

Product Information

RESTRICTION ENDONUCLEASE Bss HII

Product no. **R 2634**

Store 0 °C to -20 °C

Product Summary

Recognition Sequence: 5'G/C/G/C/G/C/3'

Activity: 10,000 units/ml

Cutting: 100%

Ligation: >95%

Recutting: >95%

No degradation detected with >20 units for 16 hrs.

Fold over digestion: 320 (20 units x 16 hrs.)

Package Size: 200 units

Unit Definition

One unit is the enzyme activity that completely cleaves 1 µg λ DNA in 1 hr. at 50 °C in a total volume of 25 µl of Buffer SA for restriction endonucleases.

Specificity

Bss HII recognizes the sequence G/C/G/C/G and generates fragments with 5'-overhanging ends.¹ Bss HII generates compatible to ends to Mlu I blunt ends. Bss HII is inhibited by 5'-methyl- cytosine in the sequence G/^mC/G/^mC/G. Yeast DNA, which is rich in A and T sequences, is cleaved by Bss HII to produce 30 kb fragments. Mammalian genomic DNA is cleaved by Bss HII to produce 100 kb fragments because of reduced CG content.

Comments

Digestion Buffer SA is supplied as a 10x concentrate. Heat inactivation information is not available for Bss HII.

Bss HII Storage and Dilution Buffer Composition

10 mM Tris-HCl

50 mM KCl

0.1 mM EDTA

1 mM dithiothreitol (DTT)

500 µg/ml bovine serum albumin

50% (v/v) glycerol

pH 7.4

1x Digestion Buffer SA (B 7531) Composition

for Bss HII: 100% Digestion at 37 °C.

33 mM Tris-acetate

66 mM Potassium-acetate

10 mM Magnesium acetate

0.5 mM dithiothreitol (DTT)

pH 7.9

Quality Control Testing

Absence of unspecific endonuclease activities:

1 µg λ DNA is incubated for 16 hrs. in 25 µl buffer SA with excess of Bss HII.

Ligation and Recutting Assay

Bss HII fragments, obtained by complete digestion of 1 µg λ DNA, are adjusted to pH 7.5 at 25 °C. The Bss HII fragments are then ligated with 1.0 unit T4-DNA ligase at 4 °C at pH 7.5. A 10 µl reaction mixture, incubated for

16 hrs. at 4 °C contained: 1.0 unit T4-DNA ligase, 66 mM Tris-HCl, 5 mM MgCl₂, 1 mM dithioerythritol and 1 mM ATP.

The degree of ligation and subsequent recutting with Bss HII to yield the typical pattern of λ x Bss HII fragments is determined.

References

1. Kessler, C., et. al., *Gene*, **92**, 1 (1990).