# SapI V2.0

## Product Information

| Product name | Catalog Number | Size |
|---|---|---|
| SapI V2.0 | SAP-SE102-B | 1000 U |
| | SAP-SE102-C | 10 kU |

## Product Description

SapI V2.0 is an IIS-type restriction endonuclease that can recognize non-palindromic DNA motifs and create sticky ends after cutting the DNA domain outside the recognition motif, similar to BspQI, PciSI, and LguI. Compared to SapI(Catalog No. SAP-SE101), the SapI V2 has been engineered to digest 'difficult to cut' plasmids with higher cutting efficiency. The 10×Cut Reaction Buffer contains recombinant Albumin (rAlbumin), ensuring the stability and safety of the product.

## Specifications

| Component | SAP-SE102-B (1000 U) | SAP-SE102-C (10 kU) |
|---|---|---|
| SapI V2.0 (10 U/μl) | SAP-SE102-B1 (100 μl) | SAP-SE102-C1 (1 ml) |
| 10×Cut Reaction Buffer | CUT-EE001-B2 (800 μl) | CUT-EE001-C2 (8 ml) |

## Source

*E.coli*

## Enzyme Activity Definition

One unit (1U) is defined as the amount of enzyme required to digest 1 μg of λ DNA in 1 hour at 37℃ in a total reaction volume of 50 μl.

## Storage Buffer

10 mM Tris-HCl, 300 mM NaCl, 1 mM DTT, 0.1 mM EDTA, 500 μg/ml HSA, 50% Glycerol, pH 7.4

## Restriction Cutting Site

5'…GCTCTTC$(N)_1$↓…3'
3'…CGAGAAG$(N)_4$↑…5'

## Transportation/Storage

Ship on dry ice. Store at -20 ± 5℃. Avoid repeated freeze-thaw cycles.

## Applications

Molecular cloning, restrictive site mapping, genotyping, SNP analysis.

## Protocol

(1)Prepare the reaction as follows:

| Components | Volume(μl) |
|---|---|
| DNA | 1 μg |
| 10· Cut Reaction Buffer | 5 μl |
| SapI V2.0(10 U/μl) | 1 μl* |
| Nuclease-free Water | To 50 μl |

(2)Mix well and incubate at 37℃ for 4-6 hours

(3)Add in 5 μl 0.5 M EDTA and incubate at 65℃ for 20 minutes to stop the reaction.

Note:* Add other components first before SapI V2.0. 1μl SapI is recommended for a 50 μl volume reaction. The amount is adjustable per the actual conditions but no more than 10% of the total volume to avoid star activity.

## Cautions

(1)SapI V2.0 is not sensitive to Dam, Dcm, and CpG methylation

(2)Make sure the DNA sample does not contain Phenol, Ethanol, Chloroform, EDTA or any other contaminants that may affect the digestion efficiency.

(3)Shor digestion time may lead to insufficient cutting efficiency. 4-6 hours incubation is recommended for the digestion.

(4)For research use only.



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