# i-genomic Plant DNA Extraction Mini Kit

QUICK GUIDE

**50 prep : 17371**

## 1. KIT DESCRIPTION

i-genomic Plant DNA Extraction Mini Kit provides a fast and easy way to purify DNA from plant-like samples such as various leaf, stem, root, fruit, and seed. You can see vast sample photos, vast samples, and vast practical data. i-genomic Plant DNA Mini Kit provides 7 kinds of protocols, Type A, Type B, Type C, Type D, Type E, Type F, and Type G. You can also extract genomic DNA from various plant samples in addition to 75 plant samples by selecting an appropriate protocol. If you need some more information in selecting a protocol, please do not hesitate to contact our Technical Assist Teams.

## 2. CHARACTERISTICS

- **Speed :** Takes only 20 ~ 30 minutes to extract genomic DNA.
- **Smart :** High quality and quantity of DNA recovery
- **Steady :** Complete removal of inhibitors and contaminants for accurate down stream applications. And the freeze-dried formulated enzyme has been improved DNA extraction stability.
- **Stage-up :** No need various DNA Extraction kit – vast applicability. The Kit is suitable to use various kinds of biological samples. Advanced GxN technology for rapid and efficient purification of DNA without ethanol precipitation.

## 3. INTENDED USE & APPLICATIONS

- **Intended Use :** This product is intended for professional use in molecular diagnostic research and veterinary in vitro diagnostic (IVD) workflows to extract genomic DNA for target detection and surveillance.
- **Applications :** Suitable for downstream molecular assays including PCR, real-time PCR (qPCR), Southern blotting, microarray analysis, and NGS library preparation.

## 4. KIT CONTENTS & STORAGE

| Contents | Description | Contain |
|---|---|---|
| **Buffer PG** | Lysis buffer | 30 ml |
| **Buffer PPT** | Precipitation buffer | 7 ml |
| **Buffer PB** | Binding Buffer | 50 ml |
| **Buffer PWA** | Washing Buffer A | 40 ml |
| **Buffer PWB** | Washing Buffer B (add 40 ml of EtOH) | 10 ml |
| **Buffer PE** | Elution Buffer | 20 ml |
| **Enhancer Solution** | Binding enhancer buffer | 0.5 ml |
| **Spin Columns** | Inserted into the collection tubes. (2.0ml tubes) | 50 columns |
| **RNase A** | Dissolve in 0.3ml of DW | 3 mg |
| **Proteinase K** | Dissolve in 1.1ml of DW | 22 mg |

- Storage & Stability: Store all liquid buffers and spin columns at room temperature (15–25ºC). The kit is stable for up to 24 months under recommended conditions.
- Store the Binding Enhancer Solution at 2–8°C after receiving.
- Buffer PG : Contains a chaotropic salt. Handle with care.
- Buffer PE : The final composition is 10 mM Tris-HCl (pH 8.0). An equivalent laboratory-prepared buffer may be used.

* Buffer PWB Preparation : Add absolute ethanol (96–100%) to Buffer PWB concentrate before initial use
- For Cat. 17371 (50 preps) : Add 40 ml of absolute EtOH.

** Enzyme Dissolution & Storage :
- Dissolve RNase A in 0.3 ml sterile D.W.
- Dissolve Proteinase K in 1.1 ml sterile D.W.

### ⁕ Additional Required Materials

- **Reagents** : Absolute ethanol (96–100%)
- **Equipments :** Vortex mixer | Microcentrifuge | Heating block | Pipettes & nuclease-free tips | Collection Tubes

## 5. SAFETY INFORMATION & HAZARD WARNINGS

- **Personal Protective Equipment (PPE) :** All chemical components should be handled with standard laboratory safety precautions. Always wear appropriate personal protective equipment, including disposable nitrile gloves, a chemical-resistant laboratory coat, and protective eyewear, when handling samples and kit reagents.

> **WARNING :** DO NOT add bleach (sodium hypochlorite) or acidic solutions directly to the sample preparation waste or effluents containing these buffers. Reaction of chaotropic salts with bleach or acids generates highly toxic, corrosive, and lethal gases (e.g., hydrogen cyanide, chlorine gas).

- **Flammability Hazard :** Buffer PWB (after ethanol addition) and absolute ethanol solutions are flammable. Keep away from open flames, heat sources, sparks, and hot surfaces. Do not smoke in reagent handling areas.
- **Decontamination & Waste Disposal :** If liquid spills occur, clean immediately with detergent and water. If liquid containing potential biohazards/infectious agents is spilled, clean first with detergent and water, then treat with an appropriate disinfectant. Dispose of chemical and biological liquid waste in accordance with local, regional, and national biosafety and hazardous materials regulations.

## 6. BEFORE YOU BEGIN

- **Column Specifications**
  - **Membrane** : Silica-based membrane
  - **Max. Loading Volume** : 800 µl
  - **Max. Binding Capacity** : 45 µg gDNA
  - **Recommended Elution Volume** : 50 – 100 µl
- **General Rule & Pre-handling**
  - **Pre-heating** : Set heating blocks to 65ºC prior to starting.
- **Buffer MW Preparation** :

> **Note :** Add absolute ethanol (96–100%) to Buffer PWB concentrate before initial use
> - 50 preps (Cat. 17371) : Add 40ml of absolute EtOH.

- **Enzyme Reconstitution :**

> **Note :** Reconstitute lyophilized RNase A in 0.3 ml sterile D.W., Proteinase K in 1.1 ml sterile D.W. Aliquot & store at -20 ºC.

- **Equipment Setup** : Preheat water baths or heating blocks to 37 ºc and 65 ºC as required for target sample types.

## 7. PROTOCOLS

### 7.1. SAMPLE PRE-TREATMENT WORKFLOW (BY SAMPLE MATRIX)

#### A. Lyophilized leaf

1) **Prepare lyophilized leaf sample.**
Note : Plant tissue can be lyophilized after harvesting to allow storage at room temperature (15~20℃). To ensure DNA quality, we recommend that samples should be completely lyophilized within 24 hours of collection.

2) **Measure 5 mg of lyophilized leaf, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : Static electricity in fine powder samples can be reduced by pre-chilling the spatula and tube in liquid nitrogen. Do not exceed the recommended sample amount, as this may cause inefficient lysis and reduce DNA yield and purity.

#### B. Leaf

1) **Prepare leaf sample.**
Note : If possible, collect young fresh leaves since they contain more cells per weight and therefore result in higher yields. They also contain smaller amounts of polysaccharides and polyphenolics, making them easier to handle. For storage, slice the leaves and freeze at -20°C or -80°C to facilitate disruption and homogenization.

2) **Slice off the prepared sample to small pieces by the scalpel or scissor.**
Note : To reduce disruption and homogenization time, we recommend to slice off it.

3) **Place the sliced sample in a grinding mortar and freeze with liquid nitrogen. Keep the sample frozen and grind until completely homogenized. Allow the liquid nitrogen to evaporate and proceed immediately to step 4.**
Note : Disruption and homogenization time depends on the leaf sample. Disrupt the sample completely until no tissue clumps are visible, as remaining clumps may result in lower DNA yield. Keep the sample frozen in liquid nitrogen during disruption and homogenization to prevent low DNA yields and DNA degradation. Be careful when handling liquid nitrogen.

4) **Measure 10 ~ 50 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : To prevent thawing during transfer, pre-chill the spatula and 1.5 ml tube in liquid nitrogen. Repeated freeze-thaw cycles may cause DNA degradation. Exceeding the recommended amount of starting material may result in inefficient lysis and low DNA yield and purity.

#### C. Stem

1) **Prepare stem sample.**
Note : We recommend collecting fresh or non-dried stem samples, as dried stems absorb lysis buffer and are difficult to lyse. Plant stems are tough and thick, making disruption and homogenization difficult. For storage, keep the stem frozen or in a plastic bag with a wet paper towel to prevent drying. Slicing the sample before storage facilitates disruption and homogenization.

2) **Slice off the prepared sample to small pieces by the scalpel or scissor.**
Note : For complete disruption and homogenization of tree trunks, peel the bark to prevent bark powder from affecting DNA yield and purity. Cut the sample into small pieces to reduce disruption time.

3) **Place the sliced sample in a grinding mortar and freeze with liquid nitrogen. Keep the sample frozen and grind until completely homogenized. Allow the liquid nitrogen to evaporate and proceed immediately to step 4.**
Note : Stem samples are difficult to disrupt and homogenize into a fine powder. However, disrupt the sample completely until no tissue clumps are visible, as remaining clumps may result in lower DNA yield.

4) **Measure 50 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : To prevent thawing during transfer, pre-chill the spatula and 1.5 ml tube in liquid nitrogen. Repeated freeze-thaw cycles may cause DNA degradation, while exceeding the recommended amount of sample may result in inefficient lysis and low DNA yield and purity.

#### D. Root

1) **Prepare root sample.**
Note : We recommend collecting fresh root samples under the same conditions as fresh stems. Before storage, wash the roots to remove impurities, dry the surface, slice, and freeze at -20°C or -80°C. Keep the sample frozen in liquid nitrogen during sample treatment to prevent low DNA yield and DNA degradation, and avoid repeated freeze-thaw cycles.

2) **Cut off the prepared sample to small pieces by the blade or scissor.**
Note : To reduce disruption and homogenization time, we recommend to slice off it.

3) **Place the sliced sample in a grinding mortar and freeze with liquid nitrogen. Keep the sample frozen and grind until completely homogenized. Allow the liquid nitrogen to evaporate and proceed immediately to step 4.**
Note : Disruption and homogenization time depends on the leaf sample. Disrupt the sample completely until no tissue clumps are visible, as remaining clumps may result in lower DNA yield. Keep the sample frozen in liquid nitrogen during disruption and homogenization to prevent low DNA yields and DNA degradation. Be careful when handling liquid nitrogen.

4) **Measure 50 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : To prevent thawing during transfer, pre-chill the spatula and 1.5 ml tube in liquid nitrogen. Repeated freeze-thaw cycles may cause DNA degradation. Exceeding the recommended amount of starting material may result in inefficient lysis and low DNA yield and purity.

#### E. Fruit

1) **Prepare fresh fruit sample.**
Note : Fruit contains about 80–95% water, so a larger amount of starting material may be required. For storage, peel and slice the fruit, then freeze at -80°C or lyophilize and store at room temperature (15–25°C). Generally, use the fruit flesh for DNA extraction. Keep frozen samples in liquid nitrogen during sample treatment and avoid repeated freeze-thaw cycles to prevent DNA degradation and low yield.

2) **Slice off the prepared sample to small pieces by the blade or scissor.**
Note : To reduce disruption and homogenization time, we recommend to slice off it.

3) **Place the sliced sample in a grinding mortar and freeze with liquid nitrogen. Keep the sample frozen and grind until completely homogenized. Allow the liquid nitrogen to evaporate and proceed immediately to step 4.**
Note : Disruption and homogenization time depends on the leaf sample. Disrupt the sample completely until no tissue clumps are visible, as remaining clumps may result in lower DNA yield. Keep the sample frozen in liquid nitrogen during disruption and homogenization to prevent low DNA yields and DNA degradation. Be careful when handling liquid nitrogen.

4) **Measure 100 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : To prevent thawing during transfer, pre-chill the spatula and 1.5 ml tube in liquid nitrogen and avoid repeated freeze-thaw cycles. Since fruit contains 80–95% water, use a larger amount of starting material, but do not exceed the recommended amount to prevent inefficient lysis and low DNA yield and purity.

#### F. for Seed - Other

1) **Prepare dried or fresh seed sample.**
Note : Seed samples can be stored dry at room temperature (15–25°C) or at -20°C or -80°C for long-term storage. Before storage, wash the seed surface with distilled water to remove impurities. For frozen seeds, keep the sample frozen in liquid nitrogen during treatment and avoid repeated freeze-thaw cycles to prevent low DNA yield and DNA degradation.

2) **Place the sample in a grinding mortar and freeze with liquid nitrogen. Keep the sample frozen and grind until completely homogenized. Allow the liquid nitrogen to evaporate and proceed immediately to step 3.**
Note : Seed samples have a hard outer shell, making disruption and homogenization difficult. Break the outer shell and grind the sample repeatedly with liquid nitrogen until no tissue clumps are visible. Keep the sample frozen during disruption and homogenization to prevent low DNA yield and DNA degradation. The completely homogenized sample should be a fine powder.

3) **Measure 50 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : To prevent thawing during transfer, pre-chill the spatula and 1.5 ml tube in liquid nitrogen. Repeated freeze-thaw cycles may cause DNA degradation, while exceeding the recommended amount of sample may result in inefficient lysis and low DNA yield and purity.

#### G. for Seed - gramineae

1) **Prepare dried or fresh gramineae seed sample.**
Note : Gramineae seeds may be difficult to process due to their high levels of secondary metabolites and polyphenolic compounds. Dried seeds can be stored at room temperature (15–25°C) or frozen at -20°C or -80°C for long-term storage. Keep frozen samples in liquid nitrogen during treatment and avoid repeated freeze-thaw cycles.

2) **Place the sample in a grinding mortar and freeze with liquid nitrogen. Grind thoroughly until completely homogenized, allow the liquid nitrogen to evaporate, and proceed immediately to step 3.**
Note : Gramineae seeds are thinner than other seeds and are relatively easy to grind. Disrupt the sample completely until no tissue clumps are visible, and keep it frozen in liquid nitrogen to prevent low DNA yield and DNA degradation. Generally, the sample becomes a fine powder after complete homogenization.

3) **Measure 10 mg of sample powder, and then transfer into 1.5 ml tube using a spatula. → Proceed to Section 7.2 Core Purification Workflow.**
Note : Although thin gramineae seeds are easily ground, thick seeds such as rice and wheat are difficult to grind. During lysis, they absorb Buffer PG and swell, making lysis difficult. To prevent this, use less than 10 mg of gramineae seeds, while 100 mg can be used for grass samples.

### 7.2. CORE PURIFICATION WORKFLOW

(Applicable to all samples prepared according to Section 7.1)

1) **Enzyme & Lysis : Add 390 ㎕ Buffer PG, 7 ㎕ Enhancer Solution, 20 ㎕ Proteinase K, and 5 ㎕ RNase A Solution into sample tube, and vortex vigorously.**
Note : Lyophilized leaves may absorb lysis buffer, swell, and become difficult to handle due to increased viscosity. Use the recommended amount of starting material. If necessary, use a disposable micropestle to remove remaining clumps.

2) **Incubation : Incubate the lysate for 30 min at 65℃.**
Note : For complete lysis, mix the tube 5–6 times by inversion during incubation. The incubation time may be extended to increase DNA yield. Complete lysis results in a clear lysate.

3) **Add 100 ㎕ Buffer PPT to the lysate, mix well, and incubate for 5 min on ice.**
Note : During incubation on ice, invert the tube 5–6 times until the clear lysate becomes opaque and slushy. Since plant tissues contain high levels of polysaccharides and polyphenolics, use the recommended amount of starting material to prevent impurities in the purified DNA.

4) **Centrifuge the lysate for 5 min at 13,000 rpm at room temperature.**
Note : Plant materials may produce viscous lysates and large amounts of precipitates.

5) **Transfer carefully 200 ㎕ of supernatant from step 6 into a new 1.5 ml tube.**
Note : Although the supernatant is typically 350–400 µl, recover only 200 µl to prevent DNA shearing and impurity contamination. Carefully pipette without disturbing the cell-debris pellet.

6) **Binding Preparation : Add 650 ㎕ Buffer PB to the lysate, and mix well by gently inverting 5 to 6 times or by pipetting. DO NOT vortex.**
Note : This step equilibrates the lysate for genomic DNA binding to the column membrane. Precipitate may form after adding Buffer PB, but it does not affect the procedure.

7) **Column Loading : Transfer 650 µl of the mixture, including any precipitate, to the spin column. Centrifuge for 1 min at 13,000 rpm (RT) and discard the flow-through. If any mixture remains, centrifuge again under the same conditions.**

8) **Repeat step 9 with remaining sample (maximum 200 ㎕). Discard flow-through and collection tube altogether.**
Note : If a small amount will not pass through, please centrifuge again for 1 min at 13,000 rpm.

9) **Wash : Place the spin column into a new 2.0 ml collection tube (additionally supplied), add 700 ㎕ Buffer PWA, and centrifuge for 1 min at 13,000 rpm.**

10) **Discard the flow-through and reuse the collection tube. Add 700 µl Buffer PWB to the spin column and centrifuge for 1 min at 13,000 rpm.**
Note : Ensure that 40 ml of ethanol (EtOH) has been added to Buffer PWB.

11) **Membrane Drying : Discard the flow-through and centrifuge again for 1 min to dry the membrane. Carefully remove the spin column without contacting the flow-through, as residual ethanol may inhibit subsequent reactions.**

12) **Elution : Place the spin column into a new 1.5 ml tube and add 100 µl Buffer PE directly onto the membrane. Incubate for 1 min at room temperature and centrifuge for 1 min at 13,000 rpm to elute DNA.**
Note : Elution with 50 µl increases DNA concentration but may reduce overall yield, while 200 µl may increase overall yield. For a second elution, use a new tube to keep the eluates separate or reuse the same tube to combine them.

## 8. TROUBLESHOOTING GUIDE

| Problem | Possible cause | Recommendation |
|---|---|---|
| Low flow rate in column | Clogged spin column by particulate material | Completely perform the Disruption & Homogenization step |
| | | Increase the incubation time at 65°C in Lysis step. |
| | Problem in centrifugation | Check your centrifuge, and then speed up or increase the centrifugation time. |
| Low DNA yield | Inadequate lysis | Reduce the amounts of starting material. |
| | | Increase the incubation time at 65°C in Lysis step. |
| | Error in DNA binding | Check that the amount of Buffer PB is added correctly to the supernatant. |
| | Incorrect Washing step | Check again that the amount of ethanol (EtOH) is added correctly to Washing buffer. |
| | Insufficient DNA elution | Increase the volume of Buffer PE to 100 µl. |
| | | Increase the incubation time on the column to 5 ~ 10 min at room temperature prior to centrifugation. |
| DNA sheared | Vigorously vortex | Do not vortex the mixture after adding Buffer MB as described in protocol. |
| Problems in down-stream experiments | Ethanol contamination | Ensure that during Washing Step B, the column membrane should be dried completely. Please centrifuge at full speed for 5 ~ 10 min to dry the membrane. |
| | | During Washing Step B, after centrifugation, remove carefully the spin column from the collection tubes without contacting with the flow-through. This careless contact will result in contamination of ethanol. |
| | Salt contamination | Check again to add EtOH previously into Buffer BW. |
| | | Store Buffer BW at room temperature (15 ~ 20°C). |
| | Amount of DNA used in experiments. | Optimize the amount of DNA used in your downstream experiments. |

## 9. EXPERIMENTAL INFORMATION

### ※ Experimental Data 1 : Determination of Yield and Purity Data of DNA

**Table 1. Summary of Representative DNA Yield and Purity**

| Lane | Samples | Amounts (mg) | DNA Yield (µg) | $A_{260/280}$ |
|---|---|---|---|---|
| 1 | Persimmon | 5 | 3 ~ 5 | 1.73 |
| 2 | Adray | 5 | 2 ~ 4 | 1.83 |
| 3 | Perilla | 5 | 3 ~ 6 | 1.72 |
| 4 | Lettuce | 50 | 10 ~ 12 | 1.79 |
| 5 | Green pepper | 50 | 8 ~ 12 | 1.83 |
| 6 | Peanut | 50 | 8 ~ 12 | 1.81 |
| 7 | Potato | 50 | 6 ~ 8 | 1.80 |
| 8 | Onion | 50 | 4 ~ 6 | 1.81 |
| 9 | Sesame | 50 | 4 ~ 7 | 1.80 |
| 10 | Platycodon | 50 | 5 ~ 7 | 1.83 |
| 11 | Carrot | 50 | 8 ~ 10 | 1.85 |
| 12 | Radish | 50 | 6 ~ 10 | 1.79 |
| 13 | Tomato | 100 | 3 ~ 5 | 1.82 |
| 14 | Pineapple | 100 | 3 ~ 5 | 1.79 |
| 15 | Apple | 100 | 2 ~ 4 | 1.83 |
| 16 | Black bean | 50 | 10 ~ 14 | 1.88 |
| 17 | Yellow bean | 50 | 12 ~ 15 | 1.84 |
| 18 | Mung bean | 50 | 10 ~ 12 | 1.86 |

Type A Protocol : Lane 1 ~ 3, Type B Protocol : Lane 4 ~ 6, Type C Protocol : Lane 7 ~ 9, Type D Protocol : Lane 10 ~ 12, Type E Protocol : Lane 13 ~ 15, Type F Protocol : Lane 16 ~ 18

## 10. REGULATORY & WARRANTY

### 10.1. Quality Control Compliance (ISO Standard Verification)

- ISO Quality Management: This product is manufactured under strict quality inspection and lot-by-lot QC standards in accordance with ISO 9001 and ISO 13485 certified Quality Management Systems.
- Certificate of Analysis (CoA): All released products meet the physical, chemical, and biological activity criteria specified in the product specification, with quality compliance verified via lot-specific CoA.

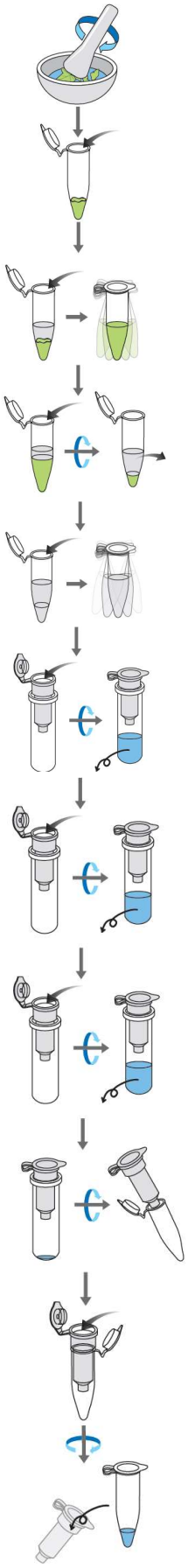
### 10.2. Product Warranty & Limitations Statement

- Warranty Scope: The manufacturer guarantees that this product will perform as specified through its expiration date when stored and operated under recommended storage conditions.
- This warranty is strictly limited to the replacement of defective products or the refund of the purchase price.
- The manufacturer assumes no liability for failures resulting from improper storage, misuse, operator error, or unauthorized application.
- For research use only (RUO) or OEM products, final validation, regulatory clearance, and application responsibilities lie entirely with the purchaser.

## 11. ORDERING INFORMATION

| Product Name | Cat. No. |
|---|---|
| G-spin™ for Bacteria Genomic DNA Extraction Kit | 17271 |
| i-genomic BYF DNA Extraction Mini Kit | 17361 |
| easy-spin™ Total RNA Extraction Kit | 17221 |
| Maxime PCR PreMix (i-Taq) | 25025 / 25026 |
| Maxime PCR PreMIx (i-StarTaq) | 25165 / 25167 |
| SiZer™-1,000 DNA Marker Solution | 24074 |
| 2X PCR Master mix Solution (i-StarTaq) | 25166 |
| RealMOD™ Probe $R^2$ 2X qPCR mix (with UDG) | 25363.200 (200 rxns)<br>25363.500 (500 rxns)<br>25363.1000 (1000 rxns) |
| RealMOD™ Probe $R^2$ 2X qRT-PCR mix (with UDG) | 25364.200 (200 rxns)<br>25364.500 (500 rxns) |

## Visual Protocol (Lyophilized leaf)



- Slice off the prepared sample
- Measure 5 ~ 100 mg of sample powder
- Transfer into 1.5 ml tube
- Buffer PG (390), Enhancer Solution (7), Proteinase K (20), RNase A Solution (5)
- Mix well, Incubation, 30 min, 65 ºC
- Buffer PPT (100), Mix well
- Incubation on ice, 5 min
- 13K rpm, 5 min, RT
- Transfer supernatant (200) into 1.5 ml tube
- Buffer PB (650), Mix well
- Transfer mixture (650)
- 13K rpm, 1min, RT
- Discard the Flow-through
- Add Buffer PWA (700)
- 13K rpm, 1min, RT
- Discard the Flow-through
- Add Buffer PWB (700)
- 13K rpm, 1min, RT
- Discard the Flow-through
- 13K rpm, 1min, RT
- Place the spin column into a new tube
- Add Buffer PE (100), Incubation, 1 min, RT
- 13K rpm, 1 min, RT, Take DNA eluate
- Remove the spin column