	/
Collect cycle	5	5	3	3	3	20	/
Collect time (s)	1	1	1	1	1	1	/
Dialog	False	False	False	False	False	False	False

9. After the program ends, remove the 96-well plate from POS6 and transfer the DNA product to a new tube.

   If the product is not used immediately, seal it and store it in a freezer at -80 ℃ .

10. Transfer the 96-well tips comb with Magnetic beads-T to the medical waste bag. Dispose of the used deep-well plates, PCR plates and waste bag.

Chapter 5 Warnings and precautions

- This product is for research use only. Please read the instructions for use carefully before use.
- Before experiment, be sure to be familiar with and master the operation methods and precautions of various devices to be used.
- It is normal that the color remains in the extracted product from stool samples, which will not affect the downstream applications, if you extract samples completely according to the instructions for use.
- Direct contact with skin and eyes should be avoided for all samples and reagents. Do not swallow. If accidental ingestion occurs, please get medical attention immediately. If skin exposure occurs, rinse with large amounts of water and get medical attention if irritation persists.
- Do not freeze and thaw frozen samples frequently. Otherwise, the DNA quality may decrease.
- Before use, take out all components in the reagent kit, equilibrate to room temperature (10 ℃ to 30 ℃) and mix them thoroughly before adding to wells. Unless otherwise specified, operate at room temperature.
- Before use, ensure that absolute ethanol is added into Buffer W1 and Buffer W2 according to the label, and that isopropanol is added into Buffer PF according to the label.
- It is normal for the Buffer PC to turn dark brown, and the quality of the reagent is not affected.
- Please use micropipette when adding sample and reagents.
- All reagents should be stored and used according to requirements. Mix thoroughly before use.
- All samples and wastes should be disposed of in accordance with relevant regulations.
- Do not use expired products.

Appendix 1 Manufacturer information

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