Effect of site-specific modification on restriction endonucleases and DNA modification methyltransferases

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ABSTRACT

Restriction endonucleases have site-specific interactions with DNA that can often be inhibited by site-specific DNA methylation and other site-specific DNA modifications. However, such inhibition cannot generally be predicted. The empirically acquired data on these effects are tabulated for over 320 restriction endonucleases. In addition, a table of known site-specific DNA modification methyltransferases and their specificities is presented along with EMBL database accession numbers for cloned genes.

We present in Table I an updated list of the sensitivities of over 320 restriction endonucleases to site-specific modification at 4-methylcytosine (^{m4}C), 5-methylcytosine (^{m5}C), 5-hydroxymethylcytosine (^{hm5}C), and 6-methyladenine (^{m6}A), four modifications that are common in the DNA of prokaryotes, eukaryotes, and their viruses (Mc2,Mc5,Mc8,Mc11,Ne3,Ne4,Mc14,Ne14).

Knowledge of the sensitivity of restriction endonucleases to site-specific modification can be used to study cellular DNA methylation. Several restriction-modification enzymes share the same recognition sequence specificity, but differ in their sensitivities to site-specific methylation. Table II lists 33 known isoschizomer pairs and one isomethylator pair, along with the modified recognition sites at which they differ. Table III lists over 240 characterized DNA methyltransferases. A detailed list of cloned restriction-modification genes can be found in Wilson (Wi4).

The data presented here and two other tables are available in printed form or as a text file on a 3.5' Macintosh diskette. The extra tables include Table IV which lists the sensitivities of 24 Type II DNA methyltransferases to ^{m4}C, ^{m5}C, ^{hm5}C, and ^{m6}A modification. Most methyltransferases are sensitive to non-canonical modifications within their recognition sequences (Bu9,Mc10,Ne3,Po4), and this sensitivity often differs from that of their restriction endonuclease partners. Table V gives a list of restriction systems in this review alphabetized by recognition sequence.

MOLECULAR BASIS FOR SENSITIVITY RESTRICTION ENZYMES TO METHYLATION

^{m4}C, ^{m5}C, ^{hm5}C, ^{hm5}U and ^{m6}A are bulky alkyl substitutions in the major groove of DNA. Site-specific DNA methylation can interfere with many sequence-specific DNA binding proteins (e.g. St2,Wa8), including restriction endonucleases and DNA methyltransferases. At the molecular level, the inability of restriction enzymes to cut modified DNA can be explained using *EcoRI* and *EcoRV* endonucleases as instructive models. DNA modification can interfere with substrate binding and/or conformational changes of the enzyme: substrate complex.

Based on the *EcoRI*: DNA co-crystal structure (Mc15,Ro8), methylation of either adenine (G^{m6}AATTC or GA^{m6}ATTC) perturbs essential hydrogen bond contacts to Glu-144 and Arg-145. Therefore aminomethylation of either adenine inhibits DNA cleavage at the level of *EcoRI*: substrate binding (Br2). In contrast, cytosine ring methylation at GAATT^{m5}C would not be expected to interfere with critical DNA: protein contacts inferred from the X-ray crystal structure (Mc15). Therefore, the reduced rate of *EcoRI* cleavage at GAATT^{m5}C can be attributed to steric distortions of the enzyme:substrate complex during catalysis (He3).

In contrast, the X-ray structure of *EcoRV* endonuclease (Wi5) predicts that hydrogen bonding of Asn-185 to the first adenine of GATATC is perturbed by 'canonical' methylation at the G^{m6}ATATC. However, it is thought that *EcoRV* cannot cleave canonically modified G^{m6}ATATC sites because non-productive enzyme: substrate complexes are formed (Ta4,Ne12). Therefore the mechanism by which canonical DNA methylation inhibits cleavage is very different for *EcoRI* and *EcoRV* endonucleases.

Although DNA modification often results in complete inhibition of restriction enzyme cleavage, a range of rate effects are observed when *non-canonically* modified DNA is used as a substrate, as listed in the footnotes to Table I. Rate effects at ^{m5}C-hemimethylated restriction endonuclease target sites are listed in Ne10.

RATE OF CLEAVAGE AT METHYLATED RESTRICTION SITES

A range of rate effects are observed when modified substrates are used in endonuclease cleavage reactions. However, in general, results can be summarized as follows.

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(1) Canonical site-specific methylation *always* inhibits DNA cleavage by a restriction endonuclease. For example, M·*Bam*HI methylase modifies GGAT^{m4}CC; and *Bam*HI endonuclease cannot cut this methylated sequence.

(2) In about one half of the cases tested, methylation at non-canonical sites inhibits the rate of duplex DNA cleavage at least ten-fold (Table I). However, in other cases non-canonical methylation has no effect on restriction cleavage. For example, *Bam*HI cuts DNA which has been modified at GGATC^{m4}C or GGATC^{m5}C, but cannot cut DNA methylated at GGAT^{m5}CC.

(3) There are a few examples in which non-canonical methylation slows the rate of cleavage or permits nicking of one strand of a hemimethylated duplex. Examples of such effects are presented in footnotes to Table I. Such nicking has proved useful in site-directed mutagenesis (US Biochemicals Inc.).

(4) Sometimes base modifications which lie *outside* a recognition sequence can influence the rate of DNA cleavage by a restriction enzyme. For example, *Nar*I does not cut at overlapping M·*Mva*I–*Nar*I GGCGCC^{m4}CCWGG sites (Ne14), *Hae*III cannot cut certain GGCC^{mT}T sites, where ^{mT}T are modified thymine residues (Wi1), and *Msp*I, *Hpa*II, *Sma*I, and *Hha*I are unable to cut DNAs in which bases adjacent to their recognition sequences are modified with hydroxymethyluracil (Ho1). Such methylation-induced 'action at a distance' may be more common than has been previously appreciated. We have tested only a few enzymes for sensitivity to base modifications *outside* their canonical recognition sequences.

DNA MODIFICATIONS OTHER THAN ^{m4}C, ^{m5}C, ^{hm5}C, ^{hm5}U, AND ^{m6}A

The effects of several other site-specific DNA modifications on the rate of restriction endonuclease cleavage, such as 5-bromodeoxycytidine, 5-bromodeoxyuridine, 5-iododeoxycytidine, deoxyinosine, 2-aminopurine, 2,6-diaminopurine, 2-chloroadenosine, 7-deazaguanosine, and deoxynucleotide phosphorothioates, are listed elsewhere (Bo1, Be6, Mo4, Br2, Ta5, He4, Gr3, Se4, Vo2).

EFFECT OF ^{m5}CG AND ^{m5}CNG ON RESTRICTION ENDONUCLEASES

Enzymes that are *not* sensitive to site-specific methylation are particularly useful for achieving complete digestion of methylated DNA. For instance, endonucleases that are unaffected by ^{m5}CG and ^{m5}CNG are useful for the digestion of plant DNA, which is frequently methylated at these positions. Endonucleases that are unaffected by these two cytosine modifications include: *Acc*III, *Afl*III, *Aha*III, *Ase*I, *Asp*700I, *Asu*II, *Bbu*I, *Bcl*II, *Bsp*HI, *Bsp*NI, *Bst*EII, *Bst*NI, *Cvi*QI, *Dpn*I, *Dra*I, *Eco*RV, *Hin*CII, *Hpa*I, *Kpn*I, *Mbo*II, *Mse*I, *Nde*I, *Nde*II, *Pac*I, *Rsa*I, *Rsp*XI, *Sfu*I, *Spe*I, *Sph*I, *Ssp*I, *Swa*I, *Taq*I, *Tsp*509I, *Tth*HBI and *Xmn*I. However, adenine methylation may also occur in plants.

CpG sequences occur infrequently and are often methylated in mammalian genomes (Mc9). Almost all the enzymes that could generate large fragments of mammalian DNA are blocked by this ^{m5}CpG modification at overlapping sites, including *Aat*II, *Ape*I, *Asc*I, *Avi*II, *Bbe*I, *Bma*DI, *Bsr*BI, *Bss*HII, *Bsp*MII, *Bst*BI, *Cl*aI, *Csp*I, *Csp*45I, *Eag*I, *Ecl*XI, *Eco*47III, *Fse*I, *Fsp*I, *Kpn*2I, *Mlu*I, *Mlu*9273I, *Mlu*9273II, *Mro*I, *Nae*I, *Nar*I, *Nor*I, *Nru*I, *Pfu*I, *Pml*I, *Ppu*AI, *Pvu*I, *Rsr*II, *Sal*I, *Sal*DI, *Sbo*13I, *Sfi*I, *Sma*I, *Sna*BI, *Spe*II, *Spo*I, *Srf*I, *Xho*I and *Xor*II (see Table I). Only ten enzymes suitable for pulsed field mapping of eukaryotic chromosomes are

known to cut ^{m5}CG-modified DNA: *Acc*III, *Asu*II, *Bsp*EI, *Cfr*9I, *Pac*I, *Pme*I, *Sfu*I, *Sse*8387I, *Swa*I, and *Xma*I.

^{m4}C, ^{m5}C, AND ^{hm5}C CYTOSINE MODIFICATIONS

In some cases, a restriction enzyme may differ in sensitivity to ^{m4}C, ^{m5}C or ^{hm5}C at a particular sequence. For example, *Bst*NI and *Mva*I cut ^{m5}C, but not ^{m4}C modified CCWGG sequences. *Rsa*I cuts GTA^{m5}C but not GTA^{m4}C. *Kpn*I cuts GGTAC^{m5}C but not GGTAC^{m4}C. *Bst*YI cuts RGAT^{m5}CY but not RGAT^{m4}CY. Similarly, *Cvi*III cuts T^{m5}CGA but not T^{hm5}CGA. These endonucleases may be used to distinguish among these modifications.

EFFECT OF SITE-SPECIFIC METHYLATION ON DNA METHYLTRANSFERASES

Twenty-three Type II methyltransferases have been tested for sensitivity to *non-canonical* DNA modifications, of which nine were blocked (Mc10 and Table IV). As with restriction endonucleases, rate effects are sometimes seen with DNA methyltransferases at non-canonically modified sequences. For example, *E. coli* *Dam* methyltransferase is unaffected by GAT^{m4}C, but methylates GAT^{m5}C relatively slowly. Such data is summarized in Table IV and footnotes to Table I.

METHYLATION-DEPENDENT RESTRICTION SYSTEMS IN BACTERIA

E. coli K-12 contains at least three different methylation-dependent restriction systems which selectively restrict methylated target sequences: *mrr* (^{m6}A), *mcrA* (^{m5}CG), *mcrB* (^{Rm5}C) (Br5, Di1, He2, Ra1, Ra2). *In vivo* or *in vitro* modified DNA is inefficiently cloned into *E. coli*. For example, human DNA which is extensively methylated at ^{m5}CpG is restricted by *mcrA* (Wo3) and other systems (Bu2). Appropriate non-restricting strains of *E. coli* (Go2, Kr2, Ra1, Ra2) should be chosen for efficient transformation and cloning of methylated DNA. Other species also have such methyl-dependent restriction systems (e.g. Ma2).

ENGINEERED DNA METHYLTRANSFERASE SPECIFICITIES

Many DNA methyltransferase genes have now been sequenced. Extensive homologies between closely related enzymes (Wi3) or common motifs (Po5, Sm3) allow new specificities to be engineered (e.g. Ba4, Tr4).

DATA IN ELECTRONIC FORM

This paper is available as a text file on a 3.5' Macintosh diskette. The data can be supplied as a Microsoft Word, Macwrite or MS-DOS file. Please contact Michael McClelland at CIBR, phone (619) 535 5486, FAX (619) 535 5472.

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Table I. Methylation sensitivity of restriction endonucleases^a

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>AatI</i>	AGGCCT	?	AGG ^{m5} CCT AGGC ^{m5} CT AGGC ^{m4} CT	Ne14 So3 Ne14
<i>AatII</i>	GACGTC	?	GA ^{m5} CGTC GACGT ^{m5} C	Fo1 Ne14
<i>AccI</i>	GTMKAC	?	GTMK ^{m6} AC [#] GTMKA ^{m5} C ^b	Lu2,Mc3
<i>AccII</i>	CGCG	?	^{m5} CGCG	Ga2
<i>AccIII</i>	TCCGGA	T ^{m5} CCGGA ^b TC ^{m5} CGGA ^b	TCCGG ^{m6} A	Ke3,La2,Sc2
<i>Acc65I</i>	GGTACC	?	GGTAC ^{m5} C	Ne5
<i>AciI</i>	CCGC	?	C ^{m5} CGC	Fo1
<i>AflI</i>	GGWCC	GGWC ^{m5} C GGWC ^{m4} C ^b	?	Mc11,Wh2
<i>AflIII</i>	CTTAAG	?	^{m5} CTTAAG CTTA ^{m6} AG	Ne14
<i>AflIII</i>	ACRYGT	?	A ^{m5} CRYGT	Ne14
<i>AgeI</i>	ACCGGT	?	A ^{m5} CCGGT AC ^{m5} CGGT	Ne14
<i>AhaII</i>	GRCGYC ^b	?	GR ^{m5} CGYC GRCGY ^{m5} C	Ka2,Hu1
<i>AluI</i>	AGCT	?	^{m6} AGCT AG ^{m4} CT AG ^{m5} CT [#] AG ^{hm5} CT	Gr5,Mc11,Ne2 Hu1,Wo1,Zh1 Bu9
<i>AlwI</i>	GGATC	?	GG ^{m6} ATC GGAT ^{m4} C	Ne4
<i>Alw26I</i>	GTCTC	?	GT ^{m5} CTC [#] GAG ^{m6} AC [#]	Bi7
<i>Alw44I</i>	GTGCAC	GTGC ^{m6} AC	GTG ^{m5} CAC	Ne14
<i>AlwNI</i>	CAGN ₃ CTG	?	CAGN ₂ C ^{m5} CTG	Bo5,Ne5
<i>AmaI</i>	TCGCGA	TCGCG ^{m6} A	?	Mc13
<i>AosII</i>	GRCGYC	?	GR ^{m5} CGYC	Eh2,Gr5,Va3
<i>ApaI</i>	GGGCCC	?	GGG ^{m5} CCC [#] GGGCC ^{m5} C	La9,Gu9
<i>ApaLI</i>	GTGCAC	GTGC ^{m6} AC GTG ^{m5} CAC	GTGCA ^{m5} C	Fo1,Ho2,Ho3 Ne14
<i>ApeI</i>	ACGCGT	?	A ^{m5} CGCGT	Ne14,Qi2
<i>ApyI</i>	CCWGG	C ^{m5} CWGG	^{m5} CCWGG	Kl1,Mc11,Ra3
<i>AquI</i>	CYCGRG	?	^{m5} CYCGRG [#]	Ka7,Ka8
<i>AscI</i>	GGCGCGCC	?	GG ^{m5} CGCGCC GGCG ^{m5} CGCC GGCGCG ^{m5} CC GGCGCGC ^{m5} C	Si2
<i>AspI</i>	GWCGWC	?	GW ^{m5} CGWC	Ne14
<i>AspMDI</i>	GATC	G ^{m6} ATC	?	Ch4
<i>Asp700I</i>	GAAN ₄ TTC	GA ^{m6} AN ₄ TTC GAAN ₄ TT ^{m5} C GGT ^{m6} A ^{m5} CC ^b GGTA ^{m5} CC ^b	G ^{m6} AAN ₄ TTC	Ne14
<i>Asp718I</i>	GGTACC	GGT ^{m6} A ^{m5} CC ^b GGTA ^{m5} CC ^b	GGTAC ^{m5} C GGTA ^{m5} C ^{m5} C ^b	Mu2,Ne4
<i>AsuI</i>	GGNCC	GGNC ^{m5} C	?	Pr4
<i>AsuII</i>	TTCGAA	TT ^{m5} CGAA	?	Ne14
<i>AtuCI</i>	TGATCA	?	TG ^{m6} ATCA	Ro3,Sc12
<i>AvaI</i>	CYCGRG	C ^{m5} CCGGG	^{m5} CYCGRG CY ^{m5} CGRG CTCG ^{m6} AG ^b GGW ^{m5} CC GGWC ^{m5} C GGW ^{hm5} C ^{hm5} C	Eh2,Ne14 Ka4,Ka7,Mc11 Ne2 Ba3,Ko3 Mc10,Mc11 Hu1
<i>AvaII</i>	GGWCC	GGWC ^{m4} C ^b	TG ^{m5} CGCA ACN ₄ GTYA ^{m5} C [#] TGG ^{m5} CCA [#] TGGC ^{m5} CA ^b	Ne14 Fo1 Gi1,Gu9
<i>AviII</i>	TGCGCA	?	GGAT ^{m4} CC [#] GGAT ^{m5} CC GGAT ^{hm5} C ^{hm5} C	Br8,Dr1,Ha3,Hu1 La7
<i>BaeI</i>	ACN ₄ GTAYC	?	GGA ^{hm5} UCC	Ho1
<i>BalI</i>	TGGCCA	?	GGAT ^{m4} CC GGAT ^{m4} CC	An1,Sh1 An1,Sh1
<i>BamHI</i>	GGATCC	GGATC ^{m5} C GG ^{m6} ATCC GG ^{m6} ATC ^{m5} C GGATC ^{m4} C GG ^{m6} ATCC GG ^{m6} ATCC GG ^{m5} CGCC	?	Co3,Ka2,Ma12,Su1

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>BanII</i>	GRGCYC	GGYRC ^{m4} C	GRG ^{m5} CYC	Fo1,Ne2,Ne6
<i>BanIII</i>	ATCGAT	GRGCY ^{m5} C	ATCG ^{m6} AT #	Su1
<i>BbeI</i>	GGCGCC	? GGCG ^{m5} CC GGCGC ^{m5} C	GG ^{m5} CGCC	Co3,Ne2,Sh2
<i>BbiII</i>	GRGCYC	? CACGTG	GR ^{m5} CGYC CA ^{m5} CGTG	Co3 Wo1,Ka11
<i>BbrPI</i>	GAAGAC	? GAAGA ^{m5} C	? G ^{m6} ATGC	Fo1 Ne14
<i>BbsI</i>	GCATGC	GCATG ^{m5} C	G ^{m5} CAGC #	Do1,Ha3,Va5
<i>BbvI</i>	GCAGC	? WCCGGW	W ^{m5} CCGGW	Sc10
<i>Bca77I</i>	WCCGGW	WC ^{m5} CGGW	CG ^{m6} AN ₅ TGC #	Ra4
<i>BcgI</i>	CGCN ₅ TGC	? TGAT ^{m5} CA	TG ^{m6} ATCA TGAT ^{hm5} CA	Bi4,Br8,Eh3,Ro3 Hu1
<i>BclI</i>	TGATCA	TCAT ^{m5} CA	TCAT ^{hm5} CA	Ja3,Ja6,K11
<i>BcnI</i>	CCSGG	^{m5} CCSGG	C ^{m4} CSGG # C ^{m5} CSGG	Kr3 Ku3
<i>BepI</i>	CGCG	? CTTAAG	^{m5} CGCG ^{m5} CTTAAG	Wo1
<i>BfiI</i>	CTTAAG	? GCCN ₅ GGC	G ^{m5} CCN ₅ GGC GCCN ₅ GG ^{m5} C ^b GC ^{m4} CN ₅ GGC # ^b	Kl1,Ko3,Mc11,Ne2
<i>BglI</i>	GCCN ₅ GGC	GC ^{m5} CN ₅ GGC ^b	AGAT ^{m5} CT	Bi4,Br8,Dr1, Dy1,Eh3 Hu1,Pi6,Ho1
<i>BglIII</i>	AGATCT	AG ^{m6} ATCT	AGAT ^{hm5} CT	Bo2
<i>BinI</i>	GGATC	AGA ^{hm5} UC ^{hm5} U	GG ^{m6} ATC	Qi2
<i>BmaDI</i>	CGATCG	CG ^{m6} ATCG	CGAT ^{m6} CG	Ma9
<i>Bme216I</i>	GGWCC	? GGW ^{m5} C	GGW ^{m5} C	Ne14
<i>BnaI</i>	GGATCC	GG ^{m6} ATCC	GGAT ^{m4} CC GGAT ^{m5} CC #	Ki1
<i>BsaI</i>	GGTCTC	GAGA ^{m5} C ^{m5} C	GGTCT ^{m5} C	Fo1,Ne5
<i>BsaAI</i>	YACGTR	? YAC ^{m5} GTR	YAC ^{m5} GTR	Fo1
<i>BsaBI</i>	GATN ₄ ATC	? GATN ₄ AT ^{m5} C	GATN ₄ AT ^{m5} C	Fo1
<i>BsaHI</i>	GRGCYC	? GR ^{m5} CGYC	G ^{m6} ATN ₄ m6ATC	Fo1
<i>BsaJI</i>	CCNNGG	C ^{m5} CNNGG	GR ^{m5} CGYC	Fo1
<i>BsaWI</i>	WCCGGW	WC ^{m5} CGGW	? ATCG ^{m6} AT #	Fo1
<i>BseCI</i>	ATCGAT	? ATCG ^{m6} AT #	CTGCA ^{m5} C	Ri3,Ri4
<i>BsgI</i>	CTGCAC	? CTGCA ^{m5} C	G ^{m6} ATN ₄ ATC	Fo1
<i>Bsh1365I</i>	GATN ₄ ATC	? GATN ₄ m6ATC	GATN ₄ m6ATC	Ja3
<i>BsiBI</i>	GATN ₄ ATC	? GATN ₄ m6ATC	GATN ₄ m6ATC	Im1
<i>BsiEI</i>	CGRYCG	? m5CGRY ^{m5} CG	m5CGRY ^{m5} CG	Fo1
<i>BsiLI</i>	CCWGG	? C ^{m5} CWGG	C ^{m5} CWGG	Im1
<i>BsiMI</i>	TCCGGA	? TCCGG ^{m6} A	TCCGG ^{m6} A	Im1
<i>BsiWI</i>	CGTACG	? m5CGTA ^{m5} CG	m5CGTA ^{m5} CG	Fo1
<i>BsiXI</i>	ATCGAT	? m6ATCGAT	m6ATCGAT	Im1
<i>BslI</i>	CCN ₇ GG	? C ^{m5} CN ₇ GG	ATCG ^{m6} AT	Fo1
<i>BsmI</i>	GAATGC	GAATG ^{m5} C	C ^{m5} CN ₇ GG	Fo1,Ne14
<i>BsmAI</i>	GTCTC	G ^{m6} AGAC	G ^{m6} AAATGC	Fo1,Ne14
<i>BspDI</i>	ATCGAT	? AT ^{m5} CGAT	GTCT ^{m5} C	Fo1
<i>BspEI</i>	TCCGGA	TC ^{m5} CGGA ^b	AT ^{m5} CGAT	Fo1
<i>BspHI</i>	TCATGA	? m6ATCG ^{m6} AT	m6ATCG ^{m6} AT	Fo1
<i>BspMI</i>	ACCTGC	ACCTG ^{m5} C	TCCGG ^{m6} A	Fo1
<i>BspMII</i>	TCCGGA	TCCGG ^{m6} A	TC ^{m6} ATGA	Pa2,Se3
<i>BspXI</i>	ATCGAT	? TCATG ^{m6} A	TCATG ^{m6} A	Mc1
<i>BspXII</i>	TGATCA	? T ^{m5} CCGGA	T ^{m5} CCGGA	Fo1
<i>Bsp106I</i>	ATCGAT	? TC ^{m5} CGGA	TC ^{m5} CGGA	La2,Sc2
<i>Bsp143I</i>	GATC	? ATCG ^{m6} AT	ATCG ^{m6} AT	Zi1
<i>Bsp1286I</i>	GDGCHC	? TG ^{m6} ATCA	TG ^{m6} ATCA	Zi1
<i>BsrBI</i>	GAGCGG	? ATCG ^{m5} AT #	ATCG ^{m5} AT #	Ne5
<i>BsrFI</i>	RCCGGY	? G ^{m6} ATC	G ^{m6} ATC	Ne14
<i>BssHII</i>	GCGCGC ^b	? GDGCH ^{m5} C	GDGCH ^{m5} C	Fo1,Ne2,Ne6
<i>BstI</i>	GGATCC	? GAG ^{m5} CGG ^b	? RC ^{m5} CGGY	Fo1
<i>BstVI</i>	CTCGAG	? G ^{m6} ATCC	G ^{m5} CGCGC	Fo1
<i>BstBI</i>	TTCGAA	? GGAT ^{m4} CC	GGAT ^{m4} CC	Ne4,Qi3
		GGATC ^{m5} C	GGAT ^{m5} CC	Ne4
			GGATC ^{m4} C	Ne14
			CTCG ^{m6} AG #	Ba7
			TTCG ^{m6} AA	Ne4
			TT ^{m5} CGAA	Wo1

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>BstEII</i>	GGTNACC	GGTNA ^{m5} C ^{m5} C	GGTNA ^{hm5} C ^{hm5} C GGTNAC ^{m4} C	Hu1,Mc11 Ne14
<i>BstEIII</i>	GATC ^b	?	G ^{m6} ATC	My1,Ro3
<i>BstGI</i>	TGATCA	?	TG ^{m6} ATCA	Ro3
<i>BstNI</i>	CCWGG ^b	^{m5} CCWGG ^b C ^{m5} CWGG ^{m5} C ^{m5} CWGG ^b C ^{m5} CWGG	^{hm5} C ^{hm5} CWGG C ^{m4} CWGG #	Gr5,Hu1,Mc11 Ba12,Br8,Ne14,Ro3
<i>BstOI</i>	CCWGG	C ^{m5} CWGG	?	Sc10
<i>BstUI</i>	CGCG	?	^{m5} CGCG CG ^{m5} CG	Ne5 Ne14
<i>BstXI</i>	CCAN ₆ TGG	C ^{m5} CAN ₆ TGG	^{m5} CCAN ₆ TGG	Ne14,Ne2
<i>BstYI</i>	RGATCY	RG ^{m6} ATCY	RGAT ^{m4} CY RGAT ^{m5} CY	Ne4 Ne14
<i>Bst1107I</i>	GTATAC	?	GTATA ^{m5} C	Fo1
<i>BsuBI</i>	CTGCAG	?	CTGC ^{m6} AG #	Gal,Je1,Sh1,St5
<i>BsuEII</i>	CGCG	?	^{m5} CGCG #	Gal,Je1,Sh1,St5
<i>BsuFI</i>	CCGG	?	^{m5} CCGG #	Je1
<i>BsuMI</i>	CTCGAG	?	CT ^{m5} CGAG #	Je1
<i>BsuRI</i>	GGCC	?	GG ^{m5} CC # ^b	Gu8,Ki2,Ki3
<i>Bsu15I</i>	ATCGAT	?	ATCG ^{m6} AT #	Re6
<i>Bsu36I</i>	CCTNAGG	CCTN ^{m6} AGG	^{m5} CCTNAGG	Ne14,Ne5
<i>CbiI</i>	TTCGAA	TTCG ^{m6} AA	?	Mu1
<i>CcrI</i>	CTCGAG	?	CTCG ^{m6} AG	Ne14
<i>CfoI</i>	GCGC	?	G ^{m5} CGC GCG ^{m5} C G ^{hm5} C ^{hm5} C	Eh1 Ne14 Hu1
<i>CfrI</i>	YGGCCR	?	YGG ^{m5} CCR #	Kl1
<i>CfrAI</i>	GCAN ₈ GTGG	?	GC ^{m6} AN ₈ GTGG	Ne14
<i>CfrBI</i>	CCWWGG	?	^{m4} CCWWGG #	Za2
<i>Cfr6I</i>	CAGCTG	?	CAG ^{m4} CTG # CAG ^{m5} CTG	Bu9
<i>Cfr9I</i>	CCCGGG ^b	C ^{m5} CCGGG CC ^{m5} CGGG	^{m4} CCCGGG ^{m5} CCCGGG C ^{m4} CCGGG # CC ^{m4} CGGG	Bu10 Kl2
<i>Cfr10I</i>	RCCGGY	?	R ^{m5} CCGGY # RC ^{m5} CGGY	Bi5,Kl1 Ne14
<i>Cfr13I</i>	GGNCC	?	GGN ^{m5} CC #	Bi5,Kl1
<i>Clal</i>	ATCGAT	?	^{m6} ATCGAT AT ^{m5} CGAT ^b ATCG ^{m6} AT #	Ca4,Mc11, Mc12,Ne4 Wo1 Mc3
<i>CpeI</i>	TGATCA	?	TG ^{m6} ATCA	Fi1,Ro3
<i>CspI</i>	CGGWCCG	CGGW ^{m5} CCG	CGGW ^{m5} CCG ^{m5} CGGWCCG	Mc11
<i>Csp45I</i>	TTCGAA	?	TTCG ^{m6} AA	Ne4,Sc11
<i>CtyI</i>	GATC	?	G ^{m6} ATC #	Ri2
<i>CviAI</i>	GATC	GAT ^{m5} C	G ^{m6} ATC #	Ne14,Xi1,Xi6
<i>CviAII</i>	CATG	^{m5} CATG	C ^{m6} ATG #	Ne14,Zh2
<i>CviBI</i>	GANTC	?	G ^{m6} ANTC #	Xi3
<i>CviJI</i>	RGCY	?	RG ^{m5} CY #	Sh3,Xi2
<i>CviPI</i>	CC	C ^{m5} C	^{m5} CC #	Xi4
<i>CviQI</i>	GTAC	GTA ^{m5} C	GT ^{m6} AC #	Xi5
<i>CviQII</i>	GANTC	?	G ^{m6} ANTC #	Ne14
<i>CviQIII</i>	CATG	?	C ^{m6} ATG	Ne14
<i>CviRI</i>	TGCA	?	TGC ^{m6} A # TG ^{m5} CA GT ^{m6} AC #	Ne14 Ne14
<i>CviRII</i>	GTAC	?	TGC ^{m6} A #	Ne14
<i>CviSIII</i>	TCGA	T ^{m5} CGA	T ^{hm5} CGA	
<i>CviSIV</i>	GATC	?	G ^{m6} ATC #	Ri2
<i>DdeI</i>	CTNAG	?	^{m5} CTNAG # ^{hm5} CTNAG CTN ^{m6} AG	Ho4,Ne2 Hu1 Ne14
<i>DpnI</i>	G ^{m6} ATC ^b	G ^{m6} ATC G ^{m6} AT ^{m5} C ^b G ^{m6} AT ^{m4} C	GATC GAT ^{m4} C GAT ^{m5} C G ^{m6} ATC #	La3,Mc11,Vo1 Ne4 Ne5
<i>DpnII</i>	GATC	?	?	De1,La3,La4, La5,Ma6,Vo1
<i>DraI</i>	TTTAAA	TTTA ^{m6} AA	?	Ne14
<i>DraII</i>	RGGNCCY	?	RGGNC ^{m5} CY	Sc8
<i>DrdI</i>	GACN ₆ GTC	?	GA ^{m5} CN ₆ GT ^{m5} C	Fo1
<i>DsaV</i>	CCNGG	?	C ^{m5} CNGG	N1
<i>EaeI</i>	YGGCCR	?	YGG ^{m5} CCR #	Ja2,Wh1

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>EagI</i>	CGGCCG	?	YGGC ^{m5} CR CGG ^{m5} CCG m ⁵ CGGC ^{m5} CG	Mc11
<i>Eam1105I</i>	GACN ₅ GTC	GA ^{m5} CN ₅ GT ^{m5} C	?	Fo1
<i>EarI</i>	GAAGAG	CTCTT ^{m5} C	G ^{m6} AAGAG GAAG ^{m6} AG m ⁵ CT ^{m5} CTT ^{m5} C	Fo1,Ne4
<i>EcaI</i>	GGTNACC	?	GGTN ^{m6} ACC #	Ne14
<i>EclXI</i>	CGGCCG	?	m ⁵ CGGC ^{m5} CG	Br3
			CGG ^{m5} CCG	Qi3
<i>Ecl136II</i>	GAGCTC	?	GAGCT ^{m5} C	Fo1
<i>EcoAI</i>	GAGN ₇ GTCA ^b	?	G ^{m6} AGN ₇ G ^m TCA # ^b	Bi2,Co6,Fu2
<i>EcoBI</i>	TGAN ₈ TGCT ^b	?	TG ^{m6} AN ₈ ^m TGCT # ^b	Bi2,La10,La11
<i>EcoDI</i>	TTAN ₈ GTCY ^b	?	TT ^{m6} AN ₈ GTCY # ^b	Na6
<i>EcoDXXI</i>	TCAN ₇ AATC ^b	?	TCAN ₇ ^{m6} AA ^m TC # ^b	Pi1
<i>EcoEI</i>	GAGN ₇ ATGC ^b	?	G ^{m6} AGN ₇ ATGC # ^b	Co6,Fu2
<i>EcoHI</i>	CCSGG	?	C ^{m5} CSGG #	Kr3
<i>EcoKI</i>	AACN ₆ GTGC ^b	?	A ^{m6} ACN ₆ G ^m TGC # ^b	Bi2,Bi3,Ka1
<i>EcoO109I</i>	RGGNCCY	?	RGGNC ^{m5} CY	Sc8
<i>EcoPI</i>	AGACC ^b	AGA ^{hm5} C ^{hm5} C	AG ^{m6} ACC #	Ba1,Ba2,Ha4,Re4
<i>EcoP15I</i>	CAGCAG ^b	?	CAGC ^{m6} AG #	Hu2,Me2
<i>EcoRI</i>	GAATTC	GAATT ^{hm5} C	G ^{m6} AAATTC ^b	Mc11,Ne2,Ru1
		GAA ^{hm5} T ^{jhm5} UC	GA ^{m6} ATTC #	Br1,Br8,Du1,Ho1
			GAATT ^{m5} C ^b	Hu1,Ka3,Ta1
<i>EcoRII</i>	CCWGG	m ⁵ CCWGG ^b	m ⁴ CCWGG	Ku1,Yo1
			C ^{m4} CCWGG	Bu8,Na5,Ro3
			C ^{m5} CCWGG #	Bo7,Mc11
			CC ^{m6} AGG	Bu7
			hm ⁵ C ^{hm5} CCWGG	Hu1,Ka3
<i>EcoRV</i>	GATATC	GATAT ^{m5} C ^b	G ^{m6} ATATC #	Mc11,Ne2,Wo1
		GATAT ^{hm5} C	GAT ^{m6} ATC	Fl1,Ho1
<i>EcoT22I</i>	ATGCAT	?	ATG ^{m5} CAT	Ne14
			ATGC ^{m6} AT	
<i>Eco31I</i>	GGTCTC	?	GGT ^{m5} CTC #	Bi7
			G ^{m6} AGACC #	
<i>Eco47I</i>	GGWCC	?	GGWC ^{m5} C	Ja5
<i>Eco47II</i>	GGNCC	?	GGNC ^{m5} C	Po6
<i>Eco47III</i>	AGCGCT	m ⁶ AGCGCT	AG ^{m5} CGCT	Ne14,Ne4
<i>Eco57I</i>	CTGAAG	?	CTGA ^{m6} AG #	Ja8,Po6
			CTTC ^{m6} AG #	
<i>Eco1831I</i>	CCSGG	?	C ^{m5} CSGG #	Kr3
<i>EheI</i>	GGCGCC	?	GG ^{m5} CGCC	Co2,Ne14
			GGCG ^{m5} CC	
			GG ^{hm5} CG ^{hm5} C ^{hm5} C	
<i>EspI</i>	GCTNAGC	GCTNAG ^{m5} C	G ^{m5} CTNAGC	Ne4
<i>Esp3I</i>	CGTCTC	?	m ⁵ CGTCTC	Fo1
			CGT ^{m5} CTC #	Bi7,Ja3
			GAG ^{m6} ACG #	
<i>Esp1396I</i>	CCAN ₅ TGG	C ^{m5} CAN ₅ TGG	?	Ja3
<i>Fnu4HI</i>	GCNGC	?	G ^{m5} CNGC #	Gu9,Ko3
			GCNG ^{m5} C #	
<i>FnuDII</i>	CGCG	?	m ⁵ CGCG	Ga1,Ga2, Ne2,Ne6,St6
			CG ^{m5} CG	
<i>FnuEI</i>	GATC	G ^{m6} ATC	?	Lu1,Ne2
<i>FokI</i>	CATCC	CAT ^{m5} CC	GG ^{m6} ATG	Po3,Po4,Sc2
		CATC ^{m5} C ^b	C ^{m6} ATCC	
			CATC ^{m4} C	Ne14
<i>FseI</i>	GGCCGGCC	?	GG ^{m5} CCGG ^{m5} CC	Ne7
			GGC ^{m5} CGGCC	
			GG ^{m5} CCGGCC	
<i>FspI</i>	TGCGCA	?	TG ^{m5} CGCA	Ne4
<i>FsuI</i>	GGWCC	?	GGWC ^{m5} C	Le1
<i>HaeII</i>	RGCGCY ^b	?	RG ^{m5} CGCY	Eh2,Gr5,Ka2,Ko3,Mc11,Pi5
			RGCG ^{m5} CY	Ne14
			RG ^{hm5} CG ^{hm5} CY	Hu1
<i>HaeIII</i>	GGCC	GGC ^{m5} C	GG ^{m5} CC # ^b	Ba3,Ka2,Ko3,Ma5
			GG ^{hm5} C ^{hm5} C	Hu1
<i>HapII</i>	CCGG	?	C ^{m5} CGG #	Eh2,Wa1
<i>HgaI</i>	GACGC	?	GA ^{m5} CGC #	Ne14
			G ^{m5} CGTC #	Wi7
			GACG ^{m5} C	Mc11
<i>HgiAI</i>	GWGCWC	GWGCW ^{m5} C	GWG ^{m5} CWC	Fo1,Ne2,Wh3
<i>HgiBI</i>	GGWCC	?	GGWCC (m ⁵ C)	Du2
<i>HgiCI</i>	GGYRCC	?	GGYR ^{m5} CC #	Er1

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>Hgi</i> II	GGWCC	?	GGWC ^{m5} C	Er1
<i>Hgi</i> DI	GRCGYC	?	GRCGYC	Du4
<i>Hgi</i> EI	GGWCC	?	GGWC ^{m5} C	Er1
<i>Hgi</i> GI	GRCGYC	?	GR ^{m5} CGY ^{m5} C	Kr4,Er1
<i>Hgi</i> II	GGYRCC	?	GGYRC ^{m5} C	Wh3
<i>Hha</i> I	GCGC	?	G ^{m5} CGC #	Eh2,Sm1
			GCG ^{m5} C	Mc11,Ko3
			G ^{hm5} CG ^{hm5} C	Hu1
<i>Hha</i> II	GANTC	?	G ^{m6} ANTC #	Ma5
<i>Hinc</i> II	GTYRAC	GT ^{m5} CRAC	GTYRA ^{m5} C ^b	Bu11
			GTYR ^{m6} AC #	Gr5,Ro7
			GTYRA ^{hm5} C	Hu1
<i>Hind</i> II	GTYRAC	?	GTYR ^{m6} AC #	Ro7
			GTYRA ^{hm5} C	
<i>Hind</i> III	AAGCTT	A ^{m6} AGCTT	^{m6} AAGCTT #	Br8,Gr5,Ne14,Ro7
		AAGC ^{hm5} U ^{hm5} U	AAG ^{m5} CTT ^b	Ho1,Ne2
			AAG ^{hm5} CTT	Hu1,Ka3
<i>Hinf</i> I	GANTC	GANT ^{m5} C ^b	G ^{m6} ANTC	Ch1,Co1,Ne2,Pe1
			GANT ^{hm5} C	Hu1
<i>Hin</i> PI	GCGC	?	G ^{m5} CGC	Mc11,Ne6
<i>Hpa</i> I	GTTAAC	GT ^{m5} AA ^{m5} C	GT ^{m6} AA ^{m6} AC #	Br8,Gr5,Hu1,Yo3
			GT ^{m5} AA ^{hm5} C	Hu1
			G ^{hm5} U ^{hm5} UAAAC	Ho1
<i>Hpa</i> II	CCGG	?	^{m4} CCGG	Be3,Bu10,Eh2,Ma5
			^{m5} CCGG ^b	Ko3,Qu1,Wa5
			^{m4} CCGG ^b	
			C ^{m5} CCGG #	
			^{hm5} C ^{hm5} CCGG	
<i>Hph</i> I	TCACC	TCAC ^{m5} C	T ^{m5} CACC #	Hu1
			TCA ^{m5} CC	Fo1,Mc11,Ne2
			GGTG ^{m6} A	
<i>Kas</i> I	GGCGCC	?	GG ^{m5} CGCC	Fo1
<i>Kpn</i> I	GGTACC ^b	GGTA ^{m5} CC	GGT ^{m6} ACC #	Eh3,Ki4,Mc11
		GGTAC ^{m5} C	GGTA ^{m4} CC ^b	Ne14
			GGTA ^{m5} C ^{m5} C ^b GGTAC ^{m4} C	
<i>Kpn</i> 2I	TCCGGA	TCCGG ^{m6} A	T ^{m5} CCGGA	Mc1,Ne14
<i>Ksp</i> I	CCGCGG	?	TC ^{m5} CGGA	Ne14
			^{m5} CCGCGG	Ne14
			C ^{m5} CGCGG	Qi2
<i>Mae</i> II	ACGT	?	A ^{m5} CGT ^b	Mo2
<i>Mam</i> I	GATN ₄ ATC	?	G ^{m6} ATN ₄ m6ATC	St4
<i>Mbo</i> I	GATC ^b	GAT ^{m4} C	G ^{m6} ATC #	Br5,Ge1,Mc8
		GAT ^{m5} C ^b	GAT ^{hm5} C	Hu1,Ro3
			GA ^{hm5} UC	Ho1
<i>Mbo</i> II	GAAGA	T ^{m5} CTT ^{m5} C ^b	GAAG ^{m6} A #	Ba3,Mc11,Mc12,Ne2
		G ^{m6} AAGA	GA ^{m6} AGA	
<i>Mfi</i> I	RGATCY ^b	?	RG ^{m6} ATCY	On1
			RGAT ^{m4} CY	
			RGAT ^{m5} CY	
<i>Mlu</i> I	ACGCGT	^{m6} ACGCGT	A ^{m5} CGCGT	Mc11,Sh1,St5,Qi3
			ACG ^{m5} CGT	Ne5
<i>Mlu</i> 9273I	TCGCGA	?	T ^{m5} CGCGA	Ne14
<i>Mlu</i> 9273II	GCCGGC	?	G ^{m5} CCGGC	Ne14
			GC ^{m5} CGGC	
<i>Mme</i> II	GATC	?	G ^{m6} ATC	Bo6
<i>Mnl</i> I	CCTC	G ^{m6} AGG	^{m5} CCTC	Eh3,Mc11
			^{m5} C ^{m5} CT ^{m5} C	
<i>Mph</i> I	CCWGG	?	C ^{m5} CWGG	Ro3
<i>Mro</i> I	TCCGGA	TCCGG ^{m6} A	T ^{m5} CCGGA	Mc1,Ne14
			TC ^{m5} CGGA	Ne14
<i>Msc</i> I	TGGCCA	?	TGGC ^{m5} CA	Fo1
<i>Msp</i> I	CCGG ^b	^{m4} CCGG	^{m5} CCGG #	Eh2,Je2,Va3,Wa1,Wa5
		C ^{m4} CGG	^{hm5} C ^{hm5} CGG	Bu10,Hu1
		C ^{m5} CGG		
<i>Mst</i> II	CCTNAGG	^{m5} CCTNAGG	CCTN ^{m6} AGG	Ne5
<i>Mth</i> TI	GGCC	?	GG ^{m5} CC #	No4,No6
<i>Mth</i> ZI	CTAG	?	^{m4} CTAG #	No5
<i>Mva</i> I	CCWGG	C ^{m5} CWGG ^b	C ^{m4} CWGG #	Bu8,Ku2,K12
		^{m5} CCWGG	CC ^{m6} AGG ^b	Gr4,Ku1
			^{m4} CCWGG ^b	
			^{m5} C ^{m5} CWGG ^b	
<i>Mun</i> I	CAATTG	?	CA ^{m6} ATTG #	Ne14
<i>Mvn</i> I	CGCG	?	^{m5} CGCG	St8
<i>Nae</i> I	GCCGGC	?	G ^{m5} CCGGC	Ne14
				Eh3,K11,Mc11,Ne5

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>NanII</i>	G ^{m6} ATC ^b	G ^{m6} ATC	G ^{m5} CGGC GCCG ^{m5} C GATC G ^{m6} AT ^{m5} C ^b	Pa1,Ne5 GAT ^{m5} C
<i>NarI</i>	GGCGCC	GGCGC ^{m5} C	GG ^{m5} CGCC GGCGC ^{m4} C GG ^{hm5} CG ^{hm5} C ^{hm5} C	Ko3,Mc11,Ne5 Ne14
<i>NciI</i>	CCSGG	^{m5} CCSGG	C ^{m4} CSGG C ^{m5} CSGG ^b	Br8,Ko3,Mc11 Me3
<i>NcoI</i>	CCATGG	CC ^{m6} ATGG	^{m4} CCATGG ^b ^{m5} CCATGG	Kl1,Ne2,Ne4
<i>NciI</i>	AGATCT	AG ^{m6} ATCT ^b	?	Qi1
<i>NcuI</i>	GAAGA	?	GAAG ^{m6} A	Mc13
<i>NdeI</i>	CATATG	^{m5} CATATG ^b	CAT ^{m6} ATG [#]	Be4,Mc11,Re7,Si1,We3
<i>NdeII</i>	GATC	GAT ^{m5} C ^b	G ^{m6} ATC	Mc9
<i>NgoI^b</i>	RGCGCY	?	RG ^{m5} CGCY	Ko3,Ko5
<i>NgoII^b</i>	GGCC	?	GG ^{m5} CC [#] GGC ^{m5} C ^b	Ko3,Ko5 Su3,Su4
<i>NgoBI^b</i>	TCACC	?	T ^{m5} CACC	Pi3,Pi4
<i>NgoMI</i>	GCCGGC	?	G ^{m5} CCGCC [#] GC ^{m5} CGGC	Gu4 Fo1
<i>NheI</i>	GCTAGC	?	GCTAG ^{m5} C	Kl1,Mc11,Ne2
<i>NlaIII</i>	CATG	?	C ^{m6} ATG [#] ^{m5} CATG	La1,Mo3 Zh2
<i>NlaIV</i>	GGNNCC	?	GGNN ^{m4} CC	Ne14
<i>NmuDI</i>	G ^{m6} ATC ^b	G ^{m6} ATC	GATC	Pa1
<i>NmuEI</i>	G ^{m6} ATC ^b	G ^{m6} ATC	GATC	Pa1
<i>NorI</i>	GCGGCCGC	GCGGCCG ^{m5} C	GCGG ^{m5} CCGC GCGGC ^{m5} CGC	Mc11 St5,Qi2
<i>NruI</i>	TCGCGA	TCG ^{m5} CGA	T ^{m5} CGCGA TCGCG ^{m6} A	Ne14,Qi3 Ne2
<i>NsiI</i>	ATGCAT	?	ATG ^{m5} CAT ATGC ^{m6} AT	Be5,Wo1
<i>NspI</i>	RCATGY	?	R ^{m5} CATGY RC ^{m6} ATGY	Ne14 Ne14
<i>NspV</i>	TTCGAA [#]	?	?	Ue1
<i>NspBII</i>	CMGCKG	C ^{m5} CGCKG	?	Ne14
<i>Paer7I</i>	CTCGAG	?	CT ^{m5} CGAG ^b CTCG ^{m6} AG [#]	Gi3 Gh1
<i>PfiMI</i>	CCAN ₅ TGG	?	C ^{m4} CAN ₅ TGG C ^{m5} CAN ₅ TGG	Ne14 St7
<i>PfaI</i>	GATC	G ^{m6} ATC	?	Ro3
<i>PfuI</i>	CGTACG	?	CGTA ^{m5} CG	Ne14
<i>PmeI</i>	GTTTAAAC	GTTTAAA ^{m5} C	?	Fo1
<i>PmlI</i>	CACGTG	?	CA ^{m5} CGTG	Fo1
<i>PpuAI</i>	CGTACG	?	CGTA ^{m5} CG	Ne14
<i>PpuMI</i>	RGGWCCY	?	RGGWC ^{m5} CT	Fo1
<i>PstI</i>	CTGCAG	?	^{m5} CTGCAG ^b C ^{hm5} UGCAG CTG ^{m5} CAG CTGC ^{m6} AG [#]	Do1,Gr5,Mc11,Ne2 Ho1 Ne5
<i>PvuI</i>	CGATCG	CG ^{m6} ATCG	CGAT ^{m4} CG CGAT ^{m5} CG	Br8,Bu7,Eh3
<i>PvuII</i>	CAGCTG	?	CAG ^{m4} CTG [#] CAG ^{m5} CTG ^b	Br8,Bu9,Do1 Eh3,Ja3,Ro1
<i>RfiFI</i>	GTCGAC	?	GTCG ^{m6} AC	Mo5
<i>RfiFII</i>	AGTACT	?	AGT ^{m6} ACT	Mo5
<i>Rrh4273I</i>	GTCGAC	?	GTCG ^{m6} AC	Ba6
<i>RsaI</i>	GTAC ^b	GTA ^{m5} C ^b	GT ^{m6} AC GTA ^{m4} C ^{#b}	Eh3,Fo1,Ne14,Ne4,Ne5 Wo2
<i>RshI</i>	CGATCG	CG ^{m6} ATCG	?	Ly1
<i>RspXI</i>	TCATGA	?	TC ^{m6} ATGA TCATG ^{m6} A	Pa2 Ne4
<i>RsrI</i>	GAATTC	?	G ^{m6} AATTC GA ^{m6} ATTC ^{#b}	Mc11 Ba5
<i>RsrII</i>	CGGWCCG	?	^{m5} CGGWCCG CGGW ^{m5} CCG CGGW ^{m5} CG	Mc11,Qi3
<i>SacI</i>	GAGCTC	G ^{m6} AGCTC GAGCT ^{m5} C	GAG ^{m5} CTC	Mc11 Fo1
<i>SacII</i>	CCGCGG	?	^{m5} CCGCGG C ^{m5} CGCGG	Kl1,Ne2 Qi2
<i>SaII</i>	GTCGAC	GTCGA ^{m5} C	GT ^{m5} CGAC ^b GTCG ^{m6} AC [#]	Br8,Eh2,Lu2,Qi1 Mc3,Ro4,Ro5,Va4

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>Sal</i> DI <i>Sau</i> LPI <i>Sau</i> 3AI	TCGCGA GCCGGC GATC ^b	TCGCG ^{m6} A ? G ^{m6} ATC GA ^{hm5} UC	G ^{hm5} UCGAC T ^{m5} CGCGA G ^{m5} CCGGC [#] GAT ^{m5} C ^{#b} GAT ^{m4} C GAT ^{hm5} C GGN ^{m5} CC [#] GGNC ^{m5} C GGN ^{hm5} C ^{hm5} C	Ho1 Mc13,Ne14,Qi3 Ok1 Dr1,Eh2,Ja3,Mc3,Ro3,Se1 Ho1,Ne5 Hu1 Ko3,Ne2,Pe1
<i>Sau</i> 96I	GGNCC	?	GGN ^{m5} CC [#] GGNC ^{m5} C GGN ^{hm5} C ^{hm5} C	Hu1 Ze1
<i>Sau</i> 3239I <i>Sbo</i> 13I <i>Sca</i> I <i>Scr</i> FI	CTCGAG TCGCGA AGTACT CCNGG	? TCGCG ^{m6} A AGTA ^{m5} CT ^{m5} CCNGG	CTCG ^{m6} AG [#] T ^{m5} CGCGA ? C ^{m5} CNGG C ^{m4} CNGG G ^{m6} ATGC GGC ^{m5} CN ₃ GGCC GGCCN ₃ GGC ^{m5} C	Mc11,Ne14 Wo1 Da4,Mc11,Ne2 Ne14 Mc11,Po4 Mc11,Qi2 GG ^{m4} CCN ₃ GGCC
<i>Sfa</i> NI <i>Sfi</i> I	GATGC GGCCN ₃ GGCC	GATG ^{m5} C GG ^{m5} CCN ₃ GG ^{m5} CC	GATG ^{m5} C GG ^{m5} CCN ₃ GG ^{m5} CC	Ne5
<i>Sfi</i> I <i>Sfi</i> I <i>Sgr</i> AI <i>Sin</i> I <i>Sma</i> I	TTCGAA CTGCAG CRCCGGYG GGWCC CCCCGG	TT ^{m5} CGAA ? ? ? C ^{m5} CCGGG	TTCG ^{m6} AA CTGC ^{m6} AG CRC ^{m5} CGGYG GGW ^{m5} CC [#] m ⁴ CCCCGGG [#] m ⁵ CCCCGGG ^b C ^{m4} CCGGG ^b CC ^{m4} CGGG CC ^{m5} CGGG ^b TA ^{m5} CGTA T ^{m6} ACGT ^{m6} A GTG ^{m5} CA ^{m5} C m ⁶ ACTAGT A ^{m5} CTAGT GC ^{m6} ATGC G ^{hm5} CATG ^{hm5} C	Br8 Ta3 Ka5,Ka6 Br8,Bu10,Eh2,Ga4 Ja3,Ka7,Mc3,Qu1
<i>Sna</i> BI	TACGTA	?	TA ^{m5} CGTA T ^{m6} ACGT ^{m6} A GTG ^{m5} CA ^{m5} C m ⁶ ACTAGT A ^{m5} CTAGT GC ^{m6} ATGC G ^{hm5} CATG ^{hm5} C	Fo1,Ya1
<i>Sno</i> I <i>Spe</i> I	GTGCAC ACTAGT	? ?	GTG ^{m5} CA ^{m5} C m ⁶ ACTAGT A ^{m5} CTAGT GC ^{m6} ATGC G ^{hm5} CATG ^{hm5} C	Ho3,Wo1 Ho2 Wo1 Mc11,Mo3,Ne2
<i>Sph</i> I	GCATGC	GCATG ^{m5} C	GCATG ^{m5} C	Ne14,Ne4,Qi3
<i>Sp</i> II	CGTACG	CGT ^{m6} ACG ^b	CGTA ^{m5} CG CGTA ^{m4} CG	Ne14,Ne4
<i>Sp</i> oI	TCGCGA	TCGCG ^{m6} A	T ^{m5} CGCGA TCG ^{m5} CGA	Ma11
<i>Srf</i> I	GCCCCGGGC	?	G ^{m5} CCCCGGGC GC ^{m5} CCCCGGGC GCC ^{m5} CGGGC GCCCCGGG ^{m5} C G ^{m6} AAATTC [#] C ^{m5} CNGG m ⁵ CCNGG	Ni4 Ni1,Vi1 Gr4
<i>Sso</i> I <i>Sso</i> II	GAATTC CCNGG	? ?	TTCG ^{m6} AA GAG ^{m5} CTC GAG ^{hm5} CT ^{hm5} C m ⁵ CCGCGG C ^{m5} CGCGG GG ^{m6} ATG [#] C ^{m6} ATCC [#]	Li1 Br8,Ro1 Hu1 Ne5 Ne5 Ki5
<i>Ssp</i> RFI <i>Sst</i> I	TTCGAA GAGCTC	? ?	AGG ^{m5} CCT AGG ^{m5} CT AGG ^{m4} CT C ^{m5} CWWGG CAG ^{m6} AG [#] AACN ₆ R ^m TAYG GA ^{m6} AN ₆ R ^m TTCG [#] GA ^{m6} AN ₇ R ^m TTCG [#] GAGN ₆ G ^m TRC G ^{m6} AGN ₆ R ^m TAYG ^{#b} A ^{m6} ACN ₆ G ^m TRC ^{#b}	Ca4,Mc11 So3 Ne14 Mi3 Da5 Na2 Bi1,Pr2,Pr3 Pr1,Pr2 Ga3 Na1,Na2 Na1,Na2
<i>Ssr</i> II	CCGCGG	?	TCG ^{m6} A [#] T ^{hm5} CGA ^b G ^{m6} ACCGA	Gr5,Hu1,Mc3,Va3 Ba13,Hu1 Ne4
<i>Srs</i> I	GGATG	?	?	Gr1
<i>Sru</i> I	AGGCCT	?	?	Fo1 Sa3,Va6 Ga1,Ne14 Hu1 Fo1
<i>Sry</i> DI <i>Sry</i> LTI <i>Sry</i> QI <i>Sry</i> R124I <i>Sry</i> R124/3I <i>Sry</i> SJI <i>Sry</i> SBI <i>Sry</i> SPI <i>Taq</i> I	CCWWGG CAGAG AACN ₆ RTAYG ^b GAAN ₆ RTCG ^b GAAN ₇ RTCG ^b GAGN ₆ GTRC ^b GAGN ₆ RTAYG ^b AACN ₆ GTRC ^b TCGA	? ? ? ? ? ? ? ? ? T ^{m5} CGA ^b	?	
<i>Taq</i> II	GACCGA CACCCA CCWGG	? ? m ⁵ CCWGG C ^{m5} CWGG	?	
<i>Taq</i> XI	GAWTC TCGA CGCG	GAWT ^{m5} C ? ?	TCCG ^{m6} A m ⁵ CGCG hm ⁵ CG ^{hm5} CG	
<i>Th</i> 111I	GACN ₃ GTC	GA ^{m5} CN ₃ GTC GACN ₃ GT ^{m5} C	?	

Table I. (cont.)

Restriction enzyme	Recognition sequence	Sites cut	Sites not cut	References
<i>Tth</i> HBI	TCGA	T ^{m5} CGA	TCG ^{m6} A [#]	Sa3
<i>Tsp</i> 509I	AATT	?	^{m6} AATT	Fo1
<i>Van</i> 91I	CCAN ₅ TGG	?	C ^{m5} CAN ₅ TGG	Ja3
<i>Xba</i> I	TCTAGA	?	TCTAG ^{m6} A [#]	Mc13, We1
			T ^{m5} CTAGA ^b	Gr5, Hu1, Ne2
			T ^{hm5} CTAGA	
<i>Xcy</i> I	CCCGGG	?	C ^{m4} CCGGG [#]	Wi6
<i>Xho</i> I	CTCGAG	?	^{m5} CTCGAG	Ne2, Ka7
		CT ^{m5} CGAG ^b		Eh3
<i>Xho</i> II	RGATCY	RG ^{m6} ATCY	CTCG ^{m6} AG	Mc3, Va3
<i>Xma</i> I	CCCGGG	CC ^{m5} CGGG ^b	RGAT ^{m5} CY ^b	Br8
			^{m4} CCCGGG	Bu10, Yo5, Yo6
			^{m5} CCCGGG	
			C ^{m4} CCGGG	
			CC ^{m4} CGGG	
<i>Xma</i> III	CGGCCG	?	CGG ^{m5} CCG [#]	Gu9, Ne2, Tr5
<i>Xmn</i> I	GAAN ₄ TTC	GA ^{m6} AN ₄ TTC	G ^{m6} AAN ₄ TTC	Mc11, Ne2
			GAAN ₄ TT ^{m5} C ^b	
<i>Xor</i> II	CGATCG	?	CGAT ^{m5} CG	Br8, Eh2
			CG ^{m6} ATCG ^b	
			^{hm5} CGAT ^{hm5} CG	Hu1, Sm4

^a # denotes canonical modification MTase specificity. M = A or C, K = G or T, N = A, C, G, or T, R = A or G, Y = C or T, W = A or T, S = G or C, D = A, G or T, H = A, C or T. Sequences are in 5'-3' order. ^{m4}C = N4-methylcytosine; ^{m5}C = C5-methylcytosine; ^{hm5}C = hydroxymethylcytosine; ^{hm5}U = hydroxymethyluracil; ^mC = methylcytosine, in which N4 or C5-methylcytosine unspecified; ^{m6}A = N6-methyladenine. Nomenclature is according to (Sm2) and (Co4).

^b *Acc*I nicks slowly in the unmethylated strand of the hemimethylated sequence GTMKA^{m5}C. *Acc*I cuts slowly at hemimethylated GTMKA^{m5}C (Ne10).

*Acc*III cuts slowly at T^{m5}CCGGA and TC^{m5}CGGA (Sc10).

*Afl*I cuts slowly at GGWC^{m4}C.

*Aha*II (GRCGYC) will cut GRCGCC *faster* if these sites are methylated at GRCG^{m5}CC (Ne5), but will not cut GRCGY^{m5}C sites (Ne2, Ne5).

*Asp*718I cuts GT^{m6}AC- and ^{m5}CC-modified *Chlorella* virus NY2A DNA but does not cut GGTAC^{m5}CWGG overlapping *dcm* sites (Mu2) or ^{m5}C-substituted phage XP12 DNA. In contrast, *Kpn*I cuts these modified substrates readily (Ne4).

*Ava*I nicking occurs slowly in the unmethylated strand of the hemimethylated sequence CTCG^{m6}AG/CTCGAG (Ne5).

*Ava*II cuts slowly at GGWC^{m4}C.

Bacillus species have been surveyed for G^{m6}ATC and C^{m5}CWGG specific methylases. Many species have G^{m6}ATC specific methylases but none had C^{m5}CWGG specific methylases (Di2).

*Bal*I sites overlapping *dcm* sites (TGGC^{m5}CAGG) are 50-fold slower than unmethylated sites (Gi1).

*Ban*I gives various rate effects when its recognition sequence is ^{m4}C- or ^{m5}C-methylated at different positions.

*Bgl*I cleavage rate at certain GC^{m5}CN₅GGC, GC^{m4}CN₅GGC, and GCCN₅GG^{m5}C hemimethylated sites is extremely slow. However, ^{m5}C bi-methylated M·*Hae*III–*Bgl*I sites are completely refractory to *Bgl*I (Ko3, Ne2).

*Bsp*EI cleavage slowed by TC^{m5}CGGA (Fo1).

*Bsr*BI cleavage slowed by GAG^{m5}CGG (Fo1).

*Bss*HII does not cut M·*Hha*I-modified DNA, in which two different cytosine positions are hemimethylated, G^{m5}CGCGC/GCG^{m5}CGC (Ne4).

M·*Bst*I modifies the internal cytosine GGAT^mCC, but it is not known whether this modification is ^{m5}C or ^{m4}C (Le3).

*Bsr*EII cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5).

*Bst*NI isoschizomers that are insensitive to C^{m5}CWGG include *Aor*I, *Apy*I, *Bsp*NI, *Mva*I and *Taq*XI (Mc4).

*Bsu*RI nicking occurs in the unmethylated strand of the hemimethylated sequence GG^{m5}CC/GGCC.

*Cfr*9I, see reference Bu10 for rate effects.

Clal cuts slowly at hemimethylated AT^{m5}CGAT (Ne10).

M·*Cre*I is from the unicellular eukaryote *Chlamydomonas reinhardtii* (Sa2).

*Dpn*I requires adenine methylation on both DNA strands. Isoschizomers of *Dpn*I include *Cfu*I, *Nan*II, *Nmu*EI, *Nmu*DI and *Nsu*DI (Ca1). *Dpn*I cuts *dam* modified XP12 DNA (Ne6).

M·*Eco* *dam* modifies GAT^{m5}C at a reduced rate (Ne5). Many other bacteria that modify their DNA at G^{m6}ATC are listed in references Ba1 and Lo1.

*Eco*AI, *Eco*BI, *Eco*DI, *Eco*EI, *Eco*DXXI, *Eco*KI and others (Bi6) are Type I restriction endonucleases. ^mT represents a 6-methyladenine in the complementary strand.

*Eco*PI is a Type III restriction endonuclease (Ba1, Ba2, Ha4).

*Eco*P15I is a Type III restriction endonuclease (Hu2).

*Eco*RI cannot cut hemimethylated G^{m6}AATTC/GAATTC sites. Bimethylated GA^{m6}ATTC/GA^{m6}ATTC sites are not cut by *Eco*RI or *Rsr*I (Ne5). *Eco*RI shows a reduced rate of cleavage at hemimethylated GAATT^{m5}C (Tr1) and does not cut an oligonucleotide that contains GAATT^{m5}C in both strands (Br1).

*Eco*RII does not cleave some DNA molecules that carry only a single site. However, oligonucleotides containing the *Eco*RII site can be used to transactivate sites that are resistant to cleavage (Re5). *Eco*RII isoschizomers that are sensitive to C^{m5}CWGG include *Atu*BI, *Atu*II, *Bsr*GII, *Bin*SI, *Ecl*II, *Eca*II, *Eco*27I, *Eco*38I and *Mph*I (Ro3). *Eco*RII shows reduced rate of cleavage at hemimethylated ^{m5}CCWGG/CCWGG sites (Yo1).

*Eco*RV cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5).

*Eco*R124I and *Eco*R124/3I are now called *Spy*R124I and *Spy*R124/3I.

*Fok*I cuts about two-fold to four-fold more slowly at CATC^{m5}C than at unmodified sites (Ne5).

M·*Fok*I in ref Po3 corresponds to M·*Fok*IA in ref Po4.

*Hae*II shows a reduced rate of cleavage when its recognition sequence is modified at RGCG^{m5}CY.

*Hae*III nicking occurs in the unmethylated strand of the hemimethylated sequence GG^{m5}CC/GGCC.

*Hinf*I cuts GANT^{m5}C, however, detectable rate differences are observed between unmethylated, hemimethylated (GANT^{m5}C/GANTC) and bi-methylated (GANT^{m5}C/GANT^{m5}C) target sequences (Co1, Gr5, Ne5, Ne10). However, the rate difference between unmethylated and fully methylated *Hinf*I sites is only about ten-fold (Hu1, Ne5, Pe1).

*Hinc*II. There is conflicting data regarding cleavage of GTYRA^{m5}C.

*Hind*III cuts slowly at hemimethylated AAG^{m5}CTT (Ne10).

*Hpa*II nicking in the unmethylated strand of the hemimethylated sequence ^{m5}CCGG/CCGG is in dispute (Be3, Bu10, Ko3). *Hpa*II cuts hemimethylated mCCGG fifty

times slower and fully methylated mCCGG 3000 times slower than unmethylated DNA (Ko3). See reference (Bu10) for *HpaII* rate effects.

KpnI cuts ^{m5}C-substituted phage XP12 DNA (Ne4) but cuts slowly at hemimethylated GGTA^{m5}C^{m5}C, GGTA^{m5}CC and GGTAC^{m5}C (Ne10).

MaeII nicks slowly in the unmethylated strand of hemimethylated A^{m5}CGT/ACGT (Mo2).

MboI isoschizomers that are sensitive to G^{m6}ATC include *BssGII*, *BsaPI*, *Bsp74I*, *Bsp76I*, *Bsp105I*, *BstXII*, *BstEIII*, *BssGII*, *CpaI*, *CryI*, *CviAI*, *CviBII*, *CviHI*, *CviSVI*, *DpnII*, *FnuAII*, *FnuCI*, *HaeI*, *MaeI*, *MkrAI*, *MmeII*, *MnoIII*, *MosI*, *Msp67II*, *MthI*, *MthAI*, *NdeII*, *NfiAII*, *NfiBI*, *NfiI*, *NlaDI*, *NlaII*, *NmeCI*, *NphI*, *NsiAI*, *NspAI*, *NsuI*, *PfaI*, *RluII*, *SalAI*, *SalHI*, *Sau6782I*, *SinMI*, *TruII* (Ro3).

MboII cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5), although certain hemimethylated ^{m5}C-containing substrates are reported not to be cut (Gr5).

MflI cuts slowly at ^{m6}AGATCY sites (On1).

Mammalian methylase is the ^{m5}CG methyltransferase from *Mus musculus*. (mouse) (Be7).

MspI cuts the hemimethylated sequence C^{m5}CGG/CCGG (Wa5) and C^{m4}CGG/CCGG duplexes (Bu10). *MspI* cuts very slowly at GGC^{m5}CGG (Bu6). An M·*MspI* clone methylates ^{m5}CCGG (Wa5, Wa2). However, there is a report that *Moraxella* sp. chromosomal DNA is methylated at ^{m5}C^{m5}CGG (Je2).

MvaI nicking occurs in the unmethylated strand of the hemimethylated sequence ^{m4}CCWGG/CCWGG and CC^{m6}AGG/CCTGG (Ku1). *MvaI* cuts XP12 DNA very slowly at ^{m5}C^{m5}CWGG.

NanII requires adenine methylation on both DNA strands (Ca1). *NanII* cuts *dam* methylase-modified XP12 DNA (Ne5).

NciI ability to cut C^{m5}CGGG in dispute.

NcoI is blocked by M·*SecI* (CCNNGG) (Ne5).

NcrI is a *BglII* isoschizomer from *Nocardia carnia* Beijing (Q11).

NdeI cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5).

NdeII cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5).

Ngo. There is some confusion about naming restriction enzymes from these strains (Gu4). *NgoPI* may be *NgoI*, *NgoPII*, *NgoII* and *NgoSI* may be the same. *NgoPIII* may be *NgoIII*.

NgoII does not cut overlapping dcm sites (Su4).

NmuDI requires adenine methylation on both DNA strands (Ca1).

NmuEI requires adenine methylation on both DNA strands (Ca1).

PaeR7I cuts hemimethylated CT^{m5}CGAG/CTCGAG sites 100-fold slower and cuts fully methylated CT^{m5}CGAG/CT^{m5}CGAG 2900 fold slower than unmethylated sites (Gh1). Hemi- or full methylation at ^{m6}A completely protects against *PaeR7I* cleavage (Gh1).

PstI cuts slowly at hemimethylated ^{m5}CTG^{m5}CAG (Ne10).

PvuII cuts slowly at hemimethylated ^{m5}CAG^{m5}CTG (Ne10).

RsaI cuts the fully ^{m5}C-substituted phage XP12 DNA (Ne5), [contradicted by (Fo1) and by NEB catalog which says *RsaI* does not cut if fully ^{m5}C- methylated in both strands. It may be very slow at these sites. It is likely that M·*RsaI* modifies at GTA^{m4}C.

RsrI cannot cut hemimethylated G^{m6}AATTC/GAATTC sites.

SalI cuts slowly at hemimethylated GT^{m5}CGAC (Ne10).

Sau3AI nicking occurs in the unmethylated strand of the hemimethylated sequence GAT^{m5}C/GATC (St3). *Sau3AI* cuts at a reduced rate at ^{m6}AGATC (On1). *Sau3AI* isoschizomers that are insensitive to G^{m6}ATC include *Bce243I*, *Bsp49I*, *Bsp51I*, *Bsp52I*, *Bsp54I*, *Bsp57I*, *Bsp58I*, *Bsp59I*, *Bsp60I*, *Bsp61I*, *Bsp64I*, *Bsp65I*, *Bsp66I*, *Bsp67I*, *Bsp72I*, *BspAI*, *Bsp91I*, *BsrPII*, *CpfI*, *Csp5I*, *CpeI*, *FnuEI*, *MspBI*, *SauCI*, *SauDI*, *SauEI*, *SauFI*, *SauGI* and *SauMI* (Ro3).

SmaI nicking occurs in the unmethylated strand of the hemimethylated sequence CC^{m5}CGGG/CCCGGG (Bu10, Wa5). *SmaI* may cut C^{m5}C^{m5}CGGG methylated DNA (Br8, Je2). Possibly the second methylation negates the effect of CC^{m5}CGGG. There are conflicting results regarding *SmaI*: ^{m5}CCCGGG is not cut when modified by M·*AquI* methyltransferase (Ka7) or at overlapping M·*HaeIII*-*SmaI* sites (GG^{m5}CCCGGG, Ne5). Other investigators have reported that *SmaI* cuts at a reduced rate at hemimethylated ^{m5}CCCGGG sites (Bu10).

SpeI cuts slowly at hemimethylated A^{m5}CTAGT (Ne10).

SpII cuts GT^{m6}AC-modified *Chlorella* virus NY2A DNA, but does not cut *KpnI*-digested XP12 DNA (Ne4).

SryQI is a Type I restriction endonucleases. ^{mT} represents a 6-methyladenine in the complementary strand.

SryR124I and *SryR124/3I* are Type I restriction endonucleases formerly called *EcoR124I* and *EcoR124/3I*. ^{mT} represents a 6-methyladenine in the complementary strand.

SrySBI and *SrySPI* are Type I restriction endonucleases. ^{mT} represents a 6-methyladenine in the complementary strand.

SrySII is a Type I restriction endonucleases. ^{mT} represents a 6-methyladenine in the complementary strand.

TaqI cuts very slowly at T^{hm5}CGA (Hu1). *TaqI* cuts the fully ^{m5}C substituted phage XP12 DNA (Hu1, Ne5).

M·*TaqI* methylates T^{m5}CGA at least 20 fold slower than unmodified TCGA (Mc7).

XbaI will cut T^{m5}CTAGA/TCTAGA hemimethylated DNA at high enzyme levels (>100U *XbaI* /μg), but will not cut this sequence in twenty to forty-fold overdigestions (Ne5, Ne10).

XhoI may cut CT^{m5}CGAG according to the NEB catalog.

XhoII nicking occurs slowly in the unmethylated strand of the hemimethylated sequence RGAT^{m5}CY/RGATCY.

XmaI is claimed not cut CC^{m5}CGGG in one report (Br8). See reference Bu10 for rate effects.

XmnI cuts the fully ^{m5}C substituted phage XP12 DNA (Ne5). *XmnI* cuts slowly at some sites in DNA methylated on both strands at GAAN₄TT^{m5}C (Ne5).

XorII, according to the BRL-Gibco catalog, may cut CG^{m6}ATCG.

Table II. Isoschizomer pairs that differ in their sensitivity to sequence-specific methylation

Restriction isoschizomer pairs ^{a,b}			
Methylated sequence ^c	Cut by	Not cut by	References
^{m5} CATG	<i>CviAII</i>	<i>NlaIII</i>	Zh2
C ^{m5} CAN ₇ TGG	<i>Esp1396I</i>	<i>PfiMI</i> , <i>Van9II</i>	Ja3, St7
^{m4} CCGG	<i>MspI</i>	<i>HpaII</i>	Bu10
C ^{m5} CGG	<i>MspI</i>	<i>HpaII</i> , <i>HapII</i>	Eh2, Mc11
C ^{m4} CGG	<i>MspI</i>	<i>HpaII</i>	Bu10
CC ^{m5} CGGG	<i>Cfr9I</i> , <i>XmaI</i>	<i>SmaI</i>	Bu10
^{m5} CCTNAGG	<i>MsrII</i>	<i>Bsu36I</i>	Ne5
C ^{m5} CSGG	<i>BcnI</i>	<i>EcoHI</i> , <i>Eco183II</i>	Kr3
C ^{m5} CWGG	<i>ApyI</i> , <i>BstNI</i> , <i>MvaI</i>	<i>EcoRII^d</i>	Bu8
^{m5} CCWGG	<i>BstNI</i> , <i>EcoRII</i> , <i>MvaI</i>	<i>ApyI</i>	Ke1, Ku1, Ne3, Yo1
CG ^{m6} ATCG	<i>PvuI</i>	<i>XorII</i>	Bi3, Br8, Sm4
GAAN ₄ TT ^{m5} C	<i>Asp700I</i>	<i>XmnI</i>	Ne14, Ne2
GAGCT ^{m5} C	<i>SacI</i>	<i>Ecl136II</i>	Qi3, Fo1
G ^{m6} ATC	<i>FnuEI</i> , <i>Sau3AI</i>	<i>MboI</i> , <i>NdeII</i>	Ge1, Lu1, Mc9, Ro3
GAT ^{m5} C	<i>MboI</i>	<i>Sau3AI</i>	Ne4
GAT ^{m4} C	<i>MboI</i>	<i>Sau3AI</i>	Ne4
GGC ^{m5} C	<i>HaeIII</i>	<i>NgoII</i>	Su4

Table II. (cont.)**Restriction isoschizomer pairs ^{a,b}**

Methylated sequence ^c	Cut by	Not cut by	References
GGNC ^{m5} C	<i>AsuI</i>	<i>Sau96I</i>	Ko3
GTG ^{m5} CAC	<i>ApaLI</i>	<i>Alw44I</i>	Ne14
GGTAC ^{m5} C	<i>KpnI</i>	<i>Asp718I, Acc65I</i>	Mu2, Ne5
GGTA ^{m5} C ^{m5} C	<i>KpnI</i>	<i>Asp718I</i>	Ne4
GGWC ^{m5} C	<i>AflI</i>	<i>AvaII, Eco47I</i>	Ba3, Ja5, Wh2, Mc10, Mc11
RG ^{m6} ATCY	<i>BstYI, XhoII</i>	<i>MflI</i>	Mc9, Ne4, On1
RGAT ^{m5} CY	<i>BstYI</i>	<i>MflI, XhoII</i>	Ne4, On1
T ^{m5} CCGGA	<i>AccIII</i>	<i>BspMII, Kpn2I, MroI</i>	La2, Sc2
TC ^{m5} CGGA	<i>AccIII, BspEI</i>	<i>BspMII, Kpn2I, MroI</i>	Fo1, Sc2
TCCGG ^{m6} A	<i>BspMII, Kpn2I, MroI</i>	<i>AccIII</i>	Ke3, Ne4
T ^{hm5} CGA	<i>TaqI</i>	<i>CviSIII</i>	Ne14, Hu1
TCGCG ^{m6} A	<i>AmaI, SalDI, Sbo13I, SpoI</i>	<i>NruI</i>	Mc11, Mc13, Ne4
TCG ^{m5} CGA	<i>NruI</i>	<i>SpoI</i>	Ne14, Qi3
TT ^{m5} CGAA	<i>AsuII, SfiI</i>	<i>BstBI</i>	Ne5, Wo1
TTCG ^{m6} AA	<i>CbiI</i>	<i>BstBI, Csp45I, SspRFI</i>	Li1, Mu1, Ne4, Sc11, Wo1
CGGWC ^{m5} CG	<i>CspI</i>	<i>RsrII</i>	Qi3

Restriction isomethylator pairs ^{e,f}

Methylated sequence ^c	Methylated by	Not methylated by	References
T ^{m5} CGA	M·CviBIII (TCG ^{m6} A)	M·TaqI	We2

^a In each row the first column lists a methylated sequence, the second column lists an isoschizomer that cuts this sequence, and the third column lists an isoschizomer that does not cut this sequence.

^b An enzyme is classified as insensitive to methylation if it cuts the methylated sequence at a rate that is at least one tenth the rate at which it cuts the unmethylated sequence. An enzyme is classified as sensitive to methylation if it is inhibited at least twenty-fold by methylation relative to the unmethylated sequence.

^c See footnote 'a' of Table I.

^d See footnote 'b' of Table I.

^e In each row the first column lists a methylated sequence, the second column lists an isomethylator that modifies this sequence, and the third column lists an isomethylator that does not modify this sequence.

^f An enzyme is classified as insensitive to methylation if it modifies the methylated sequence at a rate that is at least one tenth the rate at which it modifies the unmethylated sequence. An enzyme is classified as sensitive to methylation if it is inhibited at least twenty-fold by methylation relative to the unmethylated sequence.

Table III. DNA methyltransferases and their modification specificities

Methylase ^a	Specificity ^a	EMBL accession #	References
M·AadII	GACGTC		Lu2
M·AccI	GTMK ^{m6} AC	D10671	Lu2
M·AflII	CTTAAG (^{m6} A)		Lu2
M·AlaK21	GAT ^{m5} C		Sl1
M·AluI	AG ^{m5} CT	Z11841	Kr1, Lu2, Zh1
M·Alw26I	GT ^{m5} CTC		Bi7, Bu8
	and G ^{m6} AGAC		Bu8
M·ApaI	GGG ^{m5} CCC		Gu9, Mc8
M·ApuI	^{m5} CYCGRG	M28051	Ka7, Ka8
M·AseI	ATTAAT		Mo3
M·AseII	CCSGG		Mo3
M·AvaI	CYCGRG		Lu2
M·AvaII	GGWCC		Lu2
M·AvrI	CYCGRG		Lu3
M·BaiI	TGG ^{m5} CCA		Lu2, Mc8
M·Bacillus	G ^{m6} ATC ^b		Di2
M·BamHI	GGAT ^{m4} CC	X55285	Ha3, Lu2, Na3
M·BamHII	G ^m CWGC?	M72412	Ha3
M·BaiI	GGYRCC (^{m5} C)	D00704	Lu2, Ma12, Su1
M·BanII	GRGCYC		Lu2
M·BanIII	ATCG ^{m6} AT	P22772 (protein)	Ka12
M·BbvI	G ^{m5} CAGC		Do1, Ha3, Va5
M·BbvSI	G ^m CWGC		Ha5, Va5
M·Bbv	G ^{m6} AT		Ha3
M·Bbv	A ^{m6} AG		Ha3
M·BcgI	CG ^{m6} AN ₅ TGC	L17341	Ra4
M·BcnI	C ^{m4} CSGG		Ja4, Ja6, Ja7, Pe2, Po6
M·BepI	^{m5} CGCG	X13555	Ku3
M·BglI	GCCN ₅ GGC (^{m4} C)		Lu2

Table III. (cont.)

Methylase ^a	Specificity ^a	EMBL accession #	References
M· <i>Bme</i> 216I	GGWC ^m C		Ma9
M· <i>Bna</i> I	GGAT ^m CC		Ki1
M· <i>Bse</i> CI	ATCG ^m AT		Ri3,Ri4
M· <i>Bsp</i> RI	GG ^m CC	X15758	Fe2,Ko1,Po2,Qi3,Sz4,Ve1
M· <i>Bsp</i> 106I	ATCG ^m AT		Pa2
M· <i>Bsp</i> 6I	GCNCG		Ja3
M· <i>Bst</i> I	GGAT ^m CC		Le3
M· <i>Bst</i> VI	CTCG ^m AG	L07642,L07643	Ba7
M· <i>Bst</i> NI	C ^m 4CWGG		Ba12
M· <i>Bst</i> YI	RGAT ^m CY		Va2
M· <i>Bsu</i> 15I	ATCG ^m AT		Re6
M· <i>Bsu</i> BI	CTGC ^m AG	L01541	Xu1
M· <i>Bsu</i> EII	m ⁵ CGCG		Gal,Gu9,Ik1,Je1
M· <i>Bsu</i> FI	m ⁵ CCGG	X62104,X51515	Gu9,Ik1,Je1,Wa7
M· <i>Bsu</i> H2	GG ^m CC		La8
	G ^m 5CNGC		
	GDGCHC		
M· <i>Bsu</i> MI	CT ^m 5CGAG		Gu2,Gu3,Gu9,Je1,Sh1
M· <i>Bsu</i> σ3T	GG ^m CC	M13488	Be1,Gu7,Gu6,No2,No3
	and G ^m 5CNGC		No1,Tr1
M· <i>Bsu</i> Q11I	GG ^m CC	X05242	Gu6,Gu7,Gu9,No1,No2
	and G ^m 5CNGC		
M· <i>Bsu</i> Q11s	GGCC		Be1
	and GDGCHC		
M· <i>Bsu</i> QI	m ⁵ CCGG		Je2
M· <i>Bsu</i> RI	GG ^m 5CC ^b	X02988	Gu8,Ki2,Ki3
M· <i>Bsu</i> SPb	GG ^m 5CC	M19513,M19514	Gu6,Gu7,Gu9,Je2,Ki2
	and G ^m 5CNGC		No2,Tr1,Tr3
M· <i>Bsu</i> SPRI	GG ^m 5CC	X01670,K02124	Be1,Gu5,Gu9,No2
	and m ⁵ C ^m 5CGG		Po1,Be2,Bu1,Gu5,Gu7,Ki2,Po1
M· <i>Bsu</i> SPR191	m ⁵ C ^m 5CGG		Je2,No2,Po1
	and C ^m 5CWGG		
M· <i>Bsu</i> SPR83I	GG ^m 5CC		Gu5
	and C ^m 5CWGG		
M· <i>Cfr</i> A	GCAN ₈ GTGG		Da2,Da3
M· <i>Cfr</i> BI	CCWWGG (m ⁴ C)	X57945	Za2
M· <i>Cfr</i> I	YGG ^m 5CCR		Po6
M· <i>Cfr</i> 6I	CAG ^m 4CTG		Bu9
M· <i>Cfr</i> 9I	C ^m 4CCGGG	X17022	KI2,Po6
M· <i>Cfr</i> 10I	R ^m 5CCGGY		Po6
M· <i>Cfr</i> 13I	GGN ^m 5CC		Bi5
M· <i>Cl</i> I	ATCG ^m AT		Mc3
M· <i>Cre</i> I	T ^m 5CR		Sa2
M· <i>Cyl</i> I	G ^m 6ATC		Ri2
M· <i>Cvi</i> AI	G ^m 6ATC		Ne14,Xi1,Xi6
M· <i>Cvi</i> AII	C ^m 6ATG	M86639	Ne14,Zh2
M· <i>Cvi</i> BI	G ^m 6ANTC	M96366	Xi2
M· <i>Cvi</i> BII	G ^m 6ATC		Ne14
M· <i>Cvi</i> BIII	TCG ^m 6A	X06618	Na4
M· <i>Cvi</i> JI	RG ^m 5CY	M27265	Sh3
M· <i>Cvi</i> JII	G ^m 6ANTC		Ne14
M· <i>Cvi</i> PI	m ⁵ CC		Xi4
M· <i>Cvi</i> QI	GT ^m 6AC		Xi2,Xi5
M· <i>Cvi</i> QII	G ^m 6ANTC		Ne14
M· <i>Cvi</i> QIII	C ^m 6ATG		Ne14
M· <i>Cvi</i> QIV	R ^m 6AR		Ne14
M· <i>Cvi</i> RI	TGC ^m 6A	M38173	St1
M· <i>Cvi</i> RII	GT ^m 6AC		St1
M· <i>Cvi</i> SI	TGC ^m 6A		Ne14
M· <i>Cvi</i> SII	C ^m 6ATG		Ne14
M· <i>Cvi</i> SIII	TCG ^m 6A		Ne14
M· <i>Cvi</i> SIV	G ^m 6ATC		Ne14
M· <i>Cvi</i> TI	RG ^m 5CB		Ne14
M· <i>Dde</i> I	m ⁵ CTNAG	Y00449	Ho4,Lu2,Sz3
M· <i>Dpn</i> II	G ^m 6ATC	M14339	De1,La3,La4,La5,Ma6
M· <i>Dpn</i> A	G ^m 6ATC	M14339	De1
M· <i>Eae</i> I	YGG ^m 5CCR		Ja1,Wh1
M· <i>Eag</i> I	CGGCCG		Sz2
M· <i>Eca</i> I	GGTN ^m 6ACC	X17111	Br3
M· <i>Eco</i> dam	G ^m 6ATC	V00272	Br6,Bu5,Dr1,Gi2,Ha4,He5,Ur1
M· <i>Eco</i> dcmI	C ^m 5CWGG	M32307	Bo7,Ma10,So1,Ur1
M· <i>Eco</i> dcmII	R ^m CCGG		Bu4,Ne8
M· <i>Eco</i> dcmIII	m ⁵ CCWGG		Ni2
M· <i>Eco</i> dcmIV	GGWC ^m C		Mo1,Ni2
M· <i>Eco</i> AI	G ^m 6AGN ₇ G ^m TCA ^b	J03150	Co7,Fu2

Table III. (cont.)

Methylase ^a	Specificity ^a	EMBL accession #	References
M·EcoBI	TG ^{m6} AN ₈ mTGCT ^b	J01630	Go3
M·EcoD	TTAN ₇ GTCY ^b	J01631	Go3
M·EcoDXXI	TCAN ₇ ATTCT ^b	X73984	Gu1
M·EcoEI	GAGN ₇ ATGC ^b	J03162	Fu2
M·EcoKI	AM ⁶ ACN ₆ G ^m TGC ^b	J01632, L02508	Bo3, Go3, Ka1, Lo2, Sa1
M·EcoPI	AG ^{m6} ACC ^b	X06287, X07312	Ba2, Hu2
M·Eco P1 dam	G ^{m6} ATC ^b		Co5
M·EcoP15I	CAGC ^{m6} AG	X06288, X07312	Hu2, Me2
M·EcoRI	GA ^{m6} ATTCT	J01675	Du1, Gr2, Ke2, Ne2, Ne9, Ru1
M·EcoRII	C ^{m5} CWGG	X16025, X05050	Bh1, Bu3, Bu4, Ko6, Ko7, Ko8, Ma10, Sc6, So2, Yo4
M·EcoRV	G ^{m6} ATATC	X00530	Bo4, Ga5
M·EcoR124	GA ^{m6} AAAN ₆ RTCG		Pa3, Pr2, Pr3
M·EcoR124/3	GA ^{m6} AN ₇ RTCG	X13145	Pr2, Pr3
M·EcoT1 dam	G ^{m6} ATC	J05393	Sc1, Sc7
M·EcoT2 dam	G ^{m6} AT	M22342	Br7, Ha4, Ha5, Mi1, Sc4, Sc5
M·EcoT4 dam	G ^{m6} ATC	X01416	Ha6, Ma1, Mi2, Sc3, Sc4, Sc5
M·Eco3II	GGT ^{m5} CTC and G ^{m6} AGACC		Bi7
M·Eco47II	GGNCC		Po6
M·Eco51I	CTGAAG (^{m6} A)		Po6
M·Eco57I	CTGA ^{m6} AG and CTTC ^{m6} AG	M74821, X61122	Ja8, Ja9, Po6
M·Eco64I	GGYRCC		Po6
M·Eco72I	CACGTG (^{m5} C)		Po6
M·Eco98I	AAGCTT		Po6
M·Eco105I	TACGTA		Po6
M·ErhI	G ^{m6} ATC		Ne5
M·Esp3I	GGT ^{m5} CTC and GAG ^{m6} ACC		Bi7, Ja3
M·eukaryote	^{m5} CG ^b	X14805 X63692 L10692	Be7 (Mouse) (human) Fi2 (Arabidopsis)
M·FnuDI	GG ^{m5} CC		Lu2, Va1
M·FnuDII	^{m5} CGCG		Lu2, Ne14
M·FnuDIII	GCGC		Lu2
M·FokI	GG ^{m6} ATG and C ^{m6} ATCC	J04623, M28828	La6, Lo3, Lu2, Ma8, Nw1
M·FspI	TGCGCA		Me1
M·FsuI	GGWCC (^{m5} C)		Le1
M·FV3	?? ^{m5} C??		Es1 (Frogvirus)
M·H2	GGCC and GCNGC and GDGCHC	M72412	La8
M·HaeII	RGCGCY		Lu2, Sl3
M·HaeIII	GG ^{m5} CC ^b	M24625	Lu2, Ma5, Sl3
M·HapII	C ^{m5} CGG		Wa1
M·HgaI	GA ^{m5} CGC and G ^{m5} CGTC	D90363	Lu2, Nw1 Wi7
M·HgiAI	GWGCWC		Lu2
M·HgiBI	GGWCC (^{m5} C)	X55137	Kr4, Du2
M·HgiCI	GGYRC ^{m5} C	X55138	Kr4, Er1
M·HgiCII	GGWCC (^{m5} C)	X55139	Kr4, Er1
M·HgiDI	GRCGYC (^{m5} C)	X55140	Kr4, Du4
M·HgiDII	GTCGAC (^{m5} C)	X55141	Kr4, Du3
M·HgiEI	GGWCC (^{m5} C)	X55142	Kr4
M·HgiGI	GRCGYC (^{m5} C)	X55143	Kr4, Er1
M·HhaI	G ^{m5} CGC	J02677	Ba9, Ca3, Lu2, Sm1, Wu1, Za1
M·HhaII	G ^{m6} ANTC	K00508	Ch1, Ke1, Ma3, Ma4, Sc9, Sm1
M·HincII	GTYR ^{m6} AC	X52124	Gr5, Mc8, Ro7, Re2
M·HindII	GTYR ^{m6} AC		Lu2, Re2, Ro6, Ro7
M·HindIII	^{m6} AAGCTT		Lu2, Ro6, Ro7
M·Hinfi	G ^{m6} ANTC	M22862	Ch1, Lu2
M·HinPI	GCGC		Ba9, Lu2
M·HjaI	GATATC (^{m6} A)		Da1
M·HpaI	GTTA ^{m6} AC	D10668	Br8, It1, Yo3
M·HpaII	C ^{m5} CGG	X51322	Lu2, Ma5, Qu1, Wi2, Yo2
M·HphI	T ^{m5} CACC		Mc8, Ne2, Ne4
M·KpnI	GGT ^{m6} ACC	X61796	Ch2, Ki4
M·Kpn2I	TCCGGA		Po6
M·LlaI	?	M77136	Hi1
M·MboI	G ^{m6} ATC	D13968	Mc8, Ue1
M·MboII	GAAG ^{m6} A	X56977	Mc12, Ne4, Ne2
M·MspI	^{m5} CCGG ^b	X14191	Eh2, Je2, Lu2, Nw2, Wa1, Wa5
M·MstI	TGCGCA		Me1

Table III. (cont.)

Methylase ^a	Specificity ^a	EMBL accession #	References
M·MthTI	GG ^{m5} CC	X68366,X97222	No4,No6
M·MthZI	m ⁴ CTAG	X67212,X68367	No4,No5
M·MunI	CA ^{m6} ATTG	X76192	St8
M·MvaI	C ^{m4} CWGG	X16985	Bu8,Kl2,Po6
M·MwoI	G ^{m4} CN ₇ GC (m ⁴ C)		Lu2,Lu4
M·NaeI	GCCGGC		Lu2,Va1
M·NcoI	CCATGG (m ⁴ C)		Lu2,Va1
M·NdeI	CAT ^{m6} ATG		Re7,Si1,We3
M·NgoMI	G ^{m5} CCGGC ^b	M86915	Pi5,St9
M·NgoMVI	GGNN ^{m5} CC ^b		Pi5
M·NgoI	RG ^{m5} CGCY ^b		Ko5,Ri1,St9,Su2
M·NgoAI	GG ^{m5} CC ^b		Pi3
M·NgoII	GG ^{m5} CC ^b	X52661,X06965	Ko5,Ri1,Su3,Su4
M·NgoIII	CCGCGG ^b		Ko5,Ri1,St9
M·NgoIV	G ^{m5} CCGGC ^b		Ch3,Ko15,Ri1,St9
M·NgoV	GGNN ^{m5} CC ^b		Ko5,Pi2,St9
M·NgoVI	G ^{m6} ATC ^b		Ko5,St9
M·NgoVII	G ^{m5} CSGC ^b		Gu4,Ko5,St9
M·NgoIX	GTAN ^{m5} CTC ^b		St9
M·NgoBI	T ^{m5} CACC ^b		Pi3
M·NgoBII	GTAN ₅ m ⁵ CTC ^b		Pi3
M·NlaI	GGCC		Mo3
M·NlaIII	C ^{m6} ATG	X54485	La1,Lu2,Mo3
M·NlaIV	GGNNCC (m ⁵ C)	U06074	Lu2
M·NlaV	GGNN ^{m5} CC		Mo3
M·NlaX	?? ^m C??	X54485	La1
M·NspV	TTCGAA	D14719	Ue2
M·PaeR7I	CTCG ^{m6} AG	X03274	Gi3,Th1,Th2
M·PgiI	G ^{m6} ATC	M63469	Ba10
M·PstI	CTGC ^{m6} AG	K02081	Le2,Wa3,Wa4,Wa6
M·PvuI	CGATCG	L04163	Sm5
M·PvuII	CAG ^{m4} CTG	X52681,X13778	Bl1,Ta2
M·Rrh4273I	GTCG ^{m6} AC		Ba6,Ye1
M·RsaI	GT ^{m6} AC		Ne5
M·RsrI	GA ^{m6} ATTC	X14697,X16456	Ba5,Ka10
M·SacII	CCGCGG		Lu2
M·SalI	GTCG ^{m6} AC		Lu2,Ro4,Ro5
M·SauLPI	G ^{m5} CCGGC		Ok1
M·Sau3AI	GAT ^{m5} C	M32470	Se1
M·Sau96I	GGN ^{m5} CC	X53096	Lu2,Ne14,Sz1
M·Sau3239I	CTCG ^{m6} AG		Ze1
M·ScrFI	C ^m CNGG	M87289	Da4
M·SfiI	GG ^{m4} CCN ₅ GGCC		Ba8,Ne5
M·SinI	GGW ^{m5} CC	J03391	Ka5,Ka6
M·SmaI	CC ^{m4} CGGG	X16458	He1,Po6
M·SphI	GCATGC		Lu2
M·SsoI	G ^{m6} AATTC	M97479	Ka9
M·SsoII	C ^{m5} CNGG	M86545	Ka9,Ni1,Ni3
M·SspMQI	m ⁵ CG		Nu1,Pi5,Re3
M·SssI	m ⁵ CG	X17195	Ko10,Re3
M·StsI	GG ^{m6} ATG	D11101	Ki5
	and C ^{m6} ATCC		
M·SryLTI	CAG ^{m6} AG	M90544	Da5
M·SryR124	GAAN ₆ RTCG (m ⁶ A)		Pr2,Pr3
M·SryR124/3	GAAN ₇ RTCG (m ⁶ A)		Pr2,Pr3
M·SlySBI	G ^{m6} AGN ₆ R ^m TYG ^b		Fu1,Fu3,Ga3,Na1,Na2
M·SlySPI	A ^{m6} ACN ₆ G ^m TRC ^b		Fu1,Fu3,Na1,Na2
M·SlySQ	A ^{m6} ACN ₆ R ^m TAYG ^b		Fu1,Fu3
M·SlySJ	G ^{m6} AGN ₆ G ^m TRC ^b		Ga3
M·TaqI	TCG ^{m6} A	M76680,M76681	Lu2,Mc3,Sa3,Sl2
		Y00499	Ba13
M·TthHBI	TCG ^{m6} A	M74795	Ba11,Mc3,Sa3
M·TjiI	TCG ^{m6} A		Sa3,Va6
M·Tetrahymena	?? ^{m6} A??		Ca2,Go1
M·VspI	ATTAAT (m ⁶ A)	X68658	De2
M·XbaI	TCTAG ^{m6} A		Lu2,Mc13,Va1
M·XcyI	C ^{m4} CCGGG	M98768	Wi6
M·XmaI	CCCGGG (m ⁴ C)		Ba8
M·XmaIII	CGG ^{m4} CCG		Gu9,Mc8,Tr5
M·XmnI	GAAN ₄ TTC		Fe1

^a See footnote 'a' of Table I.^b See footnote 'b' of Table I.

Cloned methylases are shown in bold face type.