REBASE—restriction enzymes and methylases

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INTRODUCTION

The restriction enzyme database, REBASE, is a collection of information about restriction enzymes and methylases. Since the last description of the contents of REBASE (1), 265 new entries have been added including 8 new Type II enzymes: *AcII*, AA¹CGTT; *Bce83I*, CTTGAG (16/14); *BscGI*, CCCGT; *BseRI*, GAGGAG (10/8); *Bsp1407I*, T¹GTACA; *BspLU11I*, A¹CATGT; *BsrDI*, GCAATG (2/0) and *SexAI* A¹CCWGGT. A complete list of these new enzymes can be found in Table I. A total of 2393 restriction enzymes is now known including 17 different Type I specificities, 188 different Type II specificities and 4 different Type III specificities. Table II contains a listing of all prototype restriction enzymes (Types I, II and III), together with their commercially available isoschizomers and neoschizomers that cleave at a position different from their prototype.

REBASE is updated daily. Each month, a set of REBASE data files are released publicly and distributed to the scientific community, at no charge, via e-mail. They can also be retrieved by anonymous ftp from vent.neb.com (192.138.220.2). These data files are flat ASCII text files, many of which are designed specifically for use with a variety of software packages such as GCG, IGSuite, GENEPRO, Staden, DNA Strider, Pro-Cite, and PC/Gene. Other data files include: a complete set of references, including abstracts, to papers on restriction enzymes and methylases; a list of all commercial suppliers of restriction enzymes and methylases, complete with contact information for each and a list of enzymes currently being sold. New data files are constantly being added and each release of REBASE includes a monthly release note indicating that the files at the ftp site have been updated, and listing new enzymes, newly available formats, enzyme name changes, etc. To join the mailing list or for more information, send a request to R.J.Roberts via e-mail to roberts@neb.com, telephone (508)927-3382 or Fax (508)921-1527.

Since last year, International Biotechnologies Inc. (IBI) and Serva have discontinued selling restriction enzymes or methylases. Listings have been added for Appligene and Angewandte Gentechnologie Systeme.

Several enzyme names have been changed recently. *Bsp1236I* (*FnuDII*) has become *Bsh1236I*. *IspI* (*Fnu4HI*) is now *ItaI*. Also it was discovered that the name *MthTI* had been used for two different enzymes. The original enzyme, *MthTI* (*AsuI*), is now called *MthBI*. The current enzyme, *MthTI* (*HaeIII*), is a new enzyme reported by Nolling and de Vos, J. Bacteriol. 174: 5719–5726 (1992). Two previously unidentified bacteria have been identified, leading to name changes of *Uba1269I* to *Mva1269I* (*BsmI*) and *Uba1285I* to *Bsh1285I* (*McrI*).

In forming these Tables, all endonucleases cleaving DNA at a specific sequence have been considered to be restriction

enzymes, although in most cases there is no direct genetic evidence for the presence of a restriction modification system. The endonucleases are named in accordance with the proposal of Smith and Nathans (2).

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Table 1.

Microorganism	Source	Enzyme ¹	Sequence ²	Reference
<i>Acinetobacter calcoaceticus</i> M4	S.K. Degtyarev	<i>AcII</i>	AA↑CGTT	3
<i>Actinomyces violaceoniger</i>	A.J. Podhajska	<i>Avcl</i> (<i>Sau96I</i>)	G↑GNCC	4
<i>Alcaligenes aquamarinus</i> 559	V.E. Repin	<i>AaqI</i> (<i>ApaLI</i>)	GTGCAC	5
<i>Alcaligenes species</i> MD1	H.X. Chiura	<i>AspMDI</i> (<i>MboI</i>)	↑GATC	6
<i>Arthrobacter citreus</i> 310	S.K. Degtyarev	<i>AcsI</i> (<i>ApoI</i>)	R↑AATTY	7
<i>Arthrobacter picolinophilus</i>	CAMB 2604	<i>Apil</i> (<i>PstI</i>)	CTGCA↑G	8
<i>Aureobacterium species</i>	K. Kaluza	<i>AspEI</i> (<i>Eam1105I</i>)	GACNNN↑NNGTC	9
<i>Bacillus Species</i> N	A.A. Janulaitis	<i>BseNI</i> (<i>BsrI</i>)	ACTGG (1/–1)	10
<i>Bacillus amyloliquefaciens</i> phage H2	T.A. Trautner	<i>M.H2I</i> (<i>HaeIII</i>)	GGCC	11
<i>Bacillus cereus</i> 83	N.I. Matvienko	<i>Bce83I</i>	CTTGAG (16/14)	12
<i>Bacillus circulans</i> 29	V.E. Repin	<i>Bci29I</i> (<i>Clal</i>)	AT↑CGAT	5
<i>Bacillus coagulans</i> 102	V.E. Repin	<i>Bco102I</i> (<i>BclI</i>)	TGATCA	5
<i>Bacillus coagulans</i> 116	V.E. Repin	<i>Bco102II</i> (<i>BbvII</i>)	GAAGAC	5
<i>Bacillus coagulans</i> 118	V.E. Repin	<i>Bco116I</i> (<i>Ksp632I</i>)	CTCTTC (1/4)	5
<i>Bacillus coagulans</i> 163	V.E. Repin	<i>Bco118I</i> (<i>Cfr10I</i>)	R↑CCGGY	5
<i>Bacillus coagulans</i> 27	V.E. Repin	<i>Bco163I</i> (<i>SfeI</i>)	CTRYAG	5
<i>Bacillus coagulans</i> 5	V.E. Repin	<i>Bco27I</i> (<i>HpaII</i>)	C↑CGG	5
<i>Bacillus coagulans</i> 6	V.E. Repin	<i>Bco5I</i> (<i>Ksp632I</i>)	CTCTTC (1/4)	5
<i>Bacillus coagulans</i> 63	V.E. Repin	<i>Bco6I</i> (<i>MstI</i>)	TGCGCA	5
<i>Bacillus licheniformis</i> HK	P.C. Shaw	<i>Bco63I</i> (<i>BsaBI</i>)	GATNNNNATC	5
<i>Bacillus megatherium</i> RFL1390	A.A. Janulaitis	<i>BliHKI</i> (<i>SauI</i>)	CC↑TNAGG	13
		<i>Bme1390I</i> (<i>ScrFI</i>)	CC↑NGG	14

Table 1. (continued)

<i>Bacillus pumilus</i>	G. Schmitz	<i>BpuAI</i> (<i>BbvII</i>)	GAAGAC (2/6)	15
<i>Bacillus pumilus</i>	P.C. Shaw	<i>BpuB5I</i> (<i>SpI</i>)	C1GTACG	16
<i>Bacillus schlegelii</i> 107	V.E. Repin	<i>Bsc107I</i> (<i>BsiYI</i>)	CCNNNNNNNGG	5
<i>Bacillus schlegelii</i> 4	V.E. Repin	<i>Bsc4I</i> (<i>BsiYI</i>)	CCNNNNNNNGG	5
<i>Bacillus species</i>	T. Schoenfeld	<i>Bsc91I</i> (<i>BbvII</i>)	GAAGAC (2/6)	17
<i>Bacillus species</i>	V. Bouriotis	<i>BseCI</i> (<i>Clal</i>)	AT1CGAT	18
<i>Bacillus species</i> 16	V.E. Repin	<i>Bse16I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus species</i> 17	V.E. Repin	<i>Bse17I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus species</i> 1H	D. Clark	<i>BscGI</i>	CCCGT	19
<i>Bacillus species</i> 23	V.E. Repin	<i>Bse23I</i> (<i>BsiYI</i>)	CCNNNNNNNGG	5
<i>Bacillus species</i> 24	V.E. Repin	<i>Bse24I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus species</i> 59	V.E. Repin	<i>Bse59I</i> (<i>BstEII</i>)	GGTNACC	5
<i>Bacillus species</i> 64	V.E. Repin	<i>Bse64I</i> (<i>BstEII</i>)	GGTNACC	5
<i>Bacillus species</i> 8	V.E. Repin	<i>Bse8I</i> (<i>BsaBI</i>)	GATNNNNATC	5
<i>Bacillus species</i> 9A	D. Clark	<i>BscJI</i> (<i>BstXI</i>)	CCANNNNNTGG	19
<i>Bacillus species</i> A	D. Clark	<i>BscHI</i> (<i>BsrI</i>)	ACTGG	19
<i>Bacillus species</i> K	V.M. Kramarov	<i>BspKI</i> (<i>HaeIII</i>)	GG1CC	20
<i>Bacillus species</i> LS2	N.I. Matvienko	<i>BspLS2I</i> (<i>SduI</i>)	GDGCH1C	21
<i>Bacillus species</i> LU11	N.I. Matvienko	<i>BspLU11I</i>	A1CATGT	22
		<i>BspLU11II</i> (<i>XbaI</i>)	TCTAGA	22
<i>Bacillus species</i> M90	V.M. Kramarov	<i>BspM90I</i> (<i>SnaI</i>)	GTA1TAC	20
<i>Bacillus species</i> N	CAMB 2677	<i>BspNI</i> (<i>EcoRII</i>)	CC1WGG	24
<i>Bacillus species</i> O-4	ATCC 21536	<i>BspO4I</i> (<i>PvuII</i>)	CAG1CTG	25
<i>Bacillus species</i> Q	V.E. Repin	<i>BseQI</i> (<i>HaeIII</i>)	GG1CC	5
<i>Bacillus species</i> Z	V.E. Repin	<i>BseZI</i> (<i>Ksp632I</i>)	CTCTTC (1/4)	5
<i>Bacillus sphaericus</i> RFL1236	A.A. Janulaitis	<i>Bsh1236I</i> (<i>FnuDII</i>)	CG1CG	26
<i>Bacillus sphaericus</i> RFL1285	A.A. Janulaitis	<i>Bsh1285I</i> (<i>McrI</i>)	CGRY1CG	27
<i>Bacillus sphaericus</i> RFL1365	A.A. Janulaitis	<i>Bsh1365I</i> (<i>BsaBI</i>)	GATNN1NNATC	28
<i>Bacillus stearothermophilus</i>	P.C. Shaw	<i>BsiHKAI</i> (<i>HgiAI</i>)	GWGCW1C	29
<i>Bacillus stearothermophilus</i> 100	V.E. Repin	<i>Bsr100I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus stearothermophilus</i> 11	V.E. Repin	<i>Bsr11I</i> (<i>BsrI</i>)	ACTGG (1/-1)	5
<i>Bacillus stearothermophilus</i> 12	V.E. Repin	<i>Bsr12I</i> (<i>BbvI</i>)	GCAGC	5
<i>Bacillus stearothermophilus</i> 1473	Z. Chen	<i>Bsr1473I</i> (<i>BstI</i>)	WCCGGW	30
		<i>Bsr1473II</i> (<i>HaeII</i>)	RGCGCY	30
<i>Bacillus stearothermophilus</i> 2	V.E. Repin	<i>Bsr2I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus stearothermophilus</i> 38	V.E. Repin	<i>Bsr38I</i> (<i>EcoRII</i>)	CC1WGG	5
<i>Bacillus stearothermophilus</i> 4Q	Z. Chen	<i>Bsr4QI</i> (<i>AvaII</i>)	GGWCC	30
<i>Bacillus stearothermophilus</i> 7Q	Z. Chen	<i>Bsr7QI</i> (<i>AvaI</i>)	CYCCRG	30
		<i>Bsr7QII</i> (<i>BstNI</i>)	CCWGG	30
<i>Bacillus stearothermophilus</i> C98	Z. Chen	<i>Bsr98I</i> (<i>Ksp632I</i>)	CTCTTC	30
<i>Bacillus stearothermophilus</i> CPW548	Z. Chen	<i>BsmPI</i> (<i>HgiAI</i>)	GWGCWC	30
<i>Bacillus stearothermophilus</i> Cpw230	Z. Chen	<i>BsaXI</i>	?	30
<i>Bacillus stearothermophilus</i> Cpw514	Z. Chen	<i>BsaZI</i> (<i>HpaII</i>)	CCGG	30
<i>Bacillus stearothermophilus</i> D170	Z. Chen	<i>Bsr170I</i> (<i>BsrGI</i>)	TGTACA	30
		<i>Bsr170II</i> (<i>HindIII</i>)	AAGCTT	30
<i>Bacillus stearothermophilus</i> D70	Z. Chen	<i>BsrDI</i>	GCAATG (2/0)	30
<i>Bacillus stearothermophilus</i> E505	Z. Chen	<i>BsmEI</i> (<i>PleI</i>)	GAGTC	30
<i>Bacillus stearothermophilus</i> F	Z. Chen	<i>BsmFI</i> (<i>FinI</i>)	GGGAC (10/14)	31
<i>Bacillus stearothermophilus</i> F6	Z. Chen	<i>BssFI</i> (<i>Fnu4HI</i>)	GCNGC	30
<i>Bacillus stearothermophilus</i> GR75	Z. Chen	<i>BsrGI</i> (<i>Bsp1407I</i>)	T1GTACA	30
		<i>BsrGII</i>	?	30
<i>Bacillus stearothermophilus</i> I224	Z. Chen	<i>Bsr224I</i> (<i>SlyI</i>)	CCWWGG	30
<i>Bacillus stearothermophilus</i> LV	C. Vasquez	<i>BsrLVI</i> (<i>Clal</i>)	ATCGAT	32
<i>Bacillus stearothermophilus</i> Lipari 28	D. Clark	<i>BsoFI</i> (<i>BsrI</i>)	ACTGG	33
<i>Bacillus stearothermophilus</i> Lipari 29	D. Clark	<i>BsoGI</i> (<i>EcoRII</i>)	CCWGG	33
		<i>BsoGII</i>	?	33
<i>Bacillus stearothermophilus</i> M16	Z. Chen	<i>Bsr16I</i> (<i>HaeII</i>)	RGCGCY	30
<i>Bacillus stearothermophilus</i> M6	N.I. Matvienko	<i>BsrM6I</i> (<i>EcoRII</i>)	CC1WGG	34
<i>Bacillus stearothermophilus</i> N365	Z. Chen	<i>BsmNI</i> (<i>SfaNI</i>)	GCATC	30
<i>Bacillus stearothermophilus</i> P158	Z. Chen	<i>Bsr158I</i> (<i>Ksp632I</i>)	CTCTTC	30
<i>Bacillus stearothermophilus</i> RFL1407	A.A. Janulaitis	<i>Bsp1407I</i>	T1GTACA	35
<i>Bacillus stearothermophilus</i> SR65	Z. Chen	<i>BsaUI</i> (<i>BbvI</i>)	GCAGC	30
<i>Bacillus stearothermophilus</i> SR65	Z. Chen	<i>BsoSI</i> (<i>ScaI</i>)	AGTACT	30
<i>Bacillus stearothermophilus</i> V35	Z. Chen	<i>BsrVI</i> (<i>BbvI</i>)	GCAGC	30
<i>Bacillus stearothermophilus</i> W493	Z. Chen	<i>BsrWI</i> (<i>BlnI</i>)	GGATC	30
<i>Bacillus stearothermophilus</i> X173	Z. Chen	<i>BsrXI</i> (<i>XbaI</i>)	TCTAGA	30
<i>Bacillus subtilis</i> 23	V.M. Kramarov	<i>Bsu23I</i> (<i>BspMII</i>)	T1CCGGA	20
<i>Bacillus subtilis</i> 54	V.M. Kramarov	<i>Bsu54I</i> (<i>AsuI</i>)	G1GNCC	20
<i>Bacillus thuringiensis</i> 33	V.E. Repin	<i>Bnu33I</i> (<i>Mbol</i>)	GATC	36
<i>Bacillus thuringiensis</i> 36	V.E. Repin	<i>Bnu36I</i> (<i>Mbol</i>)	GATC	36
<i>Bacillus thuringiensis</i> 37	V.E. Repin	<i>Bnu37I</i> (<i>Mbol</i>)	GATC	36
<i>Bacillus thuringiensis</i> 39	V.E. Repin	<i>Bnu39I</i> (<i>Mbol</i>)	GATC	36
<i>Bacillus thuringiensis</i> 41	V.E. Repin	<i>Bnu41I</i> (<i>Mbol</i>)	GATC	36

Table 1. (continued)

Bacillus thuringiensis var Kumantoensis	R.R. Azizbekyan	<i>BtkI</i> (<i>FnuDII</i>)	CGICG	37
Bacillus species R	CAMB 2669	<i>BtkII</i> (<i>MboI</i>)	IGATC	37
Bacteroides fragilis AIP10006	NCTC 9843T	<i>BseRI</i>	GAGGAG	38
Bacteroides fragilis BE3	H. Azeddoug	<i>BfrCI</i> (<i>AvaIII</i>)	ATGCAT	39
Chlorella strain NC64A (PBCV-1)	J.L. Van Etten	<i>BfrBI</i> (<i>AvaIII</i>)	ATGICAT	39
		<i>CviAII</i> (<i>NlaIII</i>)	CITATG	40
		<i>M.CviAIV</i>	RGCB	41
Clostridium acetobutylicum 824	ATCC 824	<i>Cac824I</i> (<i>Fnu4HI</i>)	GCNGC	42
Enterobacter cloacae	P.C. Shaw	<i>EclHKI</i> (<i>Eam1105I</i>)	GACNNNINNGTC	43
Enterobacter species 24I	P.C. Shaw	<i>EspHK24I</i> (<i>EaeI</i>)	YGGCCR	44
Enterobacter species N15	P.C. Shaw	<i>KspHK15I</i> (<i>EaeI</i>)	YGGCCR	44
Enterobacter species N16	P.C. Shaw	<i>EspHK16I</i> (<i>EaeI</i>)	YGGCCR	44
Enterobacter species N22	P.C. Shaw	<i>EspHK22I</i> (<i>EcoRII</i>)	CCWGG	44
Enterobacter species N26	P.C. Shaw	<i>EspHK26I</i> (<i>BspMII</i>)	TCCGGA	44
Enterobacter species N29	P.C. Shaw	<i>EspHK29I</i> (<i>AvaI</i>)	CYCGRG	44
Enterobacter species N30	P.C. Shaw	<i>EspHK30I</i> (<i>EcoRII</i>)	CCWGG	44
Enterobacter species N7	P.C. Shaw	<i>EspHK7I</i> (<i>EcoRII</i>)	CCWGG	44
Enterobacter species RFL1396	A.A. Janulaitis	<i>Esp1396I</i> (<i>PflMI</i>)	CCANNNNINTGG	45
Escherichia coli 27	A. Solonin	<i>Eco27kI</i> (<i>AvaI</i>)	CITYCGRG	46
Escherichia coli 29	A. Solonin	<i>Eco29kI</i> (<i>SacII</i>)	CCGCIGG	47
Escherichia coli K-12	M.G. Marinus	<i>M.EcoDcm</i>	CCWGG	48,49
Escherichia coli K-12	M.G. Marinus	<i>M.EcoDam</i>	GATC	49-52
Klebsiella pneumoniae 49k	A.S. Solonin	<i>Kpn49kI</i> (<i>EcoRI</i>)	GIAATTC	53
		<i>Kpn49kII</i> (<i>CauII</i>)	ICCSGG	54
Klebsiella species N12	P.C. Shaw	<i>KspHK12I</i> (<i>EcoRII</i>)	CCWGG	44
Klebsiella species N14	P.C. Shaw	<i>KspHK14I</i> (<i>EcoRII</i>)	CCWGG	44
Lactococcus lactis ssp. cremoris W56	J. Josephsen	<i>LlaBI</i> (<i>SfiI</i>)	CITRYAG	55
Lactococcus lactis ssp. cremoris W9	J. Josephsen	<i>LlaAI</i> (<i>MboI</i>)	IGATC	56
Methanobacterium thermoautrophicum	K.O. Stetter	<i>MthBI</i> (<i>AsuI</i>)	GGNCC	57
Methanobacterium thermoformicum FTF	DSM 3012	<i>MthFI</i> (<i>MaeI</i>)	CTAG	58
Methanobacterium thermoformicum Z-245	DSM 3720	<i>MthZI</i> (<i>MaeI</i>)	CITAG	58
Micrococcus luteus	ATCC 9273	<i>Mlu9273I</i> (<i>NruI</i>)	TCGCGA	59
		<i>Mlu9273II</i> (<i>NaeI</i>)	GCCGGC	59
Micrococcus luteus 113	S.K. Degtyarev	<i>Mlu113I</i> (<i>SacII</i>)	CCIGCGG	60
Micrococcus species	V. Bouriotis	<i>MspCI</i> (<i>AflII</i>)	CITTAAG	61
Mycobacterium fortuitum TMC 1529	A.K. Tyagi	<i>MfoAI</i> (<i>HaeIII</i>)	GGICC	62
Mycobacterium habana 206	A.K. Tyagi	<i>MhaAI</i> (<i>PstI</i>)	CTGCAIG	63
Neisseria lactamica	NRCC 2118	<i>M.NlaX</i>	?	64
Phormidium inundatum	CCAP 1462/9	<i>PinBI</i> (<i>AvaIII</i>)	ATGCAIT	65
		<i>PinBII</i> (<i>BspMII</i>)	TICCGGA	65
Phormidium tadschicicum	A. Podhajska	<i>PtaI</i> (<i>BspMII</i>)	TICCGGA	66
Photobacterium leiognathi	V.E. Repin	<i>Plo214I</i> (<i>HaeIII</i>)	GGCC	5
Photobacterium mandapamensis 579	V.E. Repin	<i>PmnI</i> (<i>NarI</i>)	GGCGCC	5
Photobacterium phosphoreum 1436	V.E. Repin	<i>Pph14I</i> (<i>BanI</i>)	GGYRCC	5
Photobacterium phosphoreum 1579	V.E. Repin	<i>Pph1579I</i> (<i>Sau96I</i>)	GGNCC	5
Photobacterium phosphoreum 1773	V.E. Repin	<i>Pph1773I</i> (<i>Sau96I</i>)	GGNCC	5
Photobacterium phosphoreum 2059	V.E. Repin	<i>Pph2059I</i> (<i>PstI</i>)	CTGCAG	5
Photobacterium phosphoreum 288	V.E. Repin	<i>Pph288I</i> (<i>MboI</i>)	GATC	5
Pseudomonas aeruginosa 18k	A.S. Solonin	<i>Pae18kI</i> (<i>BglII</i>)	AIGATCT	68
Pseudomonas aeruginosa 2k	A.S. Solonin	<i>Pae2kI</i> (<i>BglII</i>)	AIGATCT	68
Pseudomonas pseudoalcaligenes RFL1406	A.A. Janulaitis	<i>Psp1406I</i> (<i>AclI</i>)	AAICGTT	69
Pseudomonas species S	CAMB 2676	<i>PspSI</i> (<i>PstI</i>)	CTGCAG	70
Ruminococcus albus 8	B.A. White	<i>Ral8I</i> (<i>BlnI</i>)	GGATC	71
Ruminococcus flavefaciens FD-1	B.A. White	<i>RflFII</i> (<i>ScaI</i>)	AGTIACT	72
Streptococcus bovis II/1	P. Javorsky	<i>SbvI</i> (<i>HaeIII</i>)	GGICC	73
Streptococcus mutans E	I. Nasz	<i>SnuEI</i> (<i>AvaII</i>)	GIGWCC	74
Streptococcus species	I. Nasz	<i>SnuCI</i> (<i>AvaIII</i>)	ATGCAT	75
Streptomyces achromogenes N-J-H	A.J. Podhajska	<i>SacNI</i> (<i>HgiIII</i>)	GRGCYIC	76
Streptomyces aureofaciens 16	P. Pristas	<i>SauSI</i> (<i>NaeI</i>)	GCCIGGC	77
Streptomyces aureofaciens B-96	P. Pristas	<i>SauLPI</i> (<i>NaeI</i>)	GCCIGGC	77
Streptomyces aureofaciens NMU	P. Pristas	<i>SauNI</i> (<i>NaeI</i>)	GCCIGGC	77
Streptomyces aureofaciens R8/26	P. Pristas	<i>SauHPI</i> (<i>NaeI</i>)	GCCIGGC	77
Streptomyces diastaticus	F. Kimizuka	<i>SdiI</i> (<i>SfiI</i>)	GGCCNNNNINNGGCC	78
Streptomyces exfoliatus	B. Frey	<i>SexAI</i>	AICCWGGT	79
Streptomyces prasinus	ATCC 15825	<i>SprI</i> (<i>PstI</i>)	CTGCAG	80
Streptomyces pulveraceus	ATCC 29083	<i>Spul</i> (<i>SacII</i>)	CCGCIGG	81
Streptomyces species	V. Bouriotis	<i>SseBI</i> (<i>SnuI</i>)	AGGICCT	82
Streptomyces species	B. Frey	<i>SspBI</i> (<i>Bsp1407I</i>)	TIGTACA	79
Streptomyces species 5230	P. Westermann	<i>Ssp5230I</i> (<i>AatII</i>)	GACGTIC	83
Thermus ruber RFL1	A.A. Janulaitis	<i>TruII</i> (<i>MseI</i>)	TITAA	84
Thermus species	T. Tenkanen	<i>Tsp509I</i> (<i>TspEI</i>)	IAATT	85
Unidentified bacterium	P.C. Shaw	<i>UbaHKAI</i> (<i>SacII</i>)	CCGCGG	43
Unidentified bacterium	P.C. Shaw	<i>UbaHKBI</i> (<i>PstI</i>)	CTGCAG	43

Table 1. (continued)

Unidentified bacterium RFL1355	A.A. Janulaitis	<i>Uba1355I (HpaII)</i>	CCGG	86
Unidentified bacterium RFL1357	A.A. Janulaitis	<i>Uba1357I (HgiIII)</i>	GRGCYC	86
Unidentified bacterium RFL1362	A.A. Janulaitis	<i>Uba1362I (SduI)</i>	GDGCHC	86
Unidentified bacterium RFL1363	A.A. Janulaitis	<i>Uba1363I (HgiIII)</i>	GRGCYC	86
Unidentified bacterium RFL1364	A.A. Janulaitis	<i>Uba1364I (SacII)</i>	CCGCGG	86
Unidentified bacterium RFL1366	A.A. Janulaitis	<i>Uba1366I (MboI)</i>	GATC	86
		<i>Uba1366II (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1367	A.A. Janulaitis	<i>Uba1367I (AvaIII)</i>	ATGCAT	86
Unidentified bacterium RFL1368	A.A. Janulaitis	<i>Uba1368I (ApaI)</i>	GGGCCC	86
Unidentified bacterium RFL1369	A.A. Janulaitis	<i>Uba1369I (SacII)</i>	CCGCGG	86
Unidentified bacterium RFL1370	A.A. Janulaitis	<i>Uba1370I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1371	A.A. Janulaitis	<i>Uba1371I (SnaI)</i>	AGGCCT	86
Unidentified bacterium RFL1372	A.A. Janulaitis	<i>Uba1372I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1373	A.A. Janulaitis	<i>Uba1373I (AvaII)</i>	GGWCC	86
Unidentified bacterium RFL1374	A.A. Janulaitis	<i>Uba1374I (AflIII)</i>	CTTAAG	86
Unidentified bacterium RFL1375	A.A. Janulaitis	<i>Uba1375I (BspMII)</i>	TCCGGA	86
Unidentified bacterium RFL1376	A.A. Janulaitis	<i>Uba1376I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1377	A.A. Janulaitis	<i>Uba1377I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1378	A.A. Janulaitis	<i>Uba1378I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1379	A.A. Janulaitis	<i>Uba1379I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1380	A.A. Janulaitis	<i>Uba1380I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1381	A.A. Janulaitis	<i>Uba1381I (AcyI)</i>	GRCGYC	86
Unidentified bacterium RFL1382	A.A. Janulaitis	<i>Uba1382I (BsmI)</i>	GAATGC	86
Unidentified bacterium RFL1383	A.A. Janulaitis	<i>Uba1383I (BamHI)</i>	GGATCC	86
Unidentified bacterium RFL1384	A.A. Janulaitis	<i>Uba1384I (AvaIII)</i>	ATGCAT	86
Unidentified bacterium RFL1385	A.A. Janulaitis	<i>Uba1385I (AsuII)</i>	TTCGAA	86
Unidentified bacterium RFL1386	A.A. Janulaitis	<i>Uba1386I (NruI)</i>	TCGCGA	86
Unidentified bacterium RFL1387	A.A. Janulaitis	<i>Uba1387I (ApaLI)</i>	GTGCAC	86
Unidentified bacterium RFL1388	A.A. Janulaitis	<i>Uba1388I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1389	A.A. Janulaitis	<i>Uba1389I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1391	A.A. Janulaitis	<i>Uba1391I (ScrFI)</i>	CCNGG	86
Unidentified bacterium RFL1392	A.A. Janulaitis	<i>Uba1392I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1393	A.A. Janulaitis	<i>Uba1393I (SmaI)</i>	CCCGGG	86
Unidentified bacterium RFL1394	A.A. Janulaitis	<i>Uba1394I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1395	A.A. Janulaitis	<i>Uba1395I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1397	A.A. Janulaitis	<i>Uba1397I (XhoI)</i>	CTCGAG	86
Unidentified bacterium RFL1398	A.A. Janulaitis	<i>Uba1398I (BamHI)</i>	GGATCC	86
Unidentified bacterium RFL1399	A.A. Janulaitis	<i>Uba1399I (PstI)</i>	CTGCAG	86
Unidentified bacterium RFL1400	A.A. Janulaitis	<i>Uba1400I (EcoRV)</i>	GATATC	86
Unidentified bacterium RFL1401	A.A. Janulaitis	<i>Uba1401I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1402	A.A. Janulaitis	<i>Uba1402I (BamHI)</i>	GGATCC	86
Unidentified bacterium RFL1403	A.A. Janulaitis	<i>Uba1403I (SnaI)</i>	AGGCCT	86
Unidentified bacterium RFL1404	A.A. Janulaitis	<i>Uba1404I (FnuDII)</i>	CGCG	86
Unidentified bacterium RFL1405	A.A. Janulaitis	<i>Uba1405I (FnuDII)</i>	CGCG	86
Unidentified bacterium RFL1408	A.A. Janulaitis	<i>Uba1408I (HaeIII)</i>	GGCC	86
		<i>Uba1408II (HpaI)</i>	GTTAAC	86
Unidentified bacterium RFL1409	A.A. Janulaitis	<i>Uba1409I (HgiIII)</i>	GRGCYC	86
Unidentified bacterium RFL1410	A.A. Janulaitis	<i>Uba1410I (EcoRII)</i>	CCWGG	86
Unidentified bacterium RFL1411	A.A. Janulaitis	<i>Uba1411I (PstI)</i>	CTGCAG	86
Unidentified bacterium RFL1412	A.A. Janulaitis	<i>Uba1412I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1413	A.A. Janulaitis	<i>Uba1413I (AvaII)</i>	GGWCC	86
Unidentified bacterium RFL1414	A.A. Janulaitis	<i>Uba1414I (BamHI)</i>	GGATCC	86
Unidentified bacterium RFL1415	A.A. Janulaitis	<i>Uba1415I (BsmI)</i>	GAATGC	86
Unidentified bacterium RFL1416	A.A. Janulaitis	<i>Uba1416I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1417	A.A. Janulaitis	<i>Uba1417I (PstI)</i>	CTGCAG	86
Unidentified bacterium RFL1418	A.A. Janulaitis	<i>Uba1418I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1419	A.A. Janulaitis	<i>Uba1419I (SnaI)</i>	AGGCCT	86
Unidentified bacterium RFL1420	A.A. Janulaitis	<i>Uba1420I (AflIII)</i>	CTTAAG	86
Unidentified bacterium RFL1421	A.A. Janulaitis	<i>Uba1421I (HgiIII)</i>	GRGCYC	86
Unidentified bacterium RFL1422	A.A. Janulaitis	<i>Uba1422I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1423	A.A. Janulaitis	<i>Uba1423I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1424	A.A. Janulaitis	<i>Uba1424I (CauII)</i>	CCSGG	86
Unidentified bacterium RFL1425	A.A. Janulaitis	<i>Uba1425I (BspMII)</i>	TCCGGA	86
Unidentified bacterium RFL1426	A.A. Janulaitis	<i>Uba1426I (AflIII)</i>	CTTAAG	86
Unidentified bacterium RFL1427	A.A. Janulaitis	<i>Uba1427I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1428	A.A. Janulaitis	<i>Uba1428I (EcoRII)</i>	CCWGG	86
Unidentified bacterium RFL1429	A.A. Janulaitis	<i>Uba1429I (HaeIII)</i>	GGCC	86
Unidentified bacterium RFL1430	A.A. Janulaitis	<i>Uba1430I (ClaI)</i>	ATCGAT	86
Unidentified bacterium RFL1431	A.A. Janulaitis	<i>Uba1431I (BclI)</i>	TGATCA	86
Unidentified bacterium RFL1432	A.A. Janulaitis	<i>Uba1432I (XhoII)</i>	RGATCY	86
Unidentified bacterium RFL1433	A.A. Janulaitis	<i>Uba1433I (AhaI)</i>	AGCT	86
Unidentified bacterium RFL1434	A.A. Janulaitis	<i>Uba1434I (SceI)</i>	CCNNGG	86
Unidentified bacterium RFL1435	A.A. Janulaitis	<i>Uba1435I (HindIII)</i>	AAGCTT	86

Table 1. (continued)

Unidentified bacterium RFL1436	A.A. Janulaitis	<i>Uba1436I</i> (<i>AvaI</i>)	CYCGRG	86
Unidentified bacterium RFL1437	A.A. Janulaitis	<i>Uba1437I</i> (<i>GsuI</i>)	CTGGAG	86
Unidentified bacterium RFL1438	A.A. Janulaitis	<i>Uba1438I</i> (<i>AvaII</i>)	GGWCC	86
Unidentified bacterium RFL1439	A.A. Janulaitis	<i>Uba1439I</i> (<i>HpaII</i>)	CCGG	86
Unidentified bacterium RFL1440	A.A. Janulaitis	<i>Uba1440I</i> (<i>AvaI</i>)	CYCGRG	86
Unidentified bacterium RFL1441	A.A. Janulaitis	<i>Uba1441I</i> (<i>AluI</i>)	AGCT	86
Unidentified bacterium RFL1442	A.A. Janulaitis	<i>Uba1442I</i> (<i>SecI</i>)	CCNNGG	86
Unidentified bacterium RFL1443	A.A. Janulaitis	<i>Uba1443I</i> (<i>AflII</i>)	CTTAAG	86
Unidentified bacterium RFL1444	A.A. Janulaitis	<i>Uba1444I</i> (<i>GsuI</i>)	CTGGAG	86
Unidentified bacterium RFL1445	A.A. Janulaitis	<i>Uba1445I</i> (<i>NlaIV</i>)	GGNNCC	86
Unidentified bacterium RFL1446	A.A. Janulaitis	<i>Uba1446I</i> (<i>FnuDII</i>)	CGCG	86
Unidentified bacterium RFL1447	A.A. Janulaitis	<i>Uba1447I</i> (<i>BclI</i>)	TGATCA	86
Unidentified bacterium RFL1448	A.A. Janulaitis	<i>Uba1448I</i> (<i>XhoI</i>)	CTCGAG	86
Unidentified bacterium RFL1449	A.A. Janulaitis	<i>Uba1449I</i> (<i>HaeIII</i>)	GGCC	86
Unidentified bacterium RFL1450	A.A. Janulaitis	<i>Uba1450I</i> (<i>HaeIII</i>)	GGCC	86
Unidentified bacterium RFL1451	A.A. Janulaitis	<i>Uba1451I</i> (<i>Clal</i>)	ATCGAT	86
Unidentified bacterium RFL1452	A.A. Janulaitis	<i>Uba1452I</i> (<i>AsuII</i>)	TTCGAA	86
Unidentified bacterium RFL1453	A.A. Janulaitis	<i>Uba1453I</i> (<i>Clal</i>)	ATCGAT	86
Unidentified microorganism 5T	V.E. Repin	<i>Umi5I</i> (<i>AvaI</i>)	CYCGRG	5
Unidentified microorganism 7T	V.E. Repin	<i>Umi7I</i> (<i>BclI</i>)	TGATCA	5
<i>Vibrio fischeri</i> 1246	V.E. Repin	<i>VfiI</i> (<i>AflII</i>)	CTTAAG	5
<i>Vibrio harveyi</i> 1168	V.E. Repin	<i>Vha1168I</i> (<i>HaeIII</i>)	GGCC	5
<i>Vibrio harveyi</i> 44	V.E. Repin	<i>Vha44I</i> (<i>MboI</i>)	GATC	5
<i>Vibrio</i> species 2246	V.E. Repin	<i>Vsp2246I</i> (<i>BanI</i>)	GGYRCC	5

1. When two enzymes recognize the same sequence, i.e., are isoschizomers, the prototype (i.e., the first example isolated) is indicated in parentheses.
2. Recognition sequence representations use the standard abbreviations (Eur. J. Biochem. 150: 1–5, 1985) to represent ambiguity.

R = G or A
Y = C or T
M = A or C
K = G or T
S = G or C
W = A or T
B = not A (C or G or T)
D = not C (A or G or T)
H = not G (A or C or T)
V = not T (A or C or G)
N = A or C or G or T

Recognition sequences are written from 5' → 3', only one strand being given, and the point of cleavage is indicated by an arrow (†). When no arrow appears, the precise cleavage site has not been determined. For example, A†CATGT is an abbreviation for

5' A†C A T G T 3'
3' T G T A C†A 5'

For enzymes such as *Bce83I* and *BsrDI*, which cleave away from their recognition sequences, the sites of cleavage are indicated in parentheses. For example *Bce83I* CTTGAG(16/14) indicates cleavage as shown below

5'CTTGAGNNNNNNNNNNNNNNNN†3'
3'GAACTCNNNNNNNNNNNNNNNN†5'

BsrDI GCAATG(2/0) indicates cleavage as shown below

5'GCAATGNN† 3'
3'CGTTAC† 5'

In all cases the recognition sequences are oriented so that the cleavage sites lie on their 3' side.

Å is N⁶-methyladenosine. Ċ is C⁵-methylcytosine. Ċ is N⁴-methylcytosine.

Table 2.

Type I enzymes

Prototype enzyme	Recognition sequence ²	Me site ³
<i>CfrAI</i>	GCANNNNNNNNGTGG	
<i>EcoAI</i>	GAGNNNNNNNGTCA	2(6), –3(6)
<i>EcoBI</i>	TGANNNNNNNNTGCT	3(6), –4(6)
<i>EcoDI</i>	TTANNNNNNNNGTCY	
<i>EcoDR2I</i>	TCANNNNNNNGTCTG	
<i>EcoDR3I</i>	TCANNNNNNNATCG	
<i>EcoDXXI</i>	TCANNNNNNNRRTTC	
<i>EcoEI</i>	GAGNNNNNNNATGC	
<i>EcoKI</i>	AACNNNNNNNGTGC	2(6), –3(6)
<i>EcoR124I</i>	GAANNNNNNNRTCG	
<i>EcoR124/3I</i>	GAANNNNNNNRRTCG	–3(6)
<i>EcoRD2I</i>	GAANNNNNNNRRTTC	

Table 2. (continued)

	<i>Eco</i> RD3I <i>Spy</i> SBI <i>Spy</i> SJI <i>Spy</i> SPI <i>Spy</i> SQI	GAANNNNNNNRTTC GAGNNNNNNRRTAYG GAGNNNNNNNGTRC AACNNNNNNNGTRC AACNNNNNNRRTAYG	2(6), -3(6) 2(6), -3(6)	
Type III enzymes				
	Prototype enzyme <i>Eco</i> PI <i>Eco</i> P15I <i>Hin</i> III <i>Spy</i> LTI	Recognition sequence ² AGACC CAGCAG (25/27) CGAAT CAGAG	Me site ³ 3(6) 5(6) 4(6)	
Type II enzymes				
Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Aat</i> II <i>Acc</i> I <i>Acc</i> I <i>Acc</i> II		GACGT↓C GT↓MKAC CCGC (-3/-1) AA↓CGTT		ELMNOPRSUX ABDEGKLMNOPQRSUX N
<i>Acy</i> I	<i>Psp</i> 1406I	AA↓CGTT GR↓CGYC GR↓CGYC GR↓CGYC GR↓CGYC		FMN MR AK BNS DEFOU ABKNOSUX
<i>Afl</i> III <i>Afl</i> III <i>Age</i> I	<i>Bfi</i> II <i>Bsa</i> HI <i>Hin</i> II <i>Bfr</i> I	C↓TTAAG C↓TTAAG A↓CRYGT A↓CCGGT A↓CCGGT		M BMNT↓ N BM
<i>Aha</i> III	<i>Pin</i> AI	TTT↓AAA TTT↓AAA		ABDEFGKLMNOPQRSUX ABDEFGHKLMNOPQRSUX
<i>Alu</i> I <i>Alw</i> NI <i>Apa</i> I	<i>Dra</i> I	AG↓CT CAGNNN↓CTG GGGCC↓C G↓GGCCC	3(5) 4(5)	BNSU BEGKLMNOPRSUX DFN
<i>Apa</i> BI <i>Apa</i> LI	<i>Bsp</i> 120I	GCANNNNN↓TGC G↓TGCAC G↓TGCAC		DEKNSUX BFMORU N
<i>Apo</i> I <i>Asc</i> I <i>Asu</i> I	<i>Alw</i> 44I	R↓AATTY GG↓CGCGCC G↓GNCC G↓GNCC		N N W W
<i>Asu</i> II	<i>Bsi</i> ZI <i>Bsu</i> 54I <i>Cfr</i> 13I <i>Sau</i> 96I	G↓GNCC G↓GNCC G↓GNCC G↓GNCC	4(5) 4(5)	DFKOU BLMNORSUX X
<i>Ava</i> I	<i>Bsi</i> CI <i>Bsp</i> 119I <i>Bsr</i> BI <i>Csp</i> 45I <i>Lsp</i> I <i>Nsp</i> V <i>Sfi</i> I	TT↓CGAA TT↓CGAA TT↓CGAA TT↓CGAA TT↓CGAA TT↓CGAA TT↓CGAA		EUW DF NS ORU L ABKOP M
<i>Ava</i> II	<i>Bco</i> I <i>Eco</i> 88I <i>Nli</i> 387/7I	C↓YCGRG C↓YCGRG CYCGR↓G G↓GWCC G↓GWCC GGWCC G↓GWCC		ABEGKLMNOPRSUX W DF ABEGKMNPRSX DFOU N LRS
<i>Ava</i> III	<i>Eco</i> 47I <i>Msp</i> AI <i>Sin</i> I	ATGCAT ATG↓CAT ATGCA↓T ATGCA↓T ATGCA↓T A↓TGCAT C↓CTAGG C↓CTAGG	4(5)	KOU F BDELMNRSX DFN N K

Table 2. (continued)

<i>Bae</i> I		ACNNNGTAYC		
<i>Bal</i> I		TGG↓CCA	4(5)	AKRX
	<i>Msc</i> I	TGG↓CCA		BDNOSU
<i>Bam</i> HI		G↓GATCC	5(4)	ABDEFGHKL MNOPQRSUWX
	<i>Bst</i> I	G↓GATCC		P
<i>Bbv</i> I		GCAGC (8/12)	2(5), -2(5)	ENX
	<i>Bst</i> 71I	GCAGC (8/12)		R
<i>Bbv</i> II		GAAGAC (2/6)		
	<i>Bbs</i> I	GAAGAC (2/6)		NU
	<i>Bpu</i> AI	GAAGAC (2/6)		M
	<i>Bsc</i> 91I	GAAGAC (2/6)		R
<i>Bcc</i> I		CCATC		
<i>Bce</i> 83I		CTTGAG (16/14)		
<i>Bce</i> II		ACGGC (12/13)		
<i>Bcg</i> I ⁵		GCANNNNNNTCG (12/10)		NU
<i>Bcl</i> I		T↓GATCA		BDEFGHKL MNOPRSUX
	<i>Bsi</i> QI	T↓GATCA		W
	<i>Fba</i> I	T↓GATCA		K
<i>Bet</i> I		W↓CCGGW		
	<i>Bsa</i> WI	W↓CCGGW		N
<i>Bgl</i> II		GCCNNNN↓INGGC		ABDEFGHKL MNOPQRSUWX
<i>Bgl</i> III		A↓GATCT		ABDEFGHKL MNOPQRSUWX
<i>Bin</i> I		GGATC (4/5)		
	<i>Aha</i> I	GGATC (4/5)		NSU
<i>Bpu</i> 10I		CCTNAGC (-5/-2)		
<i>Bsa</i> AI		YAC↓GTR		NU
<i>Bsa</i> BI		GATNN↓NNATC		NU
	<i>Bsh</i> 1365I	GATNN↓NNATC		F
	<i>Bsi</i> BI	GATNN↓NNATC		W
	<i>Mam</i> I	GATNN↓NNATC		M
<i>Bsc</i> GI		CCCGT		
<i>Bse</i> PI		GCGCGC		
	<i>Bss</i> HII	G↓CGCGC		BDEKL MNQ RUX
<i>Bse</i> RI		GAGGAG		
<i>Bsg</i> I		GTGCAG (16/14)		N
<i>Bsi</i> I		CTCGTG (-5/-1)		
<i>Bsi</i> YI		CCNNNNN↓NNGG		MUW
	<i>Bs</i> II	CCNNNNN↓NNGG		N
<i>Bsm</i> I		GAATGC (1/-1)		BDELMNOSUX
	<i>Bsa</i> MI	GAATGC (1/-1)		R
	<i>Bsc</i> CI	GAATGC (1/-1)		W
	<i>Mva</i> 1269I	GAATGC (1/-1)		F
<i>Bsm</i> AI		GTCTC (1/5)		NU
	<i>Aha</i> 26I	GTCTC (1/5)	3(5), -4(6)	DFR
<i>Bsp</i> 1407I		T↓GTACA		FN
	<i>Bsr</i> GI	T↓GTACA		N
	<i>Ssp</i> BI	T↓GTACA		M
<i>Bsp</i> GI		CTGGAC		
<i>Bsp</i> HI		T↓CATGA		NSU
	<i>Rca</i> I	T↓CATGA		BM
<i>Bsp</i> LU11I		A↓CATGT		
<i>Bsp</i> MI		ACCTGC (4/8)		N
<i>Bsp</i> MII		T↓CCGGA		X
	<i>Acc</i> III	T↓CCGGA		EKQR
	<i>Bse</i> AI	T↓CCGGA		M
	<i>Bsi</i> MI	T↓CCGGA		W
	<i>Bsp</i> 13I	T↓CCGGA		L
	<i>Bsp</i> EI	T↓CCGGA		NS
	<i>Bsu</i> 23I	T↓CCGGA		W
	<i>Kpn</i> 2I	T↓CCGGA		BDFS
	<i>Mro</i> I	T↓CCGGA		MOU
<i>Bsr</i> I		ACTGG (1/-1)		NU
	<i>Bse</i> NI	ACTGG (1/-1)		DF
<i>Bsr</i> BI		GAGCGG (-3/-3)		N
<i>Bsr</i> DI		GCAATG (2/0)		N
<i>Bst</i> EII		G↓GTNACC		BGHL MNOPQRSUX
	<i>Bsr</i> PI	G↓GTNACC		K
	<i>Eco</i> 91I	G↓GTNACC		DF
	<i>Eco</i> O65I	G↓GTNACC		K
<i>Bst</i> XI		CCANNNNN↓NTGG		BDEGHKL MNQ RSRUX
<i>Cac</i> 8I		GCN↓NGC		
<i>Cau</i> II		CC↓SGG		
	<i>Bcn</i> I	CC↓SGG	2(4)	DFK

Table 2. (continued)

	<i>Eco</i> HI	CCSGIG		
	<i>Kpn</i> 49kII	ICCSGG		
	<i>Nci</i> I	CCISGG		BELMNORSUWX
<i>Cfr</i> I		YIGGCCR	4(5)	
	<i>Eae</i> I	YIGGCCR	4(5)	DKLMNSUX
<i>Cfr</i> 10I		RICCGGY	2(5)	ADFKMOUX
	<i>Bsr</i> FI	RICCGGY		N
<i>Cla</i> I		ATICGAT	5(6)	ABKMNPQRSWX
	<i>Ban</i> III	ATICGAT		OU
	<i>Bsc</i> I	ATICGAT		L
	<i>Bsi</i> XI	ATICGAT		W
	<i>Bsp</i> 106I	ATICGAT		E
	<i>Bsp</i> DI	ATICGAT		N
	<i>Bsp</i> XI	ATICGAT		G
	<i>Bsu</i> 15I	ATICGAT	5(6)	DF
<i>Cvi</i> II		RGICY	3(5)	
<i>Cvi</i> RI		TGICA	4(6)	
<i>Dde</i> I		CITNAG	1(5)	BEGLMNOPRUX
<i>Dpn</i> I*		GAITC		ABLMNRSUX
<i>Dra</i> II		RGIGNCCY		GMU
	<i>Eco</i> O109I	RGIGNCCY		BDEFKLNOSX
	<i>Pss</i> I	RGGNCICY		
<i>Dra</i> III		CACNNNIGTG		EGMNSUX
<i>Drd</i> I		GACNNNNINNGTC		NU
<i>Drd</i> II		GAACCA		
<i>Dsa</i> I		CICRYGG		M
<i>Eam</i> 1105I		GACNNNINNGTC		DFKN
	<i>Asp</i> EI	GACNNNINNGTC		M
	<i>Ecl</i> HKI	GACNNNINNGTC		R
<i>Eci</i> I		TCCGCC		
<i>Eco</i> 31I		GGTCTC (1/5)	4(5), -4(6)	DF
	<i>Bsa</i> I	GGTCTC (1/5)		N
<i>Eco</i> 47III		AGCIGCT		BDEFLMNORU
	<i>Aor</i> 51HI	AGCIGCT		K
<i>Eco</i> 57I		CTGAAG (16/14)	5(6), -5(6)	DFN
<i>Eco</i> NI		CCTNNINNNAGG		NSU
<i>Eco</i> RI		GIAATTC	3(6)	ABDEFGHKMNOPQRSUWX
<i>Eco</i> RII ⁺		ICCWGG	2(5)	BEMOSU
+	<i>Bsi</i> LI	CCIWGG		W
+	<i>Bst</i> NI	CCIWGG	2(4)	ENSX
+	<i>Bst</i> OI	CCIWGG		R
+	<i>Mva</i> I	CCIWGG	2(4)	ADFKMOU
<i>Eco</i> RV		GATATC	2(6)	ABDEGHKLMNOPQRSUWX
	<i>Eco</i> 32I	GATATC		F
<i>Esp</i> I		GCITNAGC		U
	<i>Bpu</i> 1102I	GCITNAGC		BDEFKN
	<i>Cel</i> II	GCITNAGC		LM
<i>Esp</i> 3I		CGTCTC (1/5)	4(5), -4(6)	DFNR
<i>Fau</i> I		CCCGC (4/6)		
<i>Fin</i> I		GGGAC		
	<i>Bsm</i> FI	GGGAC (10/14)		N
<i>Fnu</i> 4HI		GCINGC		N
	<i>Ita</i> I	GCINGC		M
<i>Fnu</i> DII		CGICG		
	<i>Acc</i> II	CGICG		KQX
	<i>Bsh</i> 1236I	CGICG		DEF
	<i>Bst</i> UI	CGICG		NSU
	<i>Mvn</i> I	CGICG		M
	<i>Se</i> I	ICGCG		
	<i>Tha</i> I	CGICG		B
<i>Fok</i> I		GGATG (9/13)	3(6), -2(6)	GKMNRUX
	<i>Sts</i> I	GGATG (10/14)		
<i>Fse</i> I		GGCCGGICC		
<i>Gdi</i> II		YGGCCG (-5/-1)		
<i>Gsu</i> I		CTGGAG (16/14)		DFS
	<i>Bpm</i> I	CTGGAG (16/14)		N
<i>Hae</i> I		WGGICCW		
<i>Hae</i> II		RGCGCIY		BDEGKLMNOPRSUX
	<i>Bme</i> 142I	RGCGCIY		
	<i>Bsp</i> 143II	RGCGCIY		F
<i>Hae</i> III		GGICC	3(5)	ABDGHKLMNOPQRSUX
	<i>Bsh</i> I	GGICC		W
	<i>Bsp</i> KI	GGICC		W

Table 2. (continued)

	<i>BsuRI</i>	GG↓CC	3(5)	F
	<i>Pall</i>	GG↓CC		EP
<i>HgaI</i>		GACGC (5/10)	3(5), -2(5)	NSUX
<i>HgiAI</i>		GWGCW↓C		NX
	<i>Atw21I</i>	GWGCW↓C		BDF
	<i>AspHI</i>	GWGCW↓C		M
	<i>BstHKA I</i>	GWGCW↓C		N
<i>HgiCI</i>		G↓GYRCC	?(5)	
	<i>BanI</i>	G↓GYRCC	?(5)	EMNOPRSUX
	<i>Eco64I</i>	G↓GYRCC		DF
<i>HgiEII</i>		ACCNNNNNNGGT		
<i>HgiJII</i>		GRG↓CY↓C		
	<i>BanII</i>	GRG↓CY↓C		BKLMNOPRSUX
	<i>Eco24I</i>	GRG↓CY↓C		DF
<i>HhaI</i>		GCG↓C	2(5)	BGKNOPRSUX
	<i>CfoI</i>	GCG↓C		BLMRS
	<i>Hin6I</i>	G↓CGC		DF
	<i>HinPII</i>	G↓CGC		NSX
<i>HindII</i>		GT↓Y↓RAC	5(6)	EM
	<i>HincII</i>	GT↓Y↓RAC	5(6)	ABDFGHLKLMNOPRSUX
<i>HindIII</i>		A↓AGCTT	1(6)	ABDEFGHLKLMNOPRSUWX
<i>HinfI</i>		G↓ANTC		ABDEFGHLKLMNOPRSUWX
<i>HpaI</i>		GTT↓AAC	5(6)	ABDEFGHLKLMNOPRSUX
<i>HpaII</i>		C↓CGG	2(5)	ABDEFGHLKLMNOPRSUX
	<i>HapII</i>	C↓CGG	2(5)	K
	<i>MspI</i>	C↓CGG	1(5)	ABDEFGHLKLMNOPRSUWX
<i>HphI</i>		GGTGA (8/7)	-2(5)	NSUX
<i>KpnI</i>		GGTAC↓C	4(6)	ABDEFGHLKLMNOPRSUWX
	<i>Acc65I</i>	G↓GTACC		DFNR
	<i>Asp718I</i>	G↓GTACC		M
<i>Ksp632I</i>		CTCTTC (1/4)		M
	<i>Eam1104I</i>	CTCTTC (1/4)		DF
	<i>EarI</i>	CTCTTC (1/4)		NU
<i>MaeI</i>		C↓TAG		M
	<i>BfaI</i>	C↓TAG		N
<i>MaeII</i>		A↓CGT		M
<i>MaeIII</i>		↓GTNAC		M
<i>MboI</i> ⁷		↓GATC		BEFGKNQRSX
+	<i>Bsp143I</i>	↓GATC		F
	<i>DpnII</i>	↓GATC	2(6)	NU
	<i>NdeII</i>	↓GATC		BDM
+	<i>Sau3AI</i>	↓GATC	4(5)	ABDEGHLKLMNOPRSUX
<i>MboII</i>		GAAGA (8/7)	5(6)	BDFKNOQRSUX
<i>McrI</i>		CGR↓Y↓CG		M
	<i>BsaOI</i>	CGR↓Y↓CG		R
	<i>Bsh1285I</i>	CGR↓Y↓CG		DF
	<i>BsiEI</i>	CGR↓Y↓CG		NW
<i>MfeI</i>		C↓AATTG		
	<i>MunI</i>	C↓AATTG	3(6)	BDEFKMN
<i>MluI</i>		A↓CGCGT		ABDEFGHLKLMNOPRSUWX
<i>MlyI</i>		GACTC (5/5)		
<i>MmeI</i>		TCCRAC (20/18)		
<i>MnlI</i>		CCTC (7/6)		ENQUX
<i>MseI</i>		T↓TAA		BNS
	<i>TruII</i>	T↓TAA		F
	<i>Tru9I</i>	T↓TAA		LMR
<i>MsiI</i>		CAYNN↓NNRTG		N
<i>MstI</i>		TGC↓GCA		X
	<i>AvII</i>	TGC↓GCA		M
	<i>FdiII</i>	TGC↓GCA		U
	<i>FspI</i>	TGC↓GCA		BKNOSU
<i>MwoI</i>		GCNNNNN↓NNGC		N
	<i>BspWI</i>	GCNNNNN↓NNGC		M
<i>NaeI</i>		GCC↓GGC		DEKLMNOUX
	<i>NgoMI</i>	G↓CCGGC		N
<i>NarI</i>		GG↓CGCC		BEMNOPRSUX
	<i>BbeI</i>	GGCGC↓C		K
	<i>EheI</i>	GGC↓GCC		DFOU
	<i>KasI</i>	G↓GCGCC		N
<i>NcoI</i>		C↓CATGG		ABDEFGHLKLMNOPRSUWX
<i>NdeI</i>		CA↓TATG	4(6)	BDEFGKLMNPRSUX
<i>NheI</i>		G↓CTAGC		BDEFGKLMNOPRSUX
<i>NlaIII</i>		CATG↓	2(6)	NOSU

Table 2. (continued)

	CviAII	C↓ATG	2(6)	NSU
NlaIV		GGN↓NCC		W
	BscBI	GGN↓NCC		ABDEFGKLMNOPQRSUWX
NotI		GC↓GGCCGC		BDEFGKLMNOPQRSUWX
NruI		TCG↓CGA		F
	Bsp68I	TCG↓CGA		ABKMU
NspI		RCATG↓Y		U
NspBII		CMG↓CKG		R
	MspAII	CMG↓CKG		NU
PacI		TTAAT↓TAA		
Pfi1108I		TCGTAG		NSU
PfiMI		CCANNNN↓NTGG		R
	AccB7I	CCANNNN↓NTGG		F
	Esp1396I	CCANNNN↓NTGG		DFM
	Van91I	CCANNNN↓NTGG		N
PleI		GAGTC (4/5)		AK
PmaCI		CAC↓GTG		M
	BbrPI	CAC↓GTG		DEFR
	Eco72I	CAC↓GTG		N
	PmlI	CAC↓GTG		N
PmeI		GTTT↓AAAC		NSU
PpuMI		RG↓GWCCY		BDF
	Psp5II	RG↓GWCCY		K
PshAI		GACNN↓NNGTC		ABDEFGHKLMNOPQRSUWX
PstI		CTGCA↓G	5(6)	ABDEFGKLMNOPQRSUX
PvuI		CGAT↓CG		
	Afa22MI	CGA↓TCG		E
	BspCI	CGAT↓CG		BS
	XorII	CGAT↓CG		ABDEFGHKLMNOPQRSUWX
PvuII		CAG↓CTG	4(4)	
RleAI		CCCACA (12/9)		ABDEGLMNOPQRSUWX
RsaI		GT↓AC		K
	AfaI	GT↓AC		DFN
	Csp6I	G↓TAC		BMNSUX
RsrII		CG↓GWCCG		DFK
	CpoI	CG↓GWCCG		EORU
	CspI	CG↓GWCCG		AEGHKLMNOPQRSUWX
SacI		GAGCT↓C		DFN
	Ecl136II	GAG↓CTC		R
	EcoICRI	GAG↓CTC		BS
	SstI	GAGCT↓C		EGHLNOPQRSUX
SacII		CCGC↓GG		DF
	Cfr42I	CCGC↓GG		M
	KspI	CCGC↓GG		BS
	Mlu113I	CC↓GCGG		ABDEFGHKLMNOPQRSUWX
	SstII	CCGC↓GG		N
SalI		G↓TCGAC		M
SapI		GCTCTC (1/4)		ENRS
SauI		CC↓TNAGG		BS
	Bsu36I	CC↓TNAGG		DFKOU
	CviI	CC↓TNAGG		X
	Eco81I	CC↓TNAGG		ABDEFGKLMNOPQRSUX
	MstII	CC↓TNAGG		DMNOSUX
ScaI		AGT↓ACT		M
ScrFI		CC↓NGG		F
	DsaV	↓CCNGG		M
SduI		GDGCH↓C		DKNRUX
	BmyI	GDGCH↓C		
	Bsp1286I	GDGCH↓C		BNU
SecI		C↓CNNGG		M
	BsaII	C↓CNNGG		NSX
SexAI		A↓CCWGGT		
SfaNI		GCATC (5/9)		
	BscAI	GCATC (4/6)		
SfeI		C↓TRYAG		N
	SfcI	C↓TRYAG		ABDEGLMNOPQRSUX
SfiI		GGCCNNNN↓NGGCC		M
SgrAI		CR↓CCGGYG		ABDEFGHKLMNOPQRSUWX
SmaI		CCC↓GGG	2(4)	DFOU
	Cfr9I	C↓CCGGG	2(4)	E
	PspAI	C↓CCGGG		NRSUWX
	XmaI	C↓CCGGG		
SnaI		GTATAC		

Table 2. (continued)

	<i>Bsp</i> M90I	GTA↓TAC		W
	<i>Bsr</i> 1107I	GTA↓TAC		DFKMN
<i>Sna</i> BI		TAC↓GTA		EKLMNRSX
	<i>Eco</i> 105I	TAC↓GTA		BDFOU
<i>Spe</i> I		A↓CTAGT		BDEKLMNORSUWX
<i>Sph</i> I		GCATG↓C		ABDEGHKLMNOPQRSUX
	<i>Bbu</i> I	GCATG↓C		R
	<i>Pae</i> I	GCATG↓C		F
<i>Sp</i> II		C↓GTACG		AK
	<i>Bst</i> WI	C↓GTACG		MNUW
	<i>Pft</i> 23II	C↓GTACG		DF
	<i>Sun</i> I	C↓GTACG		B
<i>Srf</i> I		GCCC↓GGGC		EO
<i>Sse</i> 8387I		CCTGCA↓GG		K
<i>Ssp</i> I		AAT↓ATT		BDEFKLMNORUX
<i>Stu</i> I		AGG↓CCT		ABEGKLMNPQRSX
	<i>Aat</i> I	AGG↓CCT		OU
	<i>Eco</i> 147I	AGG↓CCT		DF
<i>Sry</i> I		C↓CWWGG		BEMNRSX
	<i>Eco</i> 130I	C↓CWWGG		DFU
	<i>Eco</i> T14I	C↓CWWGG		AK
<i>Swa</i> I		ATTT↓AAAT		M
<i>Taq</i> I		T↓CGA	4(6)	ABDEFGMLNOPQRSUWX
	<i>Tth</i> HB8I	T↓CGA	4(6)	K
<i>Taq</i> II ⁸		CACCCA (11/9)		
		GACCGA (11/9)		
<i>Tfi</i> I		G↓AWTC		NU
<i>Tsp</i> 45I		GTSAC		
<i>Tsp</i> EI		AATT		
	<i>Tsp</i> 509I	↓AATT		N
<i>Tth</i> 111I		GACN↓NNGTC		DKNPQRUX
	<i>Asp</i> I	GACN↓NNGTC		M
<i>Tth</i> 111II		CAARCA (11/9)		
<i>Vsp</i> I		AT↓TAAT		BDEFKR
	<i>Ase</i> I	AT↓TAAT		NOSU
	<i>Asn</i> I	AT↓TAAT		M
<i>Xba</i> I		T↓CTAGA	6(6)	ABDEFGHKLMNOPQRSUWX
<i>Xcm</i> I		CCANNNNN↓NNNTGG		NU
<i>Xho</i> I		C↓TCGAG		ADEFGHKLMNOPQRSUWX
	<i>Ccr</i> I	C↓TCGAG		X
	<i>Pae</i> R7I	C↓TCGAG	5(6)	NSX
	<i>Scl</i> II	CTC↓GAG		
<i>Xho</i> II		R↓GATCY		EMRX
	<i>Bst</i> YI	R↓GATCY		BNU
	<i>Mfi</i> I	R↓GATCY		AK
<i>Xma</i> III		C↓GGCCG	4(5)	BE
	<i>Bst</i> ZI	C↓GGCCG		R
	<i>Eag</i> I	C↓GGCCG		NS
	<i>Ecl</i> XI	C↓GGCCG		M
	<i>Eco</i> 52I	C↓GGCCG		DFKORU
<i>Xmn</i> I		GAANN↓NNTTC		DENX
	<i>Asp</i> 700I	GAANN↓NNTTC		M

1. * signifies that *Dpn*I requires the presence of 6-methyladenosine within the recognition sequence GATC.

2. Recognition sequence nomenclature is as in Table 1

3. The site of methylation by the cognate methylase when known is indicated as follows. The first number shows the base within the recognition sequence that is modified. A negative number indicates the complementary strand, numbered from the 5' base of that strand. The number in parentheses indicates the specific methylation involved. (6) = N6-methyladenosine; (5) = 5-methylcytosine; (4) = N4-methylcytosine.

4. Commercial sources of restriction enzymes are abbreviated as follows:

- A Amersham (5/93)
- B Life Technologies Inc, Gibco-BRL (4/93)
- D Angewandte Gentechnologie Systeme (4/93)
- E Stratagene (4/93)
- F Fermentas MBI (4/93)
- G Appligene (4/93)
- H American Allied Biochemical, Inc. (5/93)
- K Takara (5/93)
- L Northumbria Biologicals Limited (4/93)
- M Boehringer-Mannheim (4/93)
- N New England BioLabs (5/93)
- O Toyobo (5/93)
- P Pharmacia P-L Biochemicals (5/93)
- Q Molecular Biology Resources (4/93)

R Promega Corporation (4/93)

S Sigma (4/93)

U United States Biochemical Corporation (4/93)

W International Laboratory Services (4/93)

X New York Biolabs (4/93)

The date in parentheses indicates the most recent update.

5. *BcgI* cleaves on both sides of the recognition sequence: 10 bases 5' to the recognition sequence and 12 bases 3' to it on both strands. Thus the recognition site is excised in a fragment, 34 base pairs long, with 2-base 3'-extensions at each end.

6. *EcoRII* isoschizomers fall into two classes based upon their sensitivity to methylation. *EcoRII* will not cleave when the second cytosine in the recognition sequence is methylated to 5-methylcytosine whereas *MvaI* will cleave such a sequence. Isoschizomers of *EcoRII* that are like *MvaI* are indicated by +.

7. *MboI* isoschizomers fall into two classes based upon their sensitivity to methylation. *MboI* will not cleave when the recognition sequence contains 6-methyladenosine whereas *Sau3AI* will not cleave when its recognition sequence contains 5-methylcytosine. Isoschizomers of *MboI* that are like *Sau3AI* are indicated by +.

8. *TaqII* differs from other restriction enzymes in recognizing two distinct sequences: GACCG and CACCCA.