TIANGEN®

TGuide Smart Soil/Stool DNA Kit

For purification of inhibitor-free DNA from soil and stool samples.

TECHNICAL MANUAL

Cat. no. GDP612-DE

Note: To use the TGuide Smart Soil/Stool DNA Kit, you must have the TGuide Smart Soil/Stool DNA (program no. DP612) installed on the TGuide S16/S32 pro Nucleic Acid Extractor.

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This product is for scientific research use only. Do not use in medicine, clinical treatment, food or cosmetic

Table Contents

TGuide Smart Soil / Stool DNA Kit

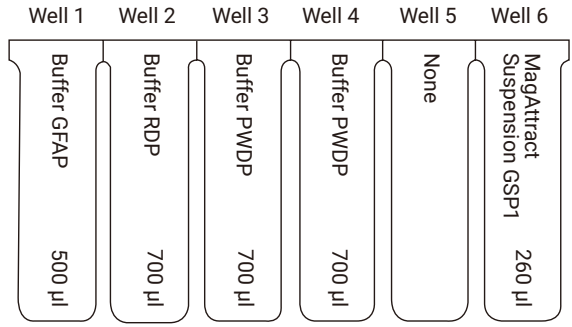
Cat. no. GDP612-DE

Kit Contents

Contents		GDP612-DE (48 preps)
GDP612-DH	Buffer SA	30 ml
	Buffer SC	5 ml
	Buffer SH	10 ml
	Soil /Stool DNA Reagents	48
	1 mm Grinding Beads	15 g
	RNase A (100 mg/ml)	200 μl
	Buffer TB	15 ml
OSE-TGA-S36	TGuide Smart Tip Comb	12 pcs

Note: OSE-TGA-S36 is shipped and packaged separately

Soil/stool DNA reagent composition



Storage condition

All components of the kit can be stored in dry conditions at room temperature (15~30°C) for 12 months. If the solution precipitates, it can be preheated in a water bath at 37°C for 10 min before use to dissolve the precipitation, without affecting the effect.

Product

This kit adopts a unique dehumification buffer system to remove humic acid from soil samples as much as possible. It is also supplied with grinding beads which effectively break up soil samples in a variety of complex components to ensure the integrity of genomic DNA extracted from soil. Besides, it is also suitable for extracting genomic DNA from stool samples.

DNA extracted by this kit has little impurity and good integrity, which can be directly used for PCR, digestion and other downstream experiments of molecular biology.

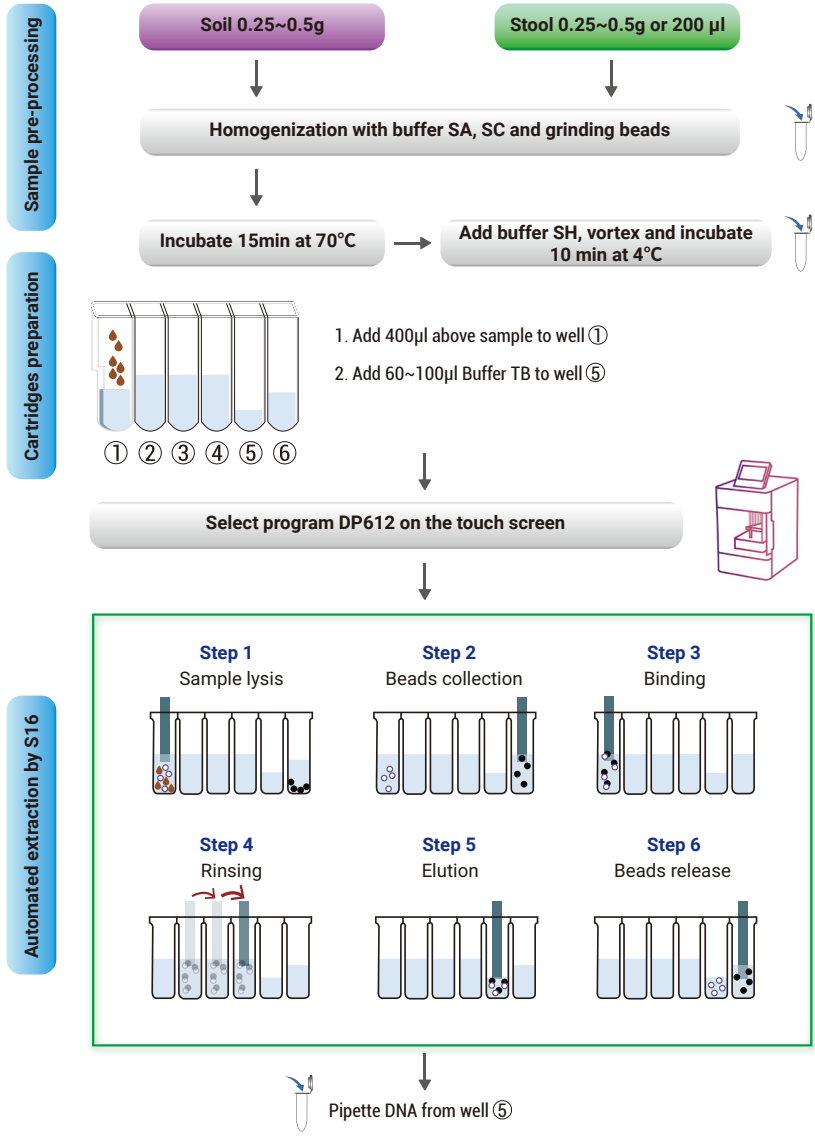
Features

- **Wide applicability:** It is suitable for flower bed soil, flower pot soil, farmland soil, forest soil, silt, red soil, black soil, dust and other soil environmental samples extraction, as well as stool sample extraction.
- **Convenient operation:** Ultra-pure genomic DNA can be obtained by running TGuide S16 for 42 minutes.
- **High purity:** Combined with magnetic bead purification, the extracted DNA with this kit has high purity and can be directly used in downstream experiments.

Notes

1. Fresh samples will ensure a higher yield. For different samples, check the corresponding optimal storage conditions before sampling.
2. At the stage where the supernatant needs to be collected, the sediment must be avoided, otherwise the purity of the product will be affected.
3. Excessive DNA input may inhibit following PCR reactions. In this case, it is recommended to dilute the DNA template before use.
4. Check buffer SC for precipitation before use. If there is precipitation, please heat it at 37°C until it is completely dissolved before use.

Operational steps



1. Prefilled single sample cartridge

1.1 Take out a prefilled single sample cartridge and invert it to re-suspend the magnetic beads; Gently shake to concentrate the reagent and magnetic beads to the bottom of the cartridge. Before use, remove sealing film carefully to avoid liquid spatter or spills.

1.2 Add proper volume (60~100 μl) of elution buffer TB to the 5th well of the cartridge.

2. Sample pre-processing

1) Soil sample processing:

Add 0.25~0.5g sample into 2 ml centrifuge tube, as well as 500 μl buffer SA, 100 μl buffer SC and 0.25 g grinding beads for 15 min vortex mixing until the sample is mixed evenly; or use the TGrinder H24 tissue homogenizer (TIANGEN, OSE-TH-01, self-prepared) for homogenization (oscillation at 6 M/S speed for 30 sec, with 30 sec interval and 2 cycles). Centrifuge it at 12,000 rpm (~13,400×g) for 1 min and transfer the supernatant (about 500 μl) to another 2 ml centrifuge tube.

Note: For some samples with low yield or requirements to extract fungal genome, it is suggested that after the samples are mixed by vortex mixing or tissue homogenizer, heat the mixture at 70°C for 15 min to improve the pyrolysis efficiency.

2) Stool sample processing:

Add 0.25~0.5 g sample into 2 ml centrifuge tube. If the sample is liquid, then transfer 200 μl sample to the centrifuge tube, and add 500 μl buffer SA, 100 μl buffer SC and 0.25 g grinding beads (Another 4 μl RNase A (100 mg/ml) is recommended for removing possible residual RNA) for vortex mixing until the sample is mixed evenly; or use the TGrinder H24 tissue homogenizer (TIANGEN, OSE-TH-01, self-prepared) for homogenization. Heat the mixture at 70°C for 15 min to improve the pyrolysis efficiency. Centrifuge it at 12,000 rpm (~13,400×g) for 1 min and transfer the supernatant (about 500 μl) to another 2 ml centrifuge tube.

Note: For gram-positive bacteria which cell wall are difficult to break , the temperature can be raised to 95°C to promote the pyrolysis.

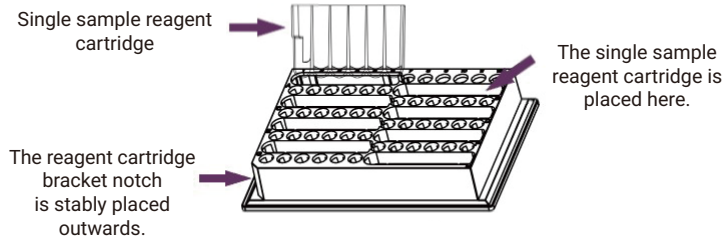
2.1 Add 200 μl buffer SH for 5 min vortex mixing and place it at 4 degrees for 10 min.

2.2 Centrifuge it at 12,000 rpm for 2 min and proceed to 3.1.

3. Operation steps of TGuide S16 Nucleic Acid Extractor

3.1 Add 400 μl above supernatant to the 1st well of the cartridge and place cartridges on the reagent tank bracket of TGuide S16 Nucleic Acid Extractor.

3.2 Place the reagent tank bracket on the plate base in the TGuide S16 Nucleic Acid Extractor. Insert the Tip Combs into the slot of the Tip Comb to ensure that they are well connected and firmed.



3.3 If you use the TGuide S16 Nucleic Acid Extractor, select the corresponding program DP612 file on the touch screen, click the icon in the lower right corner of the screen, or click the "RUN" button at the bottom of the screen to start the experiment.

3.4 At the end of the automated extraction process, take the DNA out of the 5th well of the cartridge and store it under appropriate conditions. Single sample reagent cartridge and tip comb are for single use only.

Detection of DNA concentration and purity

The size of the obtained genomic DNA fragment is affected by the sample storage time and shear force during operation. The concentration and purity of the obtained DNA fragments can be detected by agarose gel electrophoresis and UV spectrophotometer. Ideally, the DNA should absorb at most at OD_{260}, where an OD_{260} value of 1 corresponds to approximately 50 μg/ml double strand DNA and 40 μg/ml single strand DNA.The OD_{260}/OD_{280} ratio should be 1.7~1.9.

Appendix

1. Program

The extraction process of S16 provided for DP612 is shown in the following table:

Step	Hole site	Step name	Mix time (min)	Mix speed	Dry time (min)	Volume (μl)	Temp. (°C)	Segments	Every time (sec)	Magneti-zation time(sec)	Cycle	Magnet speed (mm/s)
1	6	Collect beads	0.5	8	0	260	--	5	3	0	2	2.5
2	1	Bind	8	8	0	900	--	5	4	0	2	2.5
3	2	Wash 1	5	8	0	700	--	5	3	0	2	2.5
4	3	Wash 2	3	8	0	700	--	5	3	0	2	2.5
5	4	Wash 3	3	8	5	700	--	5	3	0	2	2.5
6	5	Elution	8	8	0	100	65	3	5	2	2	2.5
7	6	Discard	0.5	5	0	260	--	1	0	0	0	--

2. Related Products

Instrument and Accessories

Product name	Packing Size	Cat.No
TGuide S16 Nucleic Acid Extractor	1 set	OSE-S16-AM
TGuide Smart Magnetic Tip Comb	200 pieces/box	OSE-TGA-S03
TGuide Single Sample Tank Bracket	5 pieces/box	OSE-TGA-S32

TGuide Smart Reagent Kits

Product name	Packing Size	Cat.No
TGuide Smart Magnetic Plant DNA Kit	48 preps	GDP607-DE
TGuide Smart Magnetic Tissue DNA Kit	48 preps	GDP602-DE
TGuide Smart Magnetic Plant RNA Kit	48 preps	GDP662-DE
TGuide Smart DNA Purification Kit	48 preps	GDP642-DE
TGuide Smart Blood/Cell/Tissue RNA Kit	48 preps	GDP661-DE
TGuide Smart Blood Genomic DNA Kit	48 preps	GDP601-DE
TGuide Smart Viral DNA/RNA Kit	48 preps	GDP604-DE
TGuide Smart Universal DNA Kit	48 preps	GDP605-DE