M0226S
100 units 4,000 U/ml Lot: 0301310
RECOMBINANT Store at –20°C Exp: 10/14

Description: The CpG Methyltransferase, M.SssI, methylates all cytosine residues (C) within the double-stranded dinucleotide recognition sequence 5’...CG...3’ (1).

Source: The CpG Methyltransferase, M.SssI, is isolated from a strain of E. coli which contains the Methyltransferase gene from Spiroplasma sp. strain MQ1 (2,3).

Applications:
- Blocking restriction endonuclease cleavage
- Studying of CpG methylation-dependent gene expression
- Probing sequence-specific contacts within the major groove of DNA
- Altering the physical properties of DNA
- Uniform [3H]-labeling of DNA
- Decreasing the number of sites cut by restriction endonucleases, yielding an apparent increase in specificity.

Reagents Supplied with Enzyme:
- 10X NEBuffer 2: 200X S-adenosylmethionine
- 50% glycerol.

Methyltransferase gene from sp. strain Spiroplasma which contains the E. coli M.SssI.

Reaction Conditions:
- Without Mg2+, methylation by M.SssI exhibits topoisomerase activity (4).
- Incubation of 100 units of M.SssI with 1 µg of plasmid DNA in a total reaction volume of 20 µl in 1 hour at 37°C resulted in no detectable endonuclease contamination.

Endonuclease Activity:
- Incubation of 50 units of M.SssI with 1 µg of λ DNA for 4 hours at 37°C in 50 µl NEBuffer 2 resulted in no detectable endonuclease contamination.

Heat Inactivation:
- 65°C for 20 minutes.

Unit Definition: One unit is defined as the amount of enzyme required to protect 1 µg of λ DNA in a total reaction volume of 20 µl in 1 hour at 37°C against cleavage by BstUI restriction endonuclease.

Quality Assurance: Purified free of contaminating endonucleases and exonucleases.

Quality Control Assays
16-Hour Incubation: Incubation of 100 units of M.SssI with 1 µg λ DNA in 50 µl of 1X NEBuffer 2 for 16 hours at 37°C resulted in no detectable endonuclease contamination.

Exonuclease Activity:
- Incubation of 100 units of M.SssI with 1 µg sonicated 3H DNA (106 cpm/µg) for 4 hours at 37°C in 50 µl NEBuffer 2 resulted in no detectable endonuclease contamination.

Endonuclease Activity:
- Incubation of 50 units of M.SssI with 1 µg of φX174 RF I DNA for 4 hours at 37°C in 50 µl reaction buffer resulted in < 5% conversion to RF II.

Heat Inactivation:
- 65°C for 20 minutes.

(See other side)
Methylation can be optimized by using fresh SAM.
This CPG Methyltransferase may be useful for studying the function of cytosine methylation in higher eukaryotes as its specificity mimics the pattern of modification found in their genomes (5). In contrast to the mammalian enzyme (6,7), both unmethylated and hemi-methylated DNA substrates are methylated with equal efficiency by the CpG Methyltransferase (2), making it a more useful tool for modifying DNA.

The CpG Methyltransferase can be used to block cleavage by a variety of restriction endonucleases whose recognition sites either contain the sequence CG, or overlap the dinucleotide. It should be noted that DNAs methylated by the CpG Methyltransferase can be used to block cleavage by a variety of restriction endonucleases whose recognition sites either contain the sequence CG, or overlap the dinucleotide. It should be noted that DNAs methylated by the CpG Methyltransferase are subject to Mcr and Mrr restriction in E. coli, and thus should be transformed into Mcr⁻ Mrr⁻ E. coli strains.

Methylation at cytosine residues has also been shown to affect the physical properties of DNA, including lowering the free energy of Z-DNA formation (8), increasing the helical pitch of DNA (6), and altering the kinetics of cruciform extrusion (9). Positions of 5-methylcytosine can be identified due to decreased reactivity to hydrazine in chemical sequencing protocols (10).

The high density of CpG dinucleotides in DNA substrates should be taken into account when methylating DNA in vitro. For example, lambda DNA (48,502 bp) contains 3112 CpG sites, and thus a 0.1 mg DNA/ml solution is 19 μM with respect to methyl acceptor sites for the Methyltransferase. This is significant because the recommended concentration of methyl donor, S-adenosylmethionine (SAM), is 160 μM, an 8-fold excess over acceptor sites. Reducing the DNA concentration (< 0.02 mg/ml) gives two advantages. First, the SAM concentration remains high enough to drive the reaction. Second, potential end product inhibition arising from S-adenosyl-L-homocysteine (AdoHcy) generated during the reaction is limited.

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