

# Site-Specific Methylation Sensitivity of Promega Restriction Enzymes

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This table lists the sensitivities of several Promega restriction enzymes to site-specific methylation at *dam*, *dcm*, CpG and CpNpG sites (p = phosphoryl group). These four modifications are frequently found in DNA of bacteria, eukaryotes or their viruses. Many strains of *E. coli* contain the site-specific *dam* and *dcm* DNA methylases. Higher eukaryotes contain the site-specific CpG and CpNpG DNA methylases. In mammalian genomes, methylation occurs mainly at the CG dinucleotide. In plant genomes, methylation may occur at both the CG and CNG sequences.

### Prokaryotic Methylation

**dcm** Cytosine methylase mutation—methylates the C5 position of the internal cytosine residue in the sequence 5'...CCTGG...3' or 5'...CCAGG...3'.

**dam** Adenine methylase mutation—methylates the N6 position of the adenine residue in the sequence 5'....GATC...3'.

### Eukaryotic Methylation

**CpG** Methylates the C5 position of the cytosine residue in the dinucleotide recognition sequence 5'...CG...3'.

**CpNpG** Methylates the C5 position of the cytosine residue in the trinucleotide recognition sequence 5'...CNG...3' (N = any base).

For further information regarding site-specific methylation, refer to McClelland, M., Nelson, M. and Raschke, E. (1994) *Nucl. Acids Res.* **22**, 3640.

### Key:

- s = sensitive to this methylation
- i = insensitive to this methylation
- s(ol) = overlapping (sensitive when restriction site overlaps methylation sequence)
- n.d. = information not available

Enzyme	Recognition Sequence	<i>dam</i>	<i>dcm</i>	CpG	CpNpG
AatII	GACGTC	i	i	s	i
AccB7I	CCANNNNNTGG	i	s(ol)	i	i
AccIII	TCCGGA	s(ol)	i	i	i
Acc65I	GGTACC	i	s(ol)	i	i
Apal	GGGCCC	i	s(ol)	s(ol)	i
Aval	CYCGRG	i	i	s	i
Avall	GGWCC	i	s(ol)	s(ol)	s(ol)
Ball	TGGCCA	i	s(ol)	i	s(ol)
BamHI	GGATCC	i	i	i	s(ol)
BanII	GRGCYC	i	i	i	i
Bbul	GCATGC	i	i	i	i
BclI	TGATCA	s	i	i	i
BglI	GCCNNNNNGGC	i	i	s(ol)	s(ol)
BglII	AGATCT	i	i	i	s(ol)
Bsp1286I	GDGCHC	i	i	i	i
BssHII	GCGCGC	i	i	s	i
BstEII	GGTNACC	i	i	i	i
BstOI	CCWGG	i	i	i	n.d.
BstXI	CCANNNNNTGG	i	i	i	i
BstZI	CGGCCG	i	i	s(ol)	s(ol)
CfoI	GCGC	i	i	s	n.d.
ClaI	ATCGAT	s(ol)	i	s	i
Cspl	CGGWCCG	i	i	i	s
Csp45I	TTCGAA	i	i	s	i
DdeI	CTNAG	i	i	i	s(ol)
Eco47III	AGCGCT	i	i	s	i
EcoRI	GAATTC	i	i	s(ol)	i
HaeIII	GGCC	i	i	i	s(ol)
HhaI	GCGC	i	i	s	s(ol)
HincII	GTYRAC	i	i	i	i
HindIII	AAGCTT	i	i	i	i
HpaII	CCGG	i	i	s	s
KpnI	GGTACC	i	i	i	i

Enzyme	Recognition Sequence	<i>dam</i>	<i>dcm</i>	CpG	CpNpG
MbolI	GAAGA(8/7)	s(ol)	i	i	i
MluI	ACGCGT	i	i	s	i
MspI	CCGG	i	i	i	s
NaeI	GCCGGC	i	i	s	s
NarI	GGCGCC	i	i	s	i
NdeI	GATC	s	i	i	i
NheI	GCTAGC	i	i	s(ol)	s(ol)
NotI	GCGGCCGC	i	i	s	s
NruI	TCGCGA	s(ol)	i	s	i
PmeI	GTTTAAAC	i	i	s(ol)*	s(ol)*
PstI	CTGCAG	i	i	i	s
PvuI	CGATCG	i	i	s	s(ol)
PvuII	CAGCTG	i	i	i	s
SacI	GAGCTC	i	i	i	i
SacII	CCGCGG	i	i	s	s
SalI	GTCGAC	i	i	s	n.d.
Sau3AI	GATC	i	i	s(ol)	s(ol)
Scal	AGTACT	i	i	i	i
SfiI	GGCCNNNNNGGCC	i	s(ol)	s(ol)	s(ol)
SgfI	GCGATCGC	i	i	s	n.d.
SinI	GGWCC	i	i	i	s(ol)
SmaI	CCCGGG	i	i	s	s
SnaBI	TACGTA	i	i	s	i
SphI	GCATGC	i	i	i	i
StuI	AGGCCT	i	s(ol)	i	s(ol)
TaqI	TCGA	s(ol)	i	i	i
XbaI	TCTAGA	s(ol)	i	i	i
XhoI	CTCGAG	i	i	s	i
XhoII	RGATCY	i	i	i	s(ol)
XmaI	CCCGGG	i	i	i	n.d.
XmnI	GAANNNN	i	i	n.d.	n.d.

\* PmeI is inhibited by methylation of cytosine residues on both strands.