REBASE — restriction enzymes and methylases

Richard J.Roberts* and Dana Macelis

New England BioLabs, 32 Tozer Road, Beverly, MA 01915, USA

ABSTRACT

REBASE is a comprehensive database of information about restriction enzymes and their associated methylases, including their recognition and cleavage sites and their commercial availability. Information from REBASE is available via monthly electronic mailings as well as via WAIS and anonymous ftp. Specialized files are available that can be used directly by many software packages.

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), 138 new entries have been added including 10 new Type II enzymes: *AceIII*, C-AGCTC (7/11); *BmgI*, GKGCCC; *Bsbl*, CAACAC; *Bsp24I*, (8/13) GACNNNNNTGG (12/7); *CjeI*, (13/7) CC-ANNNNNNGT (9/15); *CjePI*, (13/7) CCANNNNNNTC (8/14); *Hin4I*, GABNNNNVTC; *SgfI*, GCGAT[†]CGC, *TseI*, GCWGC and *UbaI* GCSGC. Note also that the recognition sequence for *BsaXI*, has now been determined as ACNNNNNC-TCC, making it a new prototype. One previously listed prototype, *MlyI*, is omitted since its recognition sequence is the complement of that of *PleI* and so it is truly an isoschizomer of the latter. This pair of isoschizomers is unique in cleaving on opposite sides of the recognition sequence. A complete list of the new enzymes can be found in Table I. A total of 2531 restriction enzymes is now known including 19 different Type I specificities, 198 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 publically 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. It should be noted that REBASE is now accessible via WAIS directly from vent.neb.com (192.138.220.2 port 210). We currently have five WAIS sources set up.

REBASE__help: general description of REBASE and the services and data files offered.

REBASE__enzymes: facts about each enzyme in REBASE.

REBASE__references: all the published references stored in REBASE complete with abstracts where available.

REBASE__suppliers: commercial sources of enzymes, includes contact information (address, telephone nos, fax nos) for each company and a list of the enzymes that they sell.

REBASE__news: a report of what's new in REBASE this month, such as any enzyme name changes, announcements of new REBASE formats and services, new commercial suppliers, etc.

Since last year, International Laboratory Services (REBASE abbreviation W) has changed its name to Immunogen International Limited. Amersham and USB have combined operations and are now listed in REBASE as a single source called Amersham Life Sciences-USB.

A small change in format should be noted. Instead of displaying the last two digits of the year in the REBASE release number, we now use only the last digit. For example, the July 1994 REBASE GCG data file which would have previously been called 'gcg.9407' becomes 'gcg.407'.

Several enzyme names have been changed recently. The enzyme previously called *BsoFI* has been renamed *BsoHI* because of duplicate use of the name. In addition, *Msp20I* (TGG[†]CCA) is now *MluNI* (strain identified as *Micrococcus luteus* N). *NgoFIII* (CCGC[†]GG) and *NgoFIV* (G[†]CCGGC) are renamed *NgoAIII* and *NgoAIV* respectively. Two previously unidentified bacteria have been identified, leading to name changes of *Uba1265I* (*AflIII*) to *BspTI* and *Uba1434I* (*SecI*) to *BseDI*. Following this renaming, it was discovered that the name *BseDI* had been used for two different enzymes. The original enzyme, *BseDI* (specificity unknown), is now called *BseEI*. The enzyme that Pharmacia sold under the name *BstDI* has been renamed *BstD102I* and is available under that name. The 'real' *BstDI* is not commercially available.

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

*To whom correspondence should be addressed

evidence for the presence of a restriction modification system. The endonucleases are named in accordance with the proposal of Smith and Nathans (2).

We request that authors wishing to cite REBASE use this article as a general reference for the complete listing that is available electronically.

ACKNOWLEDGEMENTS

Special thanks are due to the many individuals who have so kindly communicated their unpublished results for inclusion in this compilation. Work from the authors' laboratory is supported by the National Library of Medicine (LM04971).

REFERENCES

1. Roberts, R.J. and Macelis D. Nucl. Acids Res. **21**: 3125–3137 (1993).
2. Smith, H.O. and Nathans, D. J. Mol. Biol. **81**: 419–423 (1973).
3. Inagaki, K., Hikita, T., Yanagidani, S., Nomura, Y., Kishimoto, N., Tano, T. and Tanaka, H. Biosci. Biotech. Biochem. **57**: 1716–1721 (1993).
4. Miyahara, M. and Mise, K. Unpublished observations.
5. Rahman, H. and Affram, C. Unpublished observations.
6. Affram, C. and Rahman, H. Unpublished observations.
7. Torsti, A-M. Unpublished observations.
8. Matvienko, N.N., Kramarov, V.M., Zheleznyaya, L.A. and Matvienko, N.I. Biokhimiia **58**: 1139–1153 (1993).
9. Vitkute J., Markauskiene J., Valickiene D., Trinkunaite L., Kiuduliene E., Petrusyte M., Butkus V. and Janulaitis A. Unpublished observations.
10. Jurgelyte R., Maniulyte V., Lazareviciute L., Maneliene Z., Kiuduliene E., Norgeliene D., Kvietkiene E., Petrusyte M., Butkus V. and Janulaitis A. Unpublished observations.
11. Korpela, J. and Hjorleifsdottir, S. Unpublished observations.
12. Torsti, A-M. and Hjorleifsdottir, S. Unpublished observations.
13. Degtyarev, S.K., Rechkunova, N.I., Zernov, Y.P., Dedkov, V. S., Chizikov, V.E., Van Calligan, M., Williams, R. and Murray, E. Gene **131**: 93–95 (1993).
14. Shapovalova, N.I., Zheleznyaya, L.A. and Matvienko, N.I. Nucleic Acids Res. **21**: 5794 (1993).
15. Padegimiene E., Maneliene Z., Norgeliene D., Vonseviciene E., Kiuduliene E., Petrusyte M., Butkus V. and Janulaitis A.. Unpublished observations.
16. Polisson, C. Unpublished observations.
17. Maniulyte, V., Lazareviciute, L., Jurgelyte, R., Maneliene, Z., Velickiene, Z., Norgeliene, D., Petrusyte, M., Butkus, V. and Janulaitis, A. Unpublished observations.
18. Chen, Z. Unpublished observations.
19. Chen, Z. and Morgan, R. Unpublished observations.
20. Degtyarev, S.K. Unpublished observations.
21. DiFrancesco, R. and Ge, L. Unpublished observations.
22. Mattila, P. and Pitkanen, K. Unpublished observations.
23. Vitor, J.M.B., Polisson, C., Cabrita, J. and Silva, R.V.C. Acta gastroenterol. belg. **56**: 41 (1993).
24. Vitor, J.M.B. Unpublished observations.
25. Zweiger, G., Marczynski, G. and Shapiro, L. J. Mol. Biol. **235**: 472–474 (1994).
26. Zakharova, M.V., Kravetz, A.N., Beletzkaja, I.V., Repyk, A.V. and Solonin, A.S. Gene **129**: 77–81 (1993).
27. Tyndall, C., Meister, J. and Bickle, T.A. J. Mol. Biol. **237**: 266–274 (1994).
28. Kravetz, A.N., Zakharova, M.V., Beletaya, I.V., Sineva, E.V., Denjmuchametov, M.M., Petrov, S.I., Glatman, L.I. and Solonin, A.S. Gene **129**: 153–154 (1993).
29. Affram, C. Unpublished observations.
30. Lazareviciute L., Bitinaite J., Laucys V., Kvietkiene E., Kiuduliene E., Petrusyte M., Butkus V. and Janulaitis A. Unpublished observations.
31. Allen, J. Unpublished observations.
32. Vaitkevicius D., Maneliene Z., Norgeliene D., Valickiene D., Kiuduliene E., Petrusyte M., Butkus V. and Janulaitis A. Unpublished observations.
33. Romanovskaya, V.A., Alexeyev, M.F., Gun'kovskaya, N.V., Stolyar, S.M., Shatohina, E.S. and Malashenko, Y.R. Mikrobiol. J. **54**: 32–39 (1992).
34. Alexeyev, M.F., Gunkovskaya, N.V., Romanovskaya, V.A. and Malashenko, Y.R. Mikrobiol. J. **54**: 70–73 (1992).
35. Shankar, S. and Tyagi, A.K. Gene **132**: 119–123 (1993).
36. Shankar, S. and Tyagi, A.K. Gene **131**: 153–154 (1993).
37. Dybvig, K. and Yu, H. Mol. Microbiol. **12**: 547–560 (1994).
38. Gunn, J.S. and Stein, D.C. Gene **132**: 15–20 (1993).
39. Vitkute J., Markauskiene J., Maneliene Z., Valickiene, D., Trinkunaite L., Kiuduliene E., Butkus V. and Janulaitis A. Unpublished observations.
40. Leonard, J. and Morgan, R. Unpublished observations.
41. Pristas, P., Vanat, I., Godany, A. and Javorsky, P. Unpublished observations.
42. Vanat, I., Pristas, P., Rybosoval, E., Godany, A. and Javorsky, P. FEMS Microbiol. Lett. **113**: 129–132 (1993).
43. Poch, M.T. and Somkuti, G.A. ASM Abstracts O43 (1993).
44. Guimont, C., Henry, P. and Linden, G. Appl. Microbiol. Biotechnol. **39**: 216–220 (1993).
45. Bae, M., Park, J., Hwang, H-Y. and Yim, J. Unpublished observations.
46. Vesselinova, N. and Kappelman, J. Unpublished observations.
47. Kaluza, K., Frey, B. and Jarsch, M. European Patent 480343A2 (1992).
48. Hwang, H.-Y. and Yim, J. Nucleic Acids Res. **22**: 2197 (1994).
49. Korpela, J., Torsti, A-M. and Hjorleifsdottir, S. Unpublished observations.
50. Tassoni, L. and Clark, D.R. Unpublished observations.
51. Vitkute J., Jurgelyte R., Lazareviciute L., Maneliene Z., Capskaja L., Kiuduliene E., Petrusyte M., Butkus V. and Janulaitis A. Unpublished observations.
52. Bax, E. Unpublished observations.
53. Vitkute, J., Petrusyte, M., Kiuduliene, E., Butkus, V. and Janulaitis, A. Unpublished observations.

Table 1.

Microorganism	Source	Enzyme ¹	Sequence ²	Reference
<i>Acidiphilium organovorum</i> 13H	K. Inagaki	<i>Aor13HI</i> (<i>Bsp</i> MII)	T ¹ CCGGA	3
<i>Aeromonas hydrophila</i> AH63	T. Shimada	<i>AhyAI</i> (<i>Xho</i> I)	CTCGAG	4
<i>Anabaena cedrorum</i>	M.M. Wijden-bosch	<i>AceI</i> (<i>Tse</i> I)	G ¹ CWGC	5
		<i>AceII</i> (<i>Nhe</i> I)	GCTAG ¹ C	6
		<i>AceIII</i>	CAGTC (7/11)	6
<i>Bacillus cereus</i>	FZ 852	<i>BctI</i> (<i>Bce</i> II)	ACGGC	7
<i>Bacillus licheniformis</i> 736	N.I. Matvienko	<i>Bli736I</i> (<i>Eco</i> 31I)	GGTCTC (1/5)	8
<i>Bacillus megaterium</i> E11-132	A.A. Janulaitis	<i>BmgI</i>	GKGCCC	9
<i>Bacillus pumilus</i> sw 4-3	A.A. Janulaitis	<i>BpiI</i> (<i>Bbv</i> II)	GAAGAC (2/6)	10
<i>Bacillus</i> species	FZ 508	<i>Bsp508I</i> (<i>Bsp</i> MII)	TCCGGA	11
<i>Bacillus</i> species	FZ 548	<i>Bsp548I</i> (<i>Scr</i> FI)	CCNGG	12
<i>Bacillus</i> species 24	S.K. Degtyarev	<i>Bsp24I</i>	(8/13) GACNNNNNTGG (12/7)	13
<i>Bacillus</i> species KT6	N.I. Matvienko	<i>BspKT6I</i> (<i>Mbo</i> I)	G ¹ ATC	14
<i>Bacillus</i> species d 1-34	A.A. Janulaitis	<i>BspPI</i> (<i>Bln</i> I)	GGATC (4/5)	15
<i>Bacillus</i> species lp	NEB 819	<i>BlpI</i> (<i>Esp</i> I)	GCTNAGC	16
<i>Bacillus sphaericus</i> TK-45	A.A. Janulaitis	<i>BshNI</i> (<i>Hgi</i> CI)	G ¹ GYRCC	17
<i>Bacillus stearothermophilus</i> 21P	Z. Chen	<i>BsmCI</i> (<i>Bsa</i> XI)	?	18
<i>Bacillus stearothermophilus</i> 25B	Z. Chen	<i>BsmDI</i> (<i>Bsa</i> XI)	?	18
<i>Bacillus stearothermophilus</i> B61	NEB 857	<i>BsmBI</i> (<i>Esp</i> 3I)	CGTCTC (1/5) 1	9
<i>Bacillus stearothermophilus</i> BR	S.K. Degtyarev	<i>BsrBRI</i> (<i>Bsa</i> BI)	GATNN ¹ NNATC	20
<i>Bacillus stearothermophilus</i> D102	L. Ge	<i>BstD102I</i> (<i>Bsr</i> BI)	GAGCGG (-3/-3)	21
<i>Bacillus stearothermophilus</i> D88	Z. Chen	<i>BseEI</i>	?	18
<i>Bacillus stearothermophilus</i> F245	Z. Chen	<i>BseFI</i>	?	18
<i>Bacillus stearothermophilus</i> F66	Z. Chen	<i>BsoFI</i> (<i>Fnu</i> 4HI)	GC ¹ NGC	19
<i>Bacillus stearothermophilus</i> G170	Z. Chen	<i>BsmGI</i> (<i>Bsp</i> 1407I)	TGTACA	18
		<i>BsmGII</i> (<i>Hind</i> III)	AAGCTT	18
<i>Bacillus stearothermophilus</i> T889	Z. Chen	<i>BseTI</i>	?	18
<i>Bacillus stearothermophilus</i> Y36	Z. Chen	<i>BsmYI</i> (<i>Bsi</i> YI)	CCNNNNNNNGG	18
<i>Bacillus stearothermophilus</i> Z295	Z. Chen	<i>Bst295I</i> (<i>Dde</i> I)	CTNAG	18
<i>Brevibacterium helvolum</i>	ATCC 11822	<i>BheI</i> (<i>Nae</i> I)	GCCGGC	22
<i>Campylobacter coli</i> P215	J.M.B. Vitor	<i>CcoP215I</i> (<i>Fnu</i> 4HI)	GCNGC	23
<i>Campylobacter coli</i> P216	J.M.B. Vitor	<i>CcoP216I</i> (<i>Fnu</i> 4HI)	GCNGC	23
<i>Campylobacter coli</i> P219	J.M.B. Vitor	<i>CcoP219I</i> (<i>Mbo</i> I)	GATC	23
<i>Campylobacter coli</i> P31	J.M.B. Vitor	<i>CcoP31I</i> (<i>Mbo</i> I)	GATC	23
<i>Campylobacter coli</i> P73	J.M.B. Vitor	<i>CcoP73I</i> (<i>Rsa</i> I)	GTAC	23
<i>Campylobacter coli</i> P76	J.M.B. Vitor	<i>CcoP76I</i> (<i>Mbo</i> I)	GATC	23
<i>Campylobacter coli</i> P84	J.M.B. Vitor	<i>CcoP84I</i> (<i>Mbo</i> I)	GATC	23
<i>Campylobacter coli</i> P95	J.M.B. Vitor	<i>CcoP95I</i> (<i>Hha</i> I)	GCGC	23
		<i>CcoP95II</i> (<i>Mbo</i> I)	GATC	23
<i>Campylobacter jejuni</i> P116	J.M.B. Vitor	<i>CjePI</i>	(13/7) CCANNNNNNNNTC (8/14)	24
<i>Campylobacter jejuni</i> P37	J.M.B. Vitor	<i>CjeI</i>	(13/7) CCANNNNNNGT (9/15)	24
<i>Caulobacter crescentus</i>	L. Shapiro	<i>M. CcrMI</i>	G ¹ ANTC	25
<i>Citrobacter freundii</i> 4111	A.S. Solonin	<i>CfrBI</i> (<i>Sty</i> I)	C ¹ CWWGG	26
<i>Escherichia coli</i>	T.A. Bickle	<i>EcoprrI</i>	CCANNNNNNNRTGC	27
<i>Escherichia coli</i> 1831	A.S. Solonin	<i>Eco1831I</i>	TCCSGG	28
		(<i>Cau</i> II)		
<i>Fischerella uniformis</i>	M.M. Wijden-bosch	<i>FunI</i> (<i>Eco</i> 47III)	AGC ¹ GCT	29
<i>Haemophilus influenzae</i> RFL4	A.A. Janulaitis	<i>Hin4I</i>	GABNNNNNVTC	30
<i>Haemophilus</i> species 92	R. Williams	<i>Hsp92I</i> (<i>Acy</i> I)	GR ¹ CGYC	31
		<i>Hsp92II</i> (<i>Nla</i> III)	CATG ¹	31
<i>Kurthia</i> species N88	A.A. Janulaitis	<i>KspAI</i> (<i>Hpa</i> I)	GTT ¹ AAC	32
<i>Methylococcus capsulatus</i>	IMV 3494	<i>McaBI</i>	?	33
<i>Methylococcus whittenburyi</i>	IMV 3033	<i>MwhI</i> (<i>Hpa</i> I)	GTTAAC	34
<i>Methylovarius</i> species	IMV 3017	<i>MvsI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Methylovarius</i> species	IMV 3019	<i>MvsAI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Methylovarius</i> species	IMV 3027	<i>MvsBI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Methylovarius</i> species	IMV 3112	<i>MvsCI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Methylovarius</i> species	IMV 3226	<i>MvsDI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Methylovarius</i> species	IMV 3100	<i>MvsEI</i> (<i>Kpn</i> I)	GGTACC	33
<i>Mycobacterium chelonae</i>	A.K. Tyagi	<i>MchAI</i> (<i>Nor</i> I)	GC ¹ GGCCGC	35
		<i>MchAII</i> (<i>Hae</i> III)	GG ¹ CC	35
<i>Mycobacterium gordonae</i>	A.K. Tyagi	<i>MgoI</i> (<i>Mbo</i> I)	TGATC	36
<i>Mycoplasma pulmonis</i> UAB 6510	K. Dybvig	<i>MpuUI</i>	?	37
<i>Neisseria gonorrhoeae</i> WR302	D.C. Stein	<i>M. NgoBV</i>	GGCC	38
<i>Paracoccus alcaliphilus</i> ZVK3-3	A.A. Janulaitis	<i>Paul</i> (<i>Bse</i> PI)	GCGCGC	39
<i>Plesiomonas shigelloides</i> PL50	T. Shimada	<i>PshCI</i> (<i>Pma</i> CI)	CACGTG	4
<i>Plesiomonas shigelloides</i> PL59	T. Shimada	<i>PshDI</i> (<i>Pma</i> CI)	CACGTG	4
<i>Plesiomonas shigelloides</i> TPS1044	S. Matsushita	<i>PshEI</i> (<i>Pst</i> I)	CTGCAG	4
<i>Plesiomonas shigelloides</i>	S. Matsushita	<i>PshBI</i> (<i>Vsp</i> I)	AT ¹ TAAT	4

Table 1. (cont.)

Microorganism	Source	Enzyme ¹	Sequence ²	Reference
TPS970				
<i>Propionibacterium intermedium</i>	ATCC 14072	<i>PvuI</i> (<i>PvuI</i>)	CGATCG	22
<i>Pseudomonas fluorescens</i>	Viiikki 152	<i>PluI</i> (<i>SnaI</i>)	AGGCCT	22
<i>Pseudomonas oleovorans</i>	Viiikki 13	<i>PoiI</i> (<i>AvaII</i>)	GGWCC	22
<i>Pyrococcus</i> species G1H	NEB 906	<i>PspGI</i> (<i>EcoRII</i>)	CCWGG	40
<i>Rhodothermus</i> species	FZ 519	<i>Rsp519I</i> (<i>MaeI</i>)	CTAG	11
		<i>Rsp519II</i> (<i>EcoRV</i>)	GATATC	11
<i>Rhodothermus</i> species	FZ 523	<i>Rsp523I</i> (<i>MaeI</i>)	CTAG	12
<i>Rhodothermus</i> species	FZ 534	<i>Rsp534I</i> (<i>AsuII</i>)	TTCGAA	12
<i>Rhodothermus</i> species	FZ 554	<i>Rsp554I</i> (<i>AvaII</i>)	GGWCC	12
<i>Rhodothermus</i> species	FZ 556	<i>Rsp556I</i> (<i>AsuII</i>)	TTCGAA	12
<i>Salmonella enteritidis</i> PT14b	A. Nakamura	<i>SenPT14bI</i> (<i>SacII</i>)	CCGC1GG	4
<i>Salmonella enteritidis</i> PT16	A. Nakamura	<i>SenPT16I</i> (<i>XmaIII</i>)	C1GGCCG	4
<i>Selenomonas ruminantium</i>	I. Vanat	<i>Sru4DI</i> (<i>VspI</i>)	AT1TAAT	41
<i>Selenomonas ruminantium</i> 18D	I. Vanat	<i>SruI</i> (<i>AhaIII</i>)	TTT1AAA	42
<i>Streptococcus thermophilus</i>	M.T. Poch	<i>Sth132I</i>	?	43
<i>Streptococcus thermophilus</i> CNRZ 455	G. Linden	<i>Sth455I</i> (<i>EcoRII</i>)	CCWGG	44
<i>Streptomyces albidoflavus</i>	Viiikki 329	<i>SlbI</i> (<i>Eco31I</i>)	GGTCTC	22
<i>Streptomyces exfoliatus</i>	J. Yim	<i>SexBI</i> (<i>SacII</i>)	CCGC1GG	45
<i>Streptomyces griseoflavus</i>	Viiikki 346	<i>Sgil</i> (<i>PstI</i>)	CTGCAG	22
<i>Streptomyces griseoflavus</i>	Viiikki 41	<i>SriI</i> (<i>PstI</i>)	CTGCAG	22
<i>Streptomyces griseoruber</i>	R. Williams	<i>Sgfl</i>	GCGAT1CGC	46
<i>Streptomyces parvus</i>	NRRL B-1255	<i>SpvI</i> (<i>BamHI</i>)	GGATCC	22
<i>Streptomyces rimosus</i> forma <i>paramomycinus</i>	ATCC 14827	<i>SrifpI</i> (<i>XhoI</i>)	CTCGAG	22
<i>Streptomyces</i> species BMTU 4800	DSM 6181 (<i>Bsp1407I</i>)	<i>Ssp4800I</i>	T1GTACA	47
<i>Streptovorticillum olivo-verticillatum</i>	J. Yim	<i>SolI</i> (<i>BamHI</i>)	G1GATCC	48
<i>Synechococcus parietina</i>	M.M. Wijden-bosch	<i>SpaHI</i> (<i>SphI</i>)	GCATG1C	5
<i>Thermus</i> species	FZ 504	<i>Tsp504I</i> (<i>XmaIII</i>)	CGGCCG	49
<i>Thermus</i> species	FZ 505	<i>Tsp505I</i> (<i>TaqI</i>)	TCGA	11
<i>Thermus</i> species	FZ 507	<i>Tsp507I</i> (<i>BspMII</i>)	TCCGGA	11
<i>Thermus</i> species	FZ 510	<i>Tsp510I</i> (<i>TaqI</i>)	TCGA	11
<i>Thermus</i> species	FZ 513	<i>Tsp513I</i> (<i>TaqI</i>)	TCGA	11
<i>Thermus</i> species	FZ 514	<i>Tsp514I</i> (<i>BspMII</i>)	TCCGGA	11
<i>Thermus</i> species	FZ 515	<i>Tsp515I</i> (<i>BspMII</i>)	TCCGGA	11
<i>Thermus</i> species	FZ 560	<i>Tsp560I</i> (<i>HaeIII</i>)	GGCC	12
<i>Thermus</i> species 93159	D. Clark	<i>TseAI</i> (<i>SduI</i>)	GDGCHC	50
<i>Thermus</i> species 93170	D. Clark	<i>TseI</i>	GCWGC	50
<i>Thermus thermophilus</i> Ce4-1	A.A. Janulaitis	<i>TmiI</i> (<i>MaeII</i>)	ACGT	51
		<i>TmiII</i> (<i>BsePI</i>)	GCGCGC	51
<i>Tolypothrix elabens</i>	M.M. Wijden-bosch	<i>TelI</i> (<i>Tth111I</i>)	GACN1NNGTC	52
Unidentified bacterium	A. A. Janulaitis	<i>UbaII</i>	GCSGC	53
Unidentified thermophile	FZ 506	<i>Uth506I</i> (<i>BglII</i>)	GCCNNNNNGGC	11
Unidentified thermophile	FZ 511	<i>Uth511I</i> (<i>AvaII</i>)	GGWCC	11
Unidentified thermophile	FZ 512	<i>Uth512I</i> (<i>TaqI</i>)	TCGA	11
Unidentified thermophile	FZ 536	<i>Uth536I</i> (<i>AsuII</i>)	TTCGAA	12
Unidentified thermophile	FZ 537	<i>Uth537I</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 549	<i>Uth549I</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 555	<i>Uth555I</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 557	<i>Uth557I</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 558	<i>Uth558I</i> (<i>AsuII</i>)	TTCGAA	12
Unidentified thermophile	FZ 559	<i>Uth559I</i> (<i>EcoRV</i>)	GATATC	12
		<i>Uth559II</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 561	<i>Uth561I</i> (<i>HaeIII</i>)	GGCC	12
Unidentified thermophile	FZ 562	<i>Uth562I</i> (<i>HaeIII</i>)	GGCC	12
<i>Vibrio cholera</i> CY100	C. Yamada	<i>VchN100I</i> (<i>EcoRI</i>)	GAATTC	4
<i>Vibrio cholera</i> O2	T. Shimada	<i>VchO2I</i> (<i>EcoRI</i>)	GAATTC	4
<i>Vibrio cholera</i> O25	T. Shimada	<i>VchO25I</i> (<i>SnaI</i>)	GTATAC	4

Table 1. (cont.)

Microorganism	Source	Enzyme ¹	Sequence ²	Reference
<i>Vibrio cholera</i> O44	T. Shimada	<i>Vch</i> O44I (<i>Stu</i> I)	AGGCCT	4
<i>Vibrio cholera</i> O49	T. Shimada	<i>Vch</i> O49I (<i>Sca</i> I)	AGTACT	4
<i>Vibrio cholera</i> O66	T. Shimada	<i>Vch</i> O66I (<i>Asu</i> I)	GGNCC	4
<i>Vibrio cholera</i> O68	T. Shimada	<i>Vch</i> O68I (<i>Sph</i> I)	GCATGC	4
<i>Vibrio cholera</i> O70	T. Shimada	<i>Vch</i> O70I (<i>Nru</i> I)	TCGCGA	4
<i>Vibrio cholera</i> O85	T. Shimada	<i>Vch</i> O85I (<i>Asu</i> I)	GGNCC	4
<i>Vibrio cholera</i> O87	T. Shimada	<i>Vch</i> O87I (<i>Pst</i> I)	CTGCAG	4
<i>Vibrio cholera</i> O90	T. Shimada	<i>Vch</i> O90I (<i>Asu</i> I)	GGNCC	4
<i>Vibrio parahaemolyticus</i> K13	S. Matsushita	<i>Vpa</i> K13I (<i>Ava</i> II)	GGWCC	4
<i>Vibrio parahaemolyticus</i> K3	S. Matsushita	<i>Vpa</i> K3I (<i>Pma</i> CI)	CACGTG	4
<i>Vibrio parahaemolyticus</i> K4	K. Mise	<i>Vpa</i> K4I (<i>Pst</i> I)	CTGCAG	4
<i>Vibrio parahaemolyticus</i> K7	S. Matsushita	<i>Vpa</i> K7I (<i>Ava</i> II)	GGWCC	4
<i>Vibrio parahaemolyticus</i> O5	S. Matsushita	<i>Vpa</i> O5I (<i>Ksp</i> 632I)	CTCTTC	4
<i>Xanthomonas malvacearum</i> strain C	M.M. Wijden-bosch	<i>Xma</i> CI (<i>Sma</i> I)	C!CCGGG	5

¹When two enzymes recognize the same sequence, i.e., are isoschizomers, the prototype (i.e., the first example isolated) is indicated in parentheses.

²Recognition sequence representations use the standard abbreviations (Eur. J. Biochem. **150**: 1–5, 1985) to represent ambiguity.

$$R = G \text{ or } A$$

Y = C or T

$$M = A \text{ or } C$$

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

cognition sequences are written

Recognition sequences are written from 5' to 3', only one strand being given, and the point of cleavage is indicated by an arrow (→). Where the arrow appears, the precise cleavage site has not been determined. For example, A↓CATGT is an abbreviation for

5' A T C A T G T 3'

3' T G T A C $\uparrow$ A 5'

enzymes such as *Bce*

For example *Bce*83I CTTGAG(16/14) indicates cleavage as shown below

5'CTTGAGNNNNNNNNNNNNNNN†3'

3'GAACTCNNNNNNNNNNNNN†5'

-DI GCAATG(2/0) indicates cleavage as :

5'GCAATGNNI 3'

3'CGTTAC↑ 5'

all cases the recog

A* is N⁶-methyladenosine. C* is C⁵-methylcytosine. C[#] is N⁴-methylcytosine.

Table 2.

Type I enzymes

Prototype enzyme	Recognition sequence ²	Me site ³
<i>Cfr</i> AI	GCANNNNNNNNGTGG	
<i>Eco</i> AI	GAGNNNNNNNGTCA	2(6), -3(6)
<i>Eco</i> BI	TGANNNNNNNNTGCT	3(6), -4(6)
<i>Eco</i> DI	TTANNNNNNNNGTCY	
<i>Eco</i> DR2I	TCANNNNNNNNGTCG	
<i>Eco</i> DR3I	TCANNNNNNNNATCG	
<i>Eco</i> DXXI	TCANNNNNNNNRITC	
<i>Eco</i> EI	GAGNNNNNNNNATGC	
<i>Eco</i> KI	AACNNNNNNNGTGC	2(6), -3(6)
<i>Eco</i> R124I	GAANNNNNNNRITCG	3(6), 11(6)
<i>Eco</i> R124/3I	GAANNNNNNNNRITCG	-3(6)
<i>Eco</i> RD2I	GAANNNNNNNRITTC	
<i>Eco</i> RD3I	GAANNNNNNNNRITTC	
<i>Eco</i> prI	CCANNNNNNNNRITGC	
<i>Sry</i> SBI	GAGNNNNNNNRITAYG	2(6), -4(6)
<i>Sry</i> SJI	GAGNNNNNNNGTRC	
<i>Sry</i> SPI	AACNNNNNNNGTRC	2(6), -3(6)
<i>Sry</i> SQI	AACNNNNNNNRITAYG	

Table 2. (cont.)

Type III enzymes				
Prototype enzyme		Recognition sequence ²	Me site ³	
<i>EcoPI</i>		AGACC	3(6)	
<i>EcoP15I</i>		CAGCAG (25/27)	5(6)	
<i>HinfIII</i>		CGAAT		
<i>SpyLTI</i>		CAGAG	4(6)	
Type II enzymes				
Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>AarII</i>		GACGT↓C		AEFLMNOPRSX
<i>AccI</i>		GT↓MKAC	5(6)	ABDEGKLMNOPQRSX
<i>AceIII</i>		CAGCTC(7/11)		
<i>AcII</i>		CCGC(−3/−1)		N
<i>AcII</i>		AA↓CGTT		
<i>Acyl</i>	<i>Psp1406I</i>	AA↓CGTT		FMN
		GR↓CGYC		MR
	<i>BblII</i>	GR↓CGYC		K
	<i>BsaHI</i>	GR↓CGYC		BNS
	<i>HinII</i>	GR↓CGYC		DEFO
	<i>Hsp92I</i>	GR↓CGYC		R
<i>AflIII</i>		C↓TTAAG		ABKNOSX
	<i>BfrI</i>	C↓TTAAG		M
	<i>BspTI</i>	C↓TTAAG		F
	<i>Bsr98I</i>	C↓TTAAG		R
<i>AflIII</i>		A↓CRYGT		ABMN
<i>AgeI</i>		A↓CCGGT		N
	<i>PinAI</i>	A↓CCGGT		BM
<i>AhaIII</i>		TTT↓AAA		
	<i>DraI</i>	TTT↓AAA		
<i>AluI</i>		AG↓CT	3(5)	ABDEFGKLMNOPQRSWX
<i>AlwNI</i>		CAGNNN↓CTG		ABDEFGHKLMNOPQRSWX
<i>ApaI</i>		GGGCC↓C	4(5)	ABNS
	<i>Bsp120I</i>	G↓GGCCC		ABEGKLMNOPQRSX
<i>ApaBI</i>		GCANNNNN↓TGC		DFN
<i>ApalI</i>		G↓TGCAC		
	<i>Alw44I</i>	G↓TGCAC		ADEKNSX
<i>ApoI</i>		R↓AATTY		BFMOR
	<i>AcsI</i>	R↓AATTY		N
<i>AscI</i>		GG↓CGGCC		M
<i>AsuI</i>		G↓GNCC		N
	<i>BsiZI</i>	G↓GNCC		W
	<i>Cfr13I</i>	G↓GNCC	4(5)	DFKO
	<i>Sau96I</i>	G↓GNCC	4(5)	BLMNORSX
<i>AsuII</i>		TT↓CGAA		
	<i>BsiCI</i>	TT↓CGAA		W
	<i>Bsp119I</i>	TT↓CGAA		DF
	<i>BstBI</i>	TT↓CGAA		NS
	<i>Csp45I</i>	TT↓CGAA		OR
	<i>LspI</i>	TT↓CGAA		L
	<i>NspV</i>	TT↓CGAA		ABKO
	<i>SfuI</i>	TT↓CGAA		M
<i>AvaI</i>		C↓YCGRG		ABEGKLMNOPQRSX
	<i>BcoI</i>	C↓YCGRG		AW
	<i>Eco88I</i>	C↓YCGRG		DF
	<i>Nli387/7I</i>	CYCGR↓G		
<i>AvaII</i>		G↓GWCC		ABEGKMNPQRSX
	<i>Eco47I</i>	G↓GWCC		DFO
	<i>SinI</i>	G↓GWCC	4(5)	LRS
<i>AvaIII</i>		ATGCAT		
	<i>BfrBI</i>	ATG↓CAT		
	<i>EcoT22I</i>	ATGCA↓T		AKO
	<i>Mph1103I</i>	ATGCA↓T		F
	<i>NsiI</i>	ATGCA↓T		BDELMNRSX
	<i>Ppu10I</i>	A↓TGCAT		DFN
<i>AvrII</i>		C↓CTAGG		N
	<i>BlnI</i>	C↓CTAGG		AKM
<i>BaeI</i>		ACNNNNGTAYC		

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>BalI</i>	<i>MluNI</i> <i>MscI</i>	TGG↓CCA TGG↓CCA TGG↓CCA	4(5)	AKRX M BDNOS
<i>BamHI</i>	<i>BsrI</i>	G↓GATCC G↓GATCC	5(4)	ABDEFGHKLMNOPQRSWX P
<i>BbvI</i>		GCAGC(8/12)	2(5), -2(5)	NX
<i>BbvII</i>	<i>Bsf7II</i> <i>BbsI</i> <i>BpiI</i> <i>BpuAI</i>	GCAGC(8/12) GAAGAC(2/6) GAAGAC(2/6) GAAGAC(2/6) GAAGAC(2/6)		R N F M
<i>BccI</i> <i>Bce83I</i> <i>BceII</i> <i>BcgI</i> ⁵		CCATC CTTGAG(16/14) ACGGC(12/13) (10/12)GCAN- NNNNNTCG(12/10)	3(6), 3(6)	N
<i>BclI</i>	<i>FbaI</i>	T↓GATCA T↓GATCA		ABDEFGHKLMNOPRSWX K
<i>BerI</i>	<i>BsaWI</i>	W↓CCGGW W↓CCGGW		N ABDEFGHKLMNOPQRSWX ABDEFGHKLMNOPQRSWX
<i>BglI</i> <i>BglII</i> <i>BinI</i>	<i>AlwI</i>	GCCNNNN↓NGGC A↓GATCT GGATC(4/5) GGATC(4/5)		NS
<i>BmgI</i> <i>Bpu10I</i> <i>BsaAI</i> <i>BsaBI</i>		GKGGCC CCTNAGC(-5/-2) YAC↓GTR		N N F W R M
<i>BsaXI</i> <i>BsbI</i> <i>BscGI</i> <i>BsePI</i>	<i>Bsh136SI</i> <i>BsiBI</i> <i>BsrBRI</i> <i>MamI</i>	GATNN↓NNATC GATNN↓NNATC GATNN↓NNATC GATNN↓NNATC GATNN↓NNATC ACNNNNNCTCC CAACAC		N N F W R M
<i>BseRI</i> <i>BsgI</i> <i>BsiI</i> <i>BsiYI</i>	<i>BssHII</i> <i>PaulI</i>	CCCGT GCGCGC G↓CGCGC GCGCGC GAGGAG(10/8) GTGCAG(16/14) CTCGTG(-5/-1) CCNNNNN↓NNGG CCNNNNN↓NNGG		ABDEKLMNOPQRX F N N
<i>BsmI</i>	<i>BsII</i>	GAATGC(1/-1) GAATGC(1/-1) GAATGC(1/-1)		MW N ABDELMNOSX R F N
<i>BsmAI</i>	<i>BsaMI</i> <i>MvaI269I</i> <i>Alw26I</i>	GTCTC(1/5) GTCTC(1/5)	3(5), -4(6)	DFR
<i>Bsp24I</i> ⁵ <i>Bsp1407I</i>		(8/13)GACNNNNNTGG(12/7)		F N M
<i>BspGI</i> <i>BspHI</i> <i>RcaI</i> <i>BspLU11I</i> <i>BspMI</i> <i>BspMII</i>	<i>BsrGI</i> <i>SspBI</i>	T↓GTACA T↓GTACA T↓GTACA CTGGAC T↓CATGA T↓CATGA A↓CATGT ACCTGC(4/8) T↓CCGGA T↓CCGGA T↓CCGGA T↓CCGGA T↓CCGGA T↓CCGGA T↓CCGGA		AN BM N X EKQR M AW NS BDFS MO
<i>BsrI</i>	<i>BseNI</i>	ACTGG(1/-1) ACTGG(1/-1)		N DF
<i>BsrBI</i>		GAGCGG(-3/-3) GAGCGG(-3/-3)		N P
<i>BsrDI</i>	<i>BstD102I</i>	GCAATG(2/0)		N

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Bst</i> II		G↓GTNACC		BGHLMNOPRSX
	<i>Bst</i> PI	G↓GTNACC		K
	<i>Eco</i> 91I	G↓GTNACC		DF
	<i>Eco</i> O65I	G↓GTNACC		AK
<i>Bst</i> XI		CCANNNNN↓NTGG		ABDEFGHKLMNOQRSX
<i>Cac</i> 8I		GCN↓NGC		N
<i>Cau</i> II		CC↓SGG		
	<i>Bcn</i> I	CC↓SGG	2(4)	ADFKW
	<i>Eco</i> HI	↓CCSGG		
	<i>Nci</i> I	CC↓SGG		BELMNORSX
<i>Cfr</i> I		Y↓GGCCR		4(5)
	<i>Eae</i> I	Y↓GGCCR	4(5)	ADKLMNSX
<i>Cfr</i> 10I		R↓CCGGY	2(5)	ADFKMOX
	<i>Bsr</i> FI	R↓CCGGY		N
<i>Cje</i> I ⁵		(13/7)CCANNNNNNGT(9/15)		
<i>Cje</i> PI ⁵		(13/7)CCANNNNNNNTC(8/14)		
<i>Cla</i> I		AT↓CGAT	5(6)	ABKMNPRSX
	<i>Ban</i> III	AT↓CGAT		O
	<i>Bsc</i> I	AT↓CGAT		L
	<i>Bsi</i> XI	AT↓CGAT		W
	<i>Bsp</i> 106I	AT↓CGAT	5(6)	E
	<i>Bsp</i> DI	AT↓CGAT		N
	<i>Bsp</i> XI	AT↓CGAT		G
	<i>Bsu</i> 15I	AT↓CGAT	5(6)	DF
<i>Cvi</i> II		RG↓CY	3(5)	Q
<i>Cvi</i> RI		TG↓CA		4(6)
<i>Dde</i> I		C↓TNAG	1(5)	ABEGLMNOPRX
<i>Dpn</i> I		GA↓TC		ABLMNRSX
<i>Dra</i> II		RG↓GNCCY		M
	<i>Eco</i> O109I	RG↓GNCCY		ABDEFKLNSX
	<i>Pss</i> I	RGGNC↓CY		
<i>Dra</i> III		CACNNN↓GTG		AEMNSX
<i>Drd</i> I		GACNNNN↓NNGTC		N
<i>Drd</i> II		GAACCA		
<i>Dsa</i> I		C↓CRYGG		M
<i>Eam</i> 1105I		GACNNN↓NNGTC		DFKN
	<i>Ahd</i> I	GACNNNNNGTC		N
	<i>Asp</i> EI	GACNNN↓Tα		M
	<i>Ecl</i> HKI	GACNNN↓NNGTC		R
<i>Eci</i> I		TCCGCC		
<i>Eco</i> 31I		GGTCTC(1/5)	4(5), -4(6)	D
	<i>Bsa</i> I	GGTCTC(1/5)		N
<i>Eco</i> 47III		AGC↓GCT		BDEFLMNOR
	<i>Aor</i> 51HI	AGC↓GCT		AK
<i>Eco</i> 57I		CTGAAG(16/14)	5(6), -5(6)	DFN
<i>Eco</i> NI		CCTNN↓NNNAGG		ANS
<i>Eco</i> RI		G↓AATTC	3(6)	ABDEFGHKLMNOPQRSWX
<i>Eco</i> RII ⁶		↓CCWGG	2(5)	BEMOS
+	<i>Bsi</i> LI	CC↓WGG		W
+	<i>Bst</i> NI	CC↓WGG	2(4)	ENSX
+	<i>Bst</i> OI	CC↓WGG		R
+	<i>Mva</i> I	CC↓WGG	2(4)	ADFKMO
<i>Eco</i> RV		GAT↓ATC	2(6)	ABDEGHKLMNOPQRSWX
	<i>Eco</i> 32I	GAT↓ATC		F
<i>Esp</i> I		GC↓TNAGC		
	<i>Blp</i> I	GCTNAGC		N
	<i>Bpu</i> 1102I	GC↓TNAGC		BDEFK
	<i>Cel</i> II	GC↓TNAGC		ALM
<i>Esp</i> 3I		CGTCTC(1/5)	4(5), -4(6)	DF
	<i>Bsm</i> BI	CGTCTC(1/5)		N
		CCCGC(4/6)		
<i>Fau</i> I		GGGAC		
<i>Fin</i> I		GGGAC(10/14)		N
<i>Fnu</i> DII		CG↓CG		
	<i>Acc</i> II	CG↓CG		AKQX
	<i>Bsh</i> 1236I	CG↓CG		DEF
	<i>Bst</i> UI	CG↓CG		NS

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Fnu4HI</i>	<i>MvnI</i>	CG↓CG		M
	<i>SeI</i>	↓CGCG		
	<i>ThaI</i>	CG↓CG		B
		GC↓NGC		
<i>FokI</i>	<i>BsoFI</i>	GC↓NGC		N
	<i>ItaI</i>	GC↓NGC		M
		GGATG(9/13)	3(6), 2(6)	AGKLMNRX
	<i>StsI</i>	GGATG(10/14)	3(6), -2(6)	
<i>FseI</i>		GGCCGG↓CC		AK
<i>GdiII</i>		YGGCCG(-5/-1)		
<i>GsuI</i>		CTGGAG(16/14)		DFS
	<i>BpmI</i>	CTGGAG(16/14)		N
<i>HaeI</i>		WGG↓CCW		
<i>HaeII</i>		RGCGC↓Y		ABDEGKLMNOPRSX
	<i>Bsp143II</i>	RGCGC↓Y		F
	<i>LpnI</i>	RG↓GCGY		
<i>HaeIII</i>		GG↓CC	3(5)	ABDGHKLMNOPQRSX
	<i>BshI</i>	GG↓CC		W
	<i>BsuRI</i>	GG↓CC	3(5)	FW
	<i>PalI</i>	GG↓CC		EP
<i>HgaI</i>		GACGC(5/10)	3(5), -2(5)	ANSX
<i>HgiAI</i>		GWGCW↓C		X
	<i>Alw21I</i>	GWGCW↓C		BDF
	<i>AspHI</i>	GWGCW↓C		M
	<i>BsiHKAII</i>	GWGCW↓C		N
<i>HgiCI</i>		G↓GYRCC	5(5)	
	<i>BanI</i>	G↓GYRCC	?(5)	AMNOPRSX
	<i>BshNI</i>	G↓GYRCC		F
	<i>Eco64I</i>	G↓GYRCC		DF
<i>HgiEII</i>		ACCNNNNNNGGT		
<i>HgiJII</i>		GRGCG↓C		
	<i>BanII</i>	GRGCG↓C		ABKLMNOPQRSX
	<i>Eco24I</i>	GRGCG↓C		DF
<i>HhaI</i>		GCG↓C	2(5)	ABGKNOPRSX
	<i>CfoI</i>	GCG↓C		BLMRS
	<i>Hin6I</i>	G↓CGC		DF
	<i>HinPII</i>	G↓CGC		NSX
<i>Hin4I</i>		GABNNNNNVTC		
<i>HindII</i>		GTY↓RAC	5(6)	M
	<i>HincII</i>	GTY↓RAC	5(6)	ABDEFGHKLMNOPQRSWX
<i>HindIII</i>		A↓AGCTT	1(6)	ABDEFGHKLMNOPQRSWX
	<i>Eco65I</i>	AAGCTT		A
<i>Hinfi</i>		G↓ANTC		ABDEFGHKLMNOPQRSWX
<i>HpaI</i>		GTT↓AAC	5(6)	ABDEFGKLMNOPQRSWX
<i>HpaII</i>		C↓CGG	2(5)	BDEFGKLMNOPQRSWX
	<i>HapII</i>	C↓CGG	2(5)	AK
	<i>MspI</i>	C↓CGG	1(5)	ABDEFGHKLMNOPQRSWX
<i>HphI</i>		GGTGA(8/7)	-2(5)	ANSX
<i>KpnI</i>		GGTAC↓C	4(6)	ABDEFGHKLMNOPQRSWX
	<i>Acc65I</i>	G↓GTACC		DFNR
	<i>Asp718I</i>	G↓GTACC		MP
<i>Ksp632I</i>		CTCTTC(1/4)		M
	<i>Eam1104I</i>	CTCTTC(1/4)		DF
	<i>EarI</i>	CTCTTC(1/4)		N
<i>MaeI</i>		C↓TAG		M
	<i>BfaI</i>	C↓TAG		N
<i>MaeII</i>		A↓CGT		MP
<i>MaeIII</i>		↓GTNAC		MP
<i>MboI</i> ⁷		↓GATC	2(6)	ABEFGKLNQRSWX
+	<i>Bsp143I</i>	↓GATC		F
+	<i>BspKT6I</i>	G↓ATC		
	<i>DpnII</i>	↓GATC	2(6)	N
	<i>NdeII</i>	↓GATC		BDGM
+	<i>Sau3AI</i>	↓GATC	4(5)	ABDEGHKLMNOPQRSX
<i>MboII</i>		GAAGA(8/7)	5(6)	BDFKNOQRSWX
<i>McrI</i>		CGRY↓CG		M
	<i>BsaOI</i>	CGRY↓CG		R

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>MfeI</i>	<i>Bsh1285I</i>	CGRY↓CG	3(6)	DF
	<i>BsiEI</i>	CGRY↓CG		NW
	<i>MunI</i>	C↓AATTG		BDEFKMN
<i>MluI</i>	A↓CGCGT	ABDEFGKLMNOPQRSWX		
<i>MmeI</i>	TCCRAC(20/18)			
<i>MnII</i>	CCTC(7/6)	AEFNQX		
<i>MseI</i>	T↓TAA	BNS		
<i>MsII</i>	<i>TruII</i>	T↓TAA		F
	<i>Tru9I</i>	T↓TAA		LMR
	<i>AviII</i>	CAYNN↓NNRTG		N
<i>MstI</i>	TGC↓GCA	X		
<i>MwoI</i>	<i>FspI</i>	TGC↓GCA		M
	<i>BspWI</i>	TGC↓GCA		ABKNOS
		GCNNNNN↓NNGC		N
GCNNNNN↓NNGC		M		
<i>NaeI</i>	GCC↓GGC	ADEKLMNORX		
<i>NarI</i>	<i>NgoAIV</i>	G↓CCGGC		2(5)
	<i>NgoMI</i>	G↓CCGGC	NR	
	<i>BbeI</i>	GG↓CGCC	BEMNOPRSX	
<i>EheI</i>	GGCGC↓C	AK		
<i>NcoI</i>	<i>KasI</i>	GGC↓GCC	DFO	
	<i>AceII</i>	G↓GCGCC	N	
		C↓CATGG	ABDEFGHKLMNOPQRSWX	
<i>NdeI</i>		CA↓TATG	ABDEFGKLMNPRSWX	
<i>NheI</i>	G↓CTAGC	ABDEFGKLMNOPRSX		
<i>NlaIII</i>	<i>CviAII</i>	GCTAG↓C	2(6)	
	<i>Hsp92II</i>	CATG↓		2(6)
	<i>NlaIV</i>	GGN↓NCC		NS
<i>NotI</i>	GC↓GGCCGC		ABDEFGKLMNOPQRSWX	
<i>NruI</i>	TCG↓CGA		ABDEGKLMNOPQRSX	
<i>NspI</i>	<i>Bsp68I</i>	TCG↓CGA		F
<i>NspBII</i>	<i>MspAII</i>	RCATG↓Y		ABKM
<i>PacI</i>		CMG↓CKG		A
<i>Pfl1108I</i>		CMG↓CKG		NR
<i>PflMI</i>	<i>AccB7I</i>	TTAAT↓TAA		ANO
<i>PleI</i>		TCGTAG		ANS
		CCANNNN↓NTGG		R
		CCANNNN↓NTGG		F
	CCANNNN↓NTGG		DFM	
<i>PmaCI</i>	<i>MlyI</i>	GAGTC(4/5)		N
	<i>BbrPI</i>	GACTC(5/5)		AK
		CAC↓GTG		M
<i>Eco72I</i>		CAC↓GTG		DEFR
<i>PmeI</i>	<i>PmlI</i>	CAC↓GTG		N
<i>PpuMI</i>	<i>Psp5II</i>	GTTT↓AAAC		NP
<i>PshAI</i>		RG↓GWCCY		ANO
		RG↓GWCCY		BDF
		GACNN↓NNGTC		K
	<i>PstI</i>	CTGCA↓G	5(6)	ABDEFGHKLMNOPQRSWX
<i>PvuI</i>	<i>BspCI</i>	CGAT↓CG		ABDEFGKLMNOPQRSWX
<i>PvuII</i>	<i>XorII</i>	CGAT↓CG		E
	<i>RleAI</i>	CAG↓CTG	4(4)	BS
		CCCACA(12/9)		ABDEFGHKLMNOPQRSWX
<i>RsaI</i>		GT↓AC		ABDEGLMNOPQRSWX
<i>RsrII</i>	<i>AfaI</i>	GT↓AC		K
	<i>Csp6I</i>	G↓TAC		DFN
	<i>CpoI</i>	CG↓GWCCG		BMNSX
<i>SacI</i>	<i>CspI</i>	CG↓GWCCG		ADFK
	<i>Ecl136II</i>	GAGCT↓C		EOR
		<i>EcoICRI</i>	GAG↓CTC	
<i>SstI</i>		GAG↓CTC		DFN
<i>SacII</i>	<i>Cfr42I</i>	GAGCT↓C		R
		CCGC↓GG		BS
		CCGC↓GG		AEGHKLNOPQRSX
				DF

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>SalI</i> <i>SapI</i> <i>SauI</i>	<i>KspI</i>	CCGC↓GG		M
	<i>MluI</i> 113I	CC↓GCGG		
	<i>SstII</i>	CCGC↓GG		BS
		G↓TCGAC		ABDEFGHKLMNOPQRSWX
		GCTCTTC(1/4)		N
		CC↓TNAGG		M
	<i>AocI</i>	CC↓TNAGG		M
	<i>Bsu36I</i>	CC↓TNAGG		ENRS
	<i>CviI</i>	CC↓TNAGG		BS
	<i>Eco81I</i>	CC↓TNAGG		ADFKO
<i>ScaI</i> <i>ScrFI</i> <i>SduI</i> <i>SecI</i>	<i>MstII</i>	CC↓TNAGG		X
		AGT↓ACT		ABDEFGHKLMNOPQRSWX
	<i>Eco255I</i>	AGT↓ACT		F
		CC↓NGG	?(5)	DMNOSX
	<i>DsaV</i>	↓CCNGG		M
		GDGCH↓C		F
	<i>BmyI</i>	GDGCH↓C		M
	<i>Bsp1286I</i>	GDGCH↓C		ADKNRX
		C↓CNNGG		
	<i>BsaII</i>	C↓CNNGG		ABN
<i>SexAI</i> <i>SfaNI</i> <i>SfeI</i> <i>SfiI</i> <i>SgfI</i> <i>SgrAI</i> <i>SmaI</i>	<i>BseDI</i>	C↓CNNGG		F
		A↓CCWGGT		M
		GCATC(5/9)		NSX
	<i>BscAI</i>	GCATC(4/6)		
		C↓TRYAG		
	<i>SfcI</i>	C↓TRYAG		N
		GGCCNNNN↓NGGCC		ABDEGLMNOPQRSX
		GCGAT↓CGC		OR
		CR↓CCGGYG		M
		CCC↓GGG	2(4)	ABDEFGHKLMNOPQRSWX
<i>SnaI</i> <i>SnaBI</i> <i>SpeI</i> <i>SphI</i> <i>SpII</i>	<i>Cfr9I</i>	C↓CCGGG	2(4)	DFO
	<i>PspAI</i>	C↓CCGGG		E
	<i>XmaI</i>	C↓CCGGG		ANPRSWX
		GTATAC		
	<i>BspM90I</i>	GTA↓TAC		W
	<i>Bst1107I</i>	GTA↓TAC		DFKMN
		TAC↓GTA		AEKLMNPRSX
	<i>Eco105I</i>	TAC↓GTA		DFO
		A↓CTAGT		ABDEHKLMNOPQRSWX
		GCATG↓C		ABDEGHKLMNOPQRSX
<i>SrfI</i> <i>Sse8387I</i> <i>SspI</i> <i>StuI</i> <i>SryI</i> <i>SwaI</i> <i>TaqI</i> <i>TaqII</i> ⁸ <i>TaqII</i> ⁸ <i>TfiI</i> <i>TseI</i> <i>Tsp45I</i> <i>TspEI</i> <i>Tth111I</i> <i>Tth111II</i> <i>Tth111III</i> <i>UbaII</i>	<i>BbuI</i>	GCATG↓C		R
	<i>PaeI</i>	GCATG↓C		FW
		C↓GTACG		AK
	<i>BstWI</i>	C↓GTACG		MNW
	<i>Pft23II</i>	C↓GTACG		DF
	<i>SunI</i>	C↓GTACG		B
		GCCC↓GGGC		EO
		CCTGCA↓GG		AK
		AAT↓ATT		ABDEFKLMNOPRWX
		AGG↓CCT		ABEKLMPQRSX
<i>TaqII</i> ⁸ <i>TaqII</i> ⁸ <i>TfiI</i> <i>TseI</i> <i>Tsp45I</i> <i>TspEI</i> <i>Tth111I</i> <i>Tth111II</i> <i>Tth111III</i> <i>UbaII</i>	<i>AatI</i>	AGG↓CCT		O
	<i>Eco147I</i>	AGG↓CCT		DF
		C↓CWGGG		BEMNRSX
	<i>Eco130I</i>	C↓CWGGG		DF
	<i>EcoT14I</i>	C↓CWGGG		AK
		ATTT↓AAAT		M
		T↓CGA	4(6)	ABDEFGKLMNOPQRSWX
	<i>TthHB8I</i>	T↓CGA	4(6)	AK
		GACCGA(11/9)		
		CACCCA(11/9)		
<i>Tsp45I</i> <i>TspEI</i> <i>Tth111I</i> <i>Tth111II</i> <i>Tth111III</i> <i>UbaII</i>		G↓AWTC		N
		GCWGC		
	<i>AceI</i>	G↓CWGC		
		↓GTSAC		N
		↓AATT		L
	<i>Tsp509I</i>	↓AATT		N
		GACN↓NNGTC		ADKNPQRX
	<i>AspI</i>	GACN↓NNGTC		MP
		CAARCA(11/9)		
		GCSGC		

Table 2. (cont.)

Prototype ¹ enzyme	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>VspI</i>		AT↓TAAT		BDEFKR
	<i>AseI</i>	AT↓TAAT		ANOPS
	<i>AsnI</i>	AT↓TAAT		M
<i>XbaI</i>		T↓CTAGA	6(6)	ABDEFGHKL MNOPQRSWX
<i>XcmI</i>		CCANNNNN↓NNNTGG		AN
<i>XhoI</i>		C↓TCGAG		ABDEFGHKL MNOPQRSWX
	<i>CcrI</i>	C↓TCGAG		X
	<i>PaeR7I</i>	C↓TCGAG	5(6)	NSX
	<i>SciI</i>	CTC↓GAG		
<i>XhoII</i>		R↓GATCY		EMRX
	<i>BstYI</i>	R↓GATCY		BN
	<i>MflI</i>	R↓GATCY		AK
<i>XmaIII</i>		C↓GGCCG	4(5)	BE
	<i>BstZI</i>	C↓GGCCG		R
	<i>EagI</i>	C↓GGCCG		NPS
	<i>EclXI</i>	C↓GGCCG		M
	<i>Eco52I</i>	C↓GGCCG		ADFKOR
<i>XmnI</i>		GAANN↓NNTTC		DENX
	<i>Asp700I</i>	GAANN↓NNTTC		M

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

²Recognition sequence nomenclature is as in Table 1

³The 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.

⁴Commercial sources of restriction enzymes are abbreviated as follows:

- A Amersham Life Sciences-USB (7/94)
- B Life Technologies Inc, Gibco-BRL (7/94)
- D Angewandte Gentechnologie Systeme (7/94)
- E Stratagene (7/94)
- F Fermentas MBI (7/94)
- G Appligene (7/94)
- H American Allied Biochemical, Inc. (7/94)
- K Takara (7/94)
- L NBL Gene Sciences Limited (7/94)
- M Boehringer-Mannheim (7/94)
- N New England BioLabs (7/94)
- O Toyobo (7/94)
- P Pharmacia P-L Biochemicals (7/94)
- Q Molecular Biology Resources (7/94)
- R Promega Corporation (7/94)
- S Sigma (7/94)
- W Immunogen International Limited (IGI) (7/94)
- X New York Biolabs (7/94)

The date in parentheses indicates the most recent update.

⁵*BcgI*, *Bsp24I*, *CjeI* and *CjePI* all cleave on both sides of the recognition sequence. This is indicated by numbers in parentheses both before and after the recognition sequence. Thus *Bsp24I* (8/13)GACNNNNNNTGG(12/7), indicates that cleavage occurs 8 bases 5' to the recognition sequence and 12 bases 3' to it on the strand written and 7 bases 5' to the recognition sequence and 13 bases 3' to it on the complementary strand. Thus the recognition site is excised in a fragment, 32 base pairs long, with 5-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.