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Restriction enzymes and their isoschizomers

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INTRODUCTION

The restriction enzyme database, REBASE, contains information about restriction enzymes and their associated methylases. Since the last description of the contents of REBASE (1), 204 new entries have been added including 5 new Type II enzymes and 4 new Type I enzymes. A complete list of these new enzymes can be found in Table I. A total of 2103 restriction enzymes are now known and include 17 different Type I specificities, 179 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.

It should be noted that several commercial suppliers have discontinued the sale of restriction enzymes since last year and are omitted as commercial sources. These include Palliard and BioExcellence, who are no longer in business, and Janssen, who are still selling their old stock, but are not replenishing it. One new supplier, International Laboratory Services, is now included.

The complete database is available in many formats including the styles shown in Tables I and II, or as a flat file arranged in fields that can easily be reformatted. Bibliographic information from 2380 published articles describing restriction enzymes and methylases is also available, including full abstracts. It is possible to get regular monthly updates or specialized versions of the database by electronic mail. For instance, files containing the database in formats that can be used directly by the UWGCG, IGSuite and other computer software packages are available. Anyone who wishes to be included on the electronic mailing list for these regular monthly updates should send a request to roberts@cshl.org by e-mail. These data files are also available by anonymous FTP from rna.cshl.org (numerical address: 143.48.1.11)

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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REFERENCES

1. Roberts, R.J. and Macelis D. (1991) Nucl. Acids Res. 19:2077–2109.
2. Smith, H.O. and Nathans, D. (1973) J. Mol. Biol., 81:419–423.
3. Inagaki, K., Ito, T., Sagawa, H., Kotani, H., Kishimoto, N., Sugio, T., Tano, T., Tanaka, H. (1991) Nucl. Acids Res. 19: 6335
4. Inagaki, K., Ito, T., Kotani, H., Kishimoto, N., Tano, T. unpublished observations.
5. Sagawa, H., Takagi, M., Nomura, Y., Inagaki, K., Tano, T., Kishimato, N., Kotani, H., Nakajima, K. (1992) Nucl. Acids Res. 20: 365
6. Inagaki, K., Hamafuku, H., Kotani, H., Kishimoto, N., Tano, T. unpublished observations.
7. Earle-Hughes, J., Roberts, R.J. unpublished observations.
8. Polisson, C. unpublished observations.
9. Groot, E., Schouten, J.P. unpublished observations.
10. Polisson, C., Morgan, R. unpublished observations.
11. Calmero, J. unpublished observations.
12. Gubler, M., Braguglia, D., Meyer, J., Piekarowicz, A., Bickle, T.A. (1992) EMBO J. 11: 233–240
13. Connaughton, J.E., Vanek, P.G., Chirikjian, J.G. (1988) J. Cell Biol. 107: 535a
14. Schoenfeld, T. unpublished observations.
15. Sokolov, N.N., Eldarov, M.A., Samko, O.T., Karpichev, I.V., Anikeitcheva, N.V., Kalugin, A.A., Scryabin, K.G. unpublished observations.
16. Janulaitis, A.A. unpublished observations.
17. Sokolov, N.N., Eldarov, M.A., Samko, O.T., Karpichev, I.V., Kalugin, A.A., Anikeitcheva, N.V., Scryabin, K.G. unpublished observations.
18. Degtyarev, S.K., Morgan, R. unpublished observations.
19. Janulaitis, A.A., Krikstulyte, V., Trinkunaite, L., Maneliene, Z., Kiuduliene, L., Petrusyte, M., Butkus, V. unpublished observations.
20. Repin, V.E., Tereschenko, T.A. unpublished observations.
21. Clark, D. unpublished observations.
22. Dedkov, V.S., Zernov, Y.P., Rechkunova, N.I., Degtyarev, S. Kh. (1990) Mol. Genet. Mikrobiol. Virusol. 0: 17–18
23. Serov, G.D., Puchkova, L.I., Kolesnikov, V.A., Repin, V.E. unpublished observations.
24. Kong, H. unpublished observations.
25. Schoenfeld, T., Fiandt, M., Schink, M. unpublished observations.
26. Kovalevskaya, N.P., Ivanov, L.Yu., Zheleznaya, L.A., Matvienko, N.I. (1991) Nucl. Acids Res. 19: 4296
27. Chen, Z. unpublished observations.
28. Rina, M., Tsigos, I., Karagouni, A., Pagomenou, M., Bouriotis, V. (1991) Nucl. Acids Res. 19: 4776
29. Repin, V.E., Burtseva, L.I., Burlak, V.A., Trusova, S.I. unpublished observations.
30. Arif, A., Ehsan, A., Sohail, A. unpublished observations.
31. Choudry, S., Malik, K. unpublished observations.
32. Arif, A., Naeem, S., Malik, K. unpublished observations.
33. Mushtaq, R. unpublished observations.
34. Azeddoug, H., Reysset, G. (1991) FEMS Microbiol. Letts. 78: 153–156
35. Murakami, M., Ozawa, O., Kanematsu, T., Yamada, Y. (1991) Nucl. Acids Res. 19: 3458
36. Mizuno, H., Suzuki, T., Yamada, Y., Akagawa, M., Yamasato, K. (1990) Agric. Biol. Chem. 54: 2863–2867
37. Suzuki, T., Sato, Y., Yamada, Y., Akagawa-Matsushita, M., Yamasato, K. (1991) Agric. Biol. Chem. 55: 2647–2649
38. Arif, A., Malik, K., Sohail, A. unpublished observations.
39. Sokolov, N.N., Eldarov, M.A., Anikeitcheva, N.V., Karpichev, I.V., Samko, O.T., Kalugin, A.A., Fitsner, A.B., Choroshoutina, E.B., Scryabin, K.G. unpublished observations.
40. Repin, V.E., Andreeva, I.S., Puchkova, L.I. unpublished observations.

41. Qiang, B-Q., Wu, S. Kong, H. unpublished observations.
42. Janulaitis, A.A., Stakenas, P., Zareckaja, N., Petrusyte, M., Meneliene, Z., Vonseviciene, E., Klimasauskas, S., Butkus, V. unpublished observations.
43. Nomura, Y., Kotani, H., Kita, K., Sadaoka, A., Hiraoka, N., Nakamura, T., Abe, N., Izaki, K. (1990) Agric. Biol. Chem. 54: 3011–3012
44. Melnik, A.I., Rebentish, B.A., Bolotin, A.V., Mendzhul, M.I. (1991) Mikrobiol. Zh. 53: 24–28
45. Moser, D., Kallas, T. (1991) ASM Abstr. 91: 155
46. Piechula, S., Kim, S.C., Podhajska, A.J. (1992) Nucl. Acids Res. 20: 619
47. Banas, J.A., Ferretti, J.J., Progulske-Fox, A. (1991) Nucl. Acids Res. 19: 4189–4192
48. Kravetz, A.N., Tarutina, Z.E., Solonin, A.S. (1991) Nucl. Acids Res. 19: 4781
49. Choudry, S., Riazuddin, S. unpublished observations.
50. Groot, E. unpublished observations.
51. Zhou, B., Morgan, R. unpublished observations.
52. Lebedev, L.R., Andreeva, I.S., Gordienko, N.Y., Maistrenko, G.G., Repin, V.E., Pustoshilova, N.M. unpublished observations.
53. Andreeva, I.S., Afinogenova, G.N., Lebedev, L.R., Pustoshilova, N.M., Gordienko, N.Ya., Maistrenko, G.G. (1991) Mol. Genet. Mikrobiol. Virusol. 0: 30–31
54. Lebedev, L.R., Afinogenova, G.N., Andreeva, I.S., Pustoshilova, N.M., Pozdnyakov, S.G., Chizhikov, V.E. (1991) Bioorg. Khim. 17: 277–279
55. Arif, A., Mushtaq, R. unpublished observations.
56. Benbadis, L., Garel, J.R., Hartley, D.L. (1991) Appl. Environ. Microbiol. 57: 3677–3678
57. Solaiman, D.K.Y., Somkuti, G.A. (1991) FEMS Microbiol. Lett. 80: 75–80
58. Puchkova, L.I., Krivopalova, G.N., Serov, G.D., Repin, V.E. unpublished observations.
59. Muchova, J., Lacova, B., Godany, A., Sevcikova, B. (1991) J. Basic Microbiol. 31: 141–147
60. Rina, M., Karagouni, A., Pagomenou, M. Bouriotis, V. (1991) Nucl. Acids Res. 19: 6342
61. Matsushima, P., Baltz, R.H. (1989) ASM Abstracts 89: 361
62. Arif, A., Naeem, S., Sohail, A. unpublished observations.
63. Babcock, M.J., Schottel, J.L. (1991) Nucl. Acids Res. 19: 3457
64. Simcox, T.G., Marsh, S.J., Gross, E.A., Lernhardt, W., Davis, S., Simcox, M.E.C. (1991) Gene 109: 121–123
65. Rina, M., Karagouni, A., Pagomenou, M., Tsigos, I., Bouriotis, V. (1991) Nucl. Acids Res. 19: 6341
66. Klein, S., Roberts, R.J. unpublished observations.
67. Li, J-K., Tu, J. (1991) Nucl. Acids Res. 19: 4770
68. Miyahara, M., Mise, K. unpublished observations.
69. Miyahara, M., Shimada, T., Mise, K. unpublished observations.

TABLE 1

Microorganism	Source	Enzyme^1	Sequence^2	Number of Cleavage Sites^3					References
				λ	Ad2	SV40	ΦX	pBR	
Acidiphilium cryptum 25H	K. Inagaki	*Acp*I (*Asu*II)	TT↑CGAA	7	1	0	0	0	3
		*Acp*II (*Pfl*MI)	CCANNNN↑NTGG	14	18	2	2	2	4
Acidiphilium organovorum 51H	Takara	*Aor*51HI (*Eco*47III)	AGC↑GCT	2	13	1	0	4	5
Acidiphilium species 10H	K. Inagaki	*Asp*10HI (*Asu*II)	TT↑CGAA	7	1	0	0	0	4
		*Asp*10HII (*Pfl*MI)	CCANNNN↑NTGG	14	18	2	2	2	4
Acidobacterium capsulatum 1371	K. Inagaki	*Acs*1371I (*Sal*I)	GTCGAC	2	3	0	0	1	6
Acidobacterium capsulatum 1372	K. Inagaki	*Acs*1372I (*Sal*I)	GTCGAC	2	3	0	0	1	6
Acidobacterium capsulatum 1373	K. Inagaki	*Acs*1373I (*Sal*I)	GTCGAC	2	3	0	0	1	6
Acidobacterium capsulatum 1421	K. Inagaki	*Acs*1421I (*Sal*I)	GTCGAC	2	3	0	0	1	6
Acidobacterium capsulatum 1422	K. Inagaki	*Acs*1422I (*Sal*I)	GTCGAC	2	3	0	0	1	6
Actinoplanes teochomyceticus	Glaxo 2523C	*Ate*I (*Nco*I)	CCATGG	4	20	3	0	0	7
Aeromonas hydrophila	NEB #724	*Ahd*I (*Eam*1105I)	GACNNNNNGTC	9	9	0	1	1	8
Anabaena flos-aquae	J.P. Schouten	*Afl*IV (*Sca*I)	AGTACT	5	5	1	0	0	9
Arthrobacter protophormiae	NEB #723	*Apo*I (*Fsi*I)	R↑AATTY	58	0	7	7	2	10
Arthrobacter variabilis	M.M. Wijdenbosch	*Avr*BI (*Hae*III)	GGCC	149	216	18	11	22	11
		*Avr*BII (*Avr*II)	C↑CTAGG	2	2	2	0	0	11
Artificial construct	T.A. Bickle	*Eco*DR2I	TCANNNNNNGTCG	Type I Enzyme					12
Artificial construct	T.A. Bickle	*Eco*DR3I	TCANNNNNNNATCG	Type I Enzyme					12
Artificial construct	T.A. Bickle	*Eco*RD2I	GAANNNNNNRTTC	Type I Enzyme					12
Artificial construct	T.A. Bickle	*Eco*RD3I	GAANNNNNNNRTTC	Type I Enzyme					12
Bacillus amyloliquefaciens H	ATCC 49763	M.*Bam*HII	GGAT$\overset{*}{C}$C	Specific methylase					17
Bacillus caldolyticus	Promega 77	*Bca*77I (*Bet*I)	W↑CCGGW	81	28	0	3	5	14
Bacillus cereus A	N.N. Sokolov	*Bcu*AI	?	>20	?	>4	1	>6	15
Bacillus cereus RFL1247	A.A. Janulaitis	*Bce*1247I (*Mwo*I)	GCNNNNNNNGC	347	391	25	21	34	16
Bacillus polymyxa A	N.N. Sokolov	*Bpo*AI	?	>14	3	>2	2	1	17

				Number of Cleavage Sites[3]					
Microorganism	Source	Enzyme[1]	Sequence[2]	λ	Ad2	SV40	ΦX	pBR	References
Bacillus pumilus	NEB #711	*Bpm*I (*Gsu*I)	CTGGAG (16/14)	25	32	6	3	4	18
Bacillus pumilus RFL1268	A.A. Janulaitis	*Bpu*1268I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	19
Bacillus species 118	V.E. Repin	*Bse*118I (*Cfr*10I)	RCCGGY	61	40	1	0	7	20
Bacillus species A11	D. Clark	*Bsc*BI (*Nla*IV)	GGN↑NCC	82	178	16	6	24	21
Bacillus species APR91	D. Clark	*Bsc*EI (*Bse*PI)	GCGCGC	6	52	0	1	0	21
Bacillus species B2I	S.K. Degtyarev	*Bsp*B2I	?	0	0	0	0	0	22
Bacillus species JY391	D. Clark	*Bsc*FI (*Mbo*I)	GATC	116	87	8	0	22	21
Bacillus species RFL143	A.A. Janulaitis	*Bsp*143II (*Hae*II)	RGCGC↑Y	48	76	1	8	11	16
Bacillus species RFL144	A.A. Janulaitis	*Bsp*144I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Bacillus species RFL146	A.A. Janulaitis	*Bsp*146I (*Apa*LI)	GTGCAC	4	7	0	1	3	16
Bacillus species RFL147	A.A. Janulaitis	*Bsp*147I (*Mbo*I)	GATC	116	87	8	0	22	16
Bacillus species RFL148	A.A. Janulaitis	*Bsp*148I (*Asu*II)	TTCGAA	7	1	0	0	0	16
Bacillus sphaericus 45	V.E. Repin	*Bsh*45I (*Hgi*AI)	GWGCW↑C	28	38	0	3	8	23
Bacillus sphaericus RFL1260	A.A. Janulaitis	*Bsp*1260I (*Ava*II)	GGWCC	35	73	6	1	8	16
Bacillus sphaericus RFL1261	A.A. Janulaitis	*Bsp*1261I (*Hae*III)	GGCC	149	216	18	11	22	16
Bacillus stearothermophilus	NEB 547	*Bss*KI (*Scr*FI)	↑CCNGG	185	233	17	3	16	24
Bacillus stearothermophilus 71	Promega #71	*Bst*71I (*Bbv*I)	GCAGC (8/12)	199	179	22	14	21	25
Bacillus stearothermophilus AU891	D. Clark	*Bso*CI (*Sdu*I)	GDGCHC	38	105	4	3	10	21
Bacillus stearothermophilus BS	N.I. Matvienko	*Bst*BSI (*Sna*I)	GTA↑TAC	3	3	0	0	1	26
Bacillus stearothermophilus CP114	Z. Chen	*Bsm*SI (*Sty*I)	CCWWGG	10	44	8	0	1	27
Bacillus stearothermophilus CPW193	Z. Chen	*Bsr*BI	GAGCGG (-3/-3)	0	0	0	0	0	27
Bacillus stearothermophilus CPW5	Z. Chen	*Bse*HI (*Hin*dIII)	AAGCTT	6	12	6	0	1	27
Bacillus stearothermophilus H426	Z. Chen	*Bsm*HI (*Hae*II)	RGCGCY	48	76	1	8	11	27
Bacillus stearothermophilus JN1891	D. Clark	*Bso*AI (*Eco*RV)	GATATC	21	9	1	0	1	21
Bacillus stearothermophilus JN2091	D. Clark	*Bso*BI (*Ava*I)	CYCGRG	8	40	0	1	1	21
Bacillus stearothermophilus JN791	D. Clark	*Bso*I (*Scr*FI)	CCNGG	185	233	17	3	16	21
Bacillus stearothermophilus OC391	D. Clark	*Bso*EI (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	21

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3]					References
				λ	Ad2	SV40	ΦX	pBR	
Bacillus stearothermophilus SE2091	D. Clark	*Bso*DI (*Xma*III)	CGGCCG	2	19	0	0	1	21
Bacillus stearothermophilus T1544	Z. Chen	*Bsa*TI (*Mst*I)	TGCGCA	15	17	0	1	4	27
Bacillus stearothermophilus W1718	Z. Chen	*Bsa*WI (*Bet*I)	WCCGGW	81	28	0	3	5	27
Bacillus stearothermophilus	V. Bouriotis	*Bse*BI (*Eco*RII)	CC↑WGG	71	136	17	2	6	28
Bacillus thuringiensis 34	V.E. Repin	*Btu*34I (*Mbo*I)	GATC	116	87	8	0	22	29
		*Btu*34II (*Hae*II)	RGCGCY	48	76	1	8	11	29
Bacillus thuringiensis AII	CAMB 2661	*Bth*AI (*Ava*II)	G↑GWCC	35	73	6	1	8	30
Bacillus thuringiensis D4	CAMB 2657	*Bth*DI (*Eco*RII)	CC↑WGG	71	136	17	2	6	31
Bacillus thuringiensis E	CAMB 2660	*Bth*EI (*Eco*RII)	CC↑WGG	71	136	17	2	6	32
Citrobacter freundii	CAMB 2600	*Cfr*J5I (*Bse*PI)	GCGCGC	6	52	0	1	0	33
Citrobacter freundii RFL59	A.A. Janulaitis	*Cfr*59I (*Cfr*I)	YGGCCR	39	70	0	2	6	16
Clostridium acetobutylicum ABKn8	G. Reysett	*Cac*8I	GCN↑NGC	238	285	8	19	31	34
Clostridium bifermentans B-4	T. Mitsuoka	*Cbi*I (*Asu*II)	TT↑CGAA	7	1	0	0	0	35
Deleya marina	IAM 14114	*Dma*I (*Pvu*II)	CAG↑CTG	15	24	3	0	1	36
Deleya pacifica	IAM 14115	*Dpa*I (*Sca*I)	AGT↑ACT	5	5	0	0	1	37
Enterobacter aerogenes	CAMB 2670	*Eae*AI (*Sma*I)	C↑CCGGG	3	12	0	0	0	38
Enterobacter species RFL4	A.A. Janulaitis	*Ese*4I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Enterobacter species RFL6	A.A. Janulaitis	*Ese*6I (*Sac*II)	CCGCGG	4	33	0	1	0	16
		*Ese*6II (*Eco*RII)	CCWGG	71	136	17	2	6	16
Escherichia coli RFL260	A.A. Janulaitis	*Eco*260I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Escherichia coli RFL261	A.A. Janulaitis	*Eco*261I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Escherichia coli RFL262	A.A. Janulaitis	*Eco*262I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Escherichia coli RFL263	A.A. Janulaitis	*Eco*263I (*Eco*31I)	GGTCTC	2	18	0	0	1	16
Escherichia coli VKM-125	N.N. Sokolov	*Eci*125I (*Bst*EII)	G↑GTNACC	13	10	0	0	0	39
Halomonas halodurans	ATCC 29686	*Hhd*I (*Eco*RII)	CCWGG	71	136	17	2	6	27
Listeria species RFL1270	A.A. Janulaitis	*Lsp*1270I (*Nsp*I)	RCATGY	32	41	2	0	4	19
Micrococcus luteus 31	V.E. Repin	*Mlu*31I (*Bal*I)	TGG↑CCA	18	17	0	0	1	23

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3] λ	Ad2	SV40	ΦX	pBR	References
Micrococcus species 23	V.E. Repin	*Msp*23I (*Xba*I)	TCTAGA	1	5	0	0	0	40
		*Msp*23II (*Xho*I)	CTCGAG	1	6	0	1	0	40
Moraxella osloensis	NEB #722	*Msl*I	CAYNNNNRTG	62	35	5	7	7	41
Moraxella species B6	S.K. Degtyarev	*Msp*B6I	?	0	0	0	0	0	22
Mycoplasma species	A.A. Janulaitis	*Mun*I (*Mfe*I)	C↑A$\overset{*}{\text{A}}$TTG	8	4	4	1	0	42
Myxococcus xanthus F18E	K. Izaki	*Mxa*I (*Sac*I)	GAG↑CTC	2	16	0	0	0	43
Nostoc linckia	A.I. Melnik	*Nli*387/7I (*Ava*I)	CYCGR↑G	8	40	0	1	1	44
		*Nli*387/7II (*Ava*II)	GGWCC	35	73	6	1	8	44
Nostoc species	PCC 7121	*Nsp*7121I (*Asu*I)	GGNCC	74	164	11	2	15	45
Phormidium ambiguum	A. Podhajska	*Pam*I (*Mst*I)	TGC↑GCA	15	17	0	1	4	46
		*Pam*II (*Acy*I)	GR↑CGYC	40	44	0	7	6	46
Porphyromonas gingivalis	A. Progulske-Fox	M.*Pgi*I	G$\overset{*}{\text{A}}$TC	Specific methylase					47
Pseudomonas aeruginosa 4148	A. Solonin	*Pae*HI (*Hgi*JII)	GRGCY↑C	7	57	2	0	2	48
		*Pae*PI (*Pst*I)	CTGCA↑G	28	30	2	1	1	48
Pseudomonas aeruginosa Q2	CAMB 2637	*Pae*QI (*Sac*II)	CCGCGG	4	33	0	1	0	49
Pseudomonas inequalis	M.M. Wijdenbosch	*Pin*AI (*Age*I)	A↑CCGGT	13	5	0	0	0	50
Pseudomonas mendocini	NEB 698	*Pme*I	GTTT↑AAAC	2	1	0	0	0	51
Pseudomonas putida RFL1253	A.A. Janulaitis	*Ppu*1253I (*Aat*II)	GACGTC	10	3	0	1	1	16
Rhizobium leguminosarum 69	V.E. Repin	*Rle*69I (*Eco*31I)	GGTCTC	2	18	0	0	1	52
Rhizobium meliloti	I.S. Andreeva	*Rme*21I (*Cla*I)	ATCGAT	15	2	0	0	1	53
Rhizobium trifolii	L.R. Lebedev	*Rtr*I (*Sal*I)	G↑TCGAC	2	3	0	0	1	54
Rhodococcus species SE1991	D. Clark	*Rhc*I (*Bsp*HI)	TCATGA	8	3	2	3	4	21
Staphylococcus epidermidis	CAMB 2635	*Sep*I (*Ava*III)	ATGCA↑T	14	9	3	0	0	55
Streptococcus salivarius ssp thermophilus	L. Benbadis	*Ssl*I (*Eco*RII)	CC↑WGG	71	136	17	2	6	56
Streptococcus thermophilus ST117	G.A. Somkuti	*Sth*117I (*Eco*RII)	CC↑WGG	71	136	17	2	6	57
Streptomyces albus 13	V.E. Repin	*Sal*13I (*Pst*I)	CTGCAG	28	30	2	1	1	58

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3]					References
				λ	Ad2	SV40	ΦX	pBR	
Streptomyces aureofaciens 13	J. Muchova	*Sau*HI (*Sau*I)	CCTNAGG	2	7	0	0	0	59
Streptomyces griseus	V. Bouriotis	*Sgr*BI (*Sac*II)	CCGC↑GG	4	33	0	1	0	60
Streptomyces lipmanii	R.H. Baltz	*Sli*I	?	?	?	?	?	?	61
		*Sli*II	?	?	?	?	?	?	61
Streptomyces niveus	ATCC 19793	*Sni*I (*Eco*RII)	CC↑WGG	71	136	17	2	6	62
Streptomyces scabies	J.L. Schottel	*Ssb*I (*Hin*dIII)	A↑AGCTT	6	12	6	0	1	63
Streptomyces species	T.G. Simcox	*Srf*I	GCCC↑GGGC	0	1	0	0	0	64
Streptomyces species	V. Bouriotis	*Sse*AI (*Nar*I)	GG↑CGCC	1	20	0	2	4	65
Streptoverticillium cinnamoneum	Glaxo 2566C	*Sci*BI (*Xho*I)	CTCGAG	1	6	0	1	0	66
Synechococcus species RF-1	J. Tu	*Ssp*RFI (*Asu*II)	TT↑CGAA	7	1	0	0	0	67
Unidentified bacterium RFL1243	A.A. Janulaitis	*Uba*1243I (*Eco*RII)	CCWGG	71	136	17	2	6	16
Unidentified bacterium RFL1244	A.A. Janulaitis	*Uba*1244I (*Sac*II)	CCGCGG	4	33	0	1	0	16
Unidentified bacterium RFL1245	A.A. Janulaitis	*Uba*1245I (*Pvu*II)	CAGCTG	15	24	3	0	1	16
Unidentified bacterium RFL1246	A.A. Janulaitis	*Uba*1246I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1248	A.A. Janulaitis	*Uba*1248I (*Xho*I)	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1249	A.A. Janulaitis	*Uba*1249I (*Ava*II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1250	A.A. Janulaitis	*Uba*1250I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1256	A.A. Janulaitis	*Uba*1256I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1257	A.A. Janulaitis	*Uba*1257I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1258	A.A. Janulaitis	*Uba*1258I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1259	A.A. Janulaitis	*Uba*1259I (*Mbo*I)	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1262	A.A. Janulaitis	*Uba*1262I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1263	A.A. Janulaitis	*Uba*1263I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1264	A.A. Janulaitis	*Uba*1264I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1265	A.A. Janulaitis	*Uba*1265I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1266	A.A. Janulaitis	*Uba*1266I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1267	A.A. Janulaitis	*Uba*1267I (*Hpa*II)	CCGG	328	171	1	5	26	16

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3]					References
				λ	Ad2	SV40	ΦX	pBR	
Unidentified bacterium RFL1269	A.A. Janulaitis	*Uba*1269I (*Bsm*I)	GAATGC	46	10	4	4	1	16
Unidentified bacterium RFL1271	A.A. Janulaitis	*Uba*1271I (*Xho*I)	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1272	A.A. Janulaitis	*Uba*1272I (*Ava*II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1275	A.A. Janulaitis	*Uba*1275I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1276	A.A. Janulaitis	*Uba*1276I (*Ksp*632I)	CTCTTC	34	29	1	2	2	16
Unidentified bacterium RFL1278	A.A. Janulaitis	*Uba*1278I (*Ava*II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1279	A.A. Janulaitis	*Uba*1279I (*Bsp*MII)	TCCGGA	24	8	0	0	1	16
Unidentified bacterium RFL1280	A.A. Janulaitis	*Uba*1280I (*Cau*II)	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1282	A.A. Janulaitis	*Uba*1282I (*Bcl*I)	TGATCA	8	5	1	0	0	16
Unidentified bacterium RFL1283	A.A. Janulaitis	*Uba*1283I (*Bcl*I)	TGATCA	8	5	1	0	0	16
Unidentified bacterium RFL1284	A.A. Janulaitis	*Uba*1284I (*Esp*I)	GCTNAGC	6	8	1	0	0	16
Unidentified bacterium RFL1285	A.A. Janulaitis	*Uba*1285I (*Mcr*I)	CGRYCG	22	50	0	1	7	16
Unidentified bacterium RFL1286	A.A. Janulaitis	*Uba*1286I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1287	A.A. Janulaitis	*Uba*1287I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1288	A.A. Janulaitis	*Uba*1288I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1289	A.A. Janulaitis	*Uba*1289I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1290	A.A. Janulaitis	*Uba*1290I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1291	A.A. Janulaitis	*Uba*1291I (*Bst*EII)	GGTNACC	13	10	0	0	0	16
Unidentified bacterium RFL1292	A.A. Janulaitis	*Uba*1292I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1293	A.A. Janulaitis	*Uba*1293I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1294	A.A. Janulaitis	*Uba*1294I (*Sau*I)	CCTNAGG	2	7	0	0	0	16
		*Uba*1294II (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1295	A.A. Janulaitis	*Uba*1295I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1296	A.A. Janulaitis	*Uba*1296I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1297	A.A. Janulaitis	*Uba*1297I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1298	A.A. Janulaitis	*Uba*1298I (*Xho*I)	CTCGAG	1	6	0	1	0	16

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3]					References
				λ	Ad2	SV40	ΦX	pBR	
Unidentified bacterium RFL1299	A.A. Janulaitis	*Uba*1299I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1302	A.A. Janulaitis	*Uba*1302I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1303	A.A. Janulaitis	*Uba*1303I (*Mcr*I)	CGRYCG	22	50	0	1	7	16
Unidentified bacterium RFL1304	A.A. Janulaitis	*Uba*1304I (*Ava*II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1305	A.A. Janulaitis	*Uba*1305I (*Nla*IV)	GGNNCC	82	178	16	6	24	16
Unidentified bacterium RFL1306	A.A. Janulaitis	*Uba*1306I (*Sac*II)	CCGCGG	4	33	0	1	0	16
Unidentified bacterium RFL1307	A.A. Janulaitis	*Uba*1307I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1308	A.A. Janulaitis	*Uba*1308I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1309	A.A. Janulaitis	*Uba*1309I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1310	A.A. Janulaitis	*Uba*1310I (*Eco*NI)	CCTNNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1311	A.A. Janulaitis	*Uba*1311I (*Sty*I)	CCWWGG	10	44	8	0	1	16
Unidentified bacterium RFL1312	A.A. Janulaitis	*Uba*1312I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1313	A.A. Janulaitis	*Uba*1313I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1314	A.A. Janulaitis	*Uba*1314I (*Ava*II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1315	A.A. Janulaitis	*Uba*1315I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1316	A.A. Janulaitis	*Uba*1316I (*Eco*31I)	GGTCTC	2	18	0	0	1	16
Unidentified bacterium RFL1317	A.A. Janulaitis	*Uba*1317I (*Mbo*I)	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1318	A.A. Janulaitis	*Uba*1318I (*Cau*II)	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1319	A.A. Janulaitis	*Uba*1319I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1320	A.A. Janulaitis	*Uba*1320I (*Esp*I)	GCTNAGC	6	8	1	0	0	16
Unidentified bacterium RFL1321	A.A. Janulaitis	*Uba*1321I (*Fnu*DII)	CGCG	157	303	0	14	23	16
Unidentified bacterium RFL1322	A.A. Janulaitis	*Uba*1322I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1323	A.A. Janulaitis	*Uba*1323I (*Mbo*I)	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1324	A.A. Janulaitis	*Uba*1324I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1325	A.A. Janulaitis	*Uba*1325I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1326	A.A. Janulaitis	*Uba*1326I (*Dra*II)	RGGNCCY	3	44	3	0	4	16
Unidentified bacterium RFL1327	A.A. Janulaitis	*Uba*1327I (*Cfr*I)	YGGCCR	39	70	0	2	6	16

Microorganism	Source	Enzyme[1]	Sequence[2]	Number of Cleavage Sites[3]					References
				λ	Ad2	SV40	ΦX	pBR	
Unidentified bacterium RFL1328	A.A. Janulaitis	*Uba*1328I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1329	A.A. Janulaitis	*Uba*1329I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1330	A.A. Janulaitis	*Uba*1330I (*Hgi*JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1331	A.A. Janulaitis	*Uba*1331I (*Afl*II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1332	A.A. Janulaitis	*Uba*1332I (*Sau*I)	CCTNAGG	2	7	0	0	0	16
Unidentified bacterium RFL1333	A.A. Janulaitis	*Uba*1333I (*Sau*I)	CCTNAGG	2	7	0	0	0	16
Unidentified bacterium RFL1334	A.A. Janulaitis	*Uba*1334I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1335	A.A. Janulaitis	*Uba*1335I (*Xho*I)	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1336	A.A. Janulaitis	*Uba*1336I (*Hae*III)	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1337	A.A. Janulaitis	*Uba*1337I (*Pst*I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1338	A.A. Janulaitis	*Uba*1338I (*Hpa*II)	CCGG	328	171	1	5	26	16
Unidentified bacterium RFL1339	A.A. Janulaitis	*Uba*1339I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1342	A.A. Janulaitis	*Uba*1342I (*Cla*I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1343	A.A. Janulaitis	*Uba*1343I (*Eco*31I)	GGTCTC	2	18	0	0	1	16
Unidentified bacterium RFL1346	A.A. Janulaitis	*Uba*1346I (*Bam*HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1347	A.A. Janulaitis	*Uba*1347I (*Cau*II)	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1353	A.A. Janulaitis	*Uba*1353I (*Ava*III)	ATGCAT	14	9	3	0	0	16
Vibrio parahaemolyticus 1307	T. Shimada	*Vpa*K11I (*Ava*II)	GGWCC	35	73	6	1	8	68
Vibrio parahaemolyticus 4387-61	T. Shimada	*Vpa*K32I (*Sap*I)	GCTCTTC	10	7	0	1	1	69
Vibrio parahaemolyticus Takikawa 13	T. Shimada	*Vpa*K15I (*Asu*I)	GGNCC	74	164	11	2	15	68

FOOTNOTES

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 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, C↑GATCG is an abbreviation for

5′ C↑G A T C G 3′
3′ G C T A G↑C 5′

For enzymes such as *Sap*I and *Aci*I, which cleave away from their recognition sequences, the sites of cleavage are indicated in parentheses. For example *Sap*I GCTCTTC(1/4) indicates cleavage as shown below

5′ GCTCTTCN↑′ 3′
3′ CGAGAAGNNNN↑′ 5′

*Aci*I CCGC(-2/-2) indicates cleavage as shown below

5′ CC↑GC ′ 3′
3′ GG↑CG ′ 5′

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

$\overset{*}{A}$ is N^6-methyladenosine. $\overset{*}{C}$ is C^5-methylcytosine.

3. These columns indicate the frequency of cleavage by the various specific endonucleases on bacteriophage lambda DNA (λ), adenovirus-2 DNA (Ad2), simian virus 40 DNA (SV40), φX174 Rf DNA and pBR322 DNA (pBR). In all cases the sites were derived by computer search of the complete sequences obtained from GENBANK.

TABLE 2

Type I enzymes

Enzyme	Recognition sequence[2]	Me site[3]
*Cfr*AI	GCANNNNNNNNGTGG	
*Eco*AI	GAGNNNNNNNGTCA	2(6),-3(6)
*Eco*BI	TGANNNNNNNNTGCT	3(6),-4(6)
*Eco*DI	TTANNNNNNNGTCY	
*Eco*DR2I	TCANNNNNNGTCG	
*Eco*DR3I	TCANNNNNNNATCG	
*Eco*DXXI	TCANNNNNNNRTTC	
*Eco*EI	GAGNNNNNNNATGC	
*Eco*KI	AACNNNNNNGTGC	2(6),-3(6)
*Eco*R124I	GAANNNNNNRTCG	
*Eco*R124/3I	GAANNNNNNNRTCG	-3(6)
*Eco*RD2I	GAANNNNNNRTTC	
*Eco*RD3I	GAANNNNNNNRTTC	
*Sty*SBI	GAGNNNNNNRTAYG	2(6),-4(6)
*Sty*SJI	GAGNNNNNNGTRC	
*Sty*SPI	AACNNNNNNGTRC	2(6),-3(6)
*Sty*SQI	AACNNNNNNRTAYG	

Type III enzymes

Enzyme	Recognition sequence[2]	Me site[3]
*Eco*PI	AGACC	3(6)
*Eco*P15I	CAGCAG	(25/27) 5(6)
*Hin*fIII	CGAAT	
*Sty*LTI	CAGAG	4(6)

Type II enzymes

Enzyme[1]	Isoschizomers	Recognition[2] Sequence	Me[3] site	Commercial[4] source
*Aat*II		GACGT↑C		ELMNOPRSUVX
*Acc*I		GT↑MKAC		ABEIKLMNOPQRSUVX
*Aci*I		CCGC(-3/-1)		N
*Acy*I		GR↑CGYC		MRV
	*Bbi*II	GR↑CGYC		AK
	*Bsa*HI	GR↑CGYC		NS
	*Hin*1I	GR↑CGYC		EFOU
*Afl*II		C↑TTAAG		ABKNSU
	*Bfr*I	C↑TTAAG		M
	*Esp*4I	C↑TTAAG		F
*Afl*III		A↑CRYGT		BMNU
*Age*I		A↑CCGGT		N
*Aha*III		TTT↑AAA		
	*Dra*I	TTT↑AAA		ABEFIKLMNOPQRSUVX
*Alu*I		AG↑CT	3(5)	ABEFHIKLMNOPQRSUVX
*Alw*NI		CAGNNN↑CTG		NSU
*Apa*I		GGGCC↑C	4(5)	BEIKLMNOPRSUVX
	*Bsp*120I	G↑GGCCC		F
*Apa*BI		GCANNNNN↑TGC		
*Apa*LI		G↑TGCAC		AEKNSUX
	*Alw*44I	G↑TGCAC		FORU
	*Sno*I	G↑TGCAC		LMV
*Asc*I		GG↑CGCGCC		N
*Asu*I		G↑GNCC		R
	*Bsi*ZI	G↑GNCC		AW
	*Cfr*13I	G↑GNCC	4(5)	FKOU
	*Sau*96I	G↑GNCC		BELMNORSVX
*Asu*II		TT↑CGAA		
	*Bsi*CI	TT↑CGAA		AUW
	*Bsp*119I	TT↑CGAA		F
	*Bst*BI	TT↑CGAA		NS
	*Csp*45I	TT↑CGAA		ORV
	*Lsp*I	TT↑CGAA		L
	*Nsp*V	TT↑CGAA		ABKOP
	*Sfu*I	TT↑CGAA		M
*Ava*I		C↑YCGRG		ABEIKLMNOPRSUVX
	*Bco*I	C↑YCGRG		AW
	*Eco*88I	C↑YCGRG		F
	*Nsp*III	C↑YCGRG		P
*Ava*II		G↑GWCC		ABEIKMNPRSX
	*Eco*47I	G↑GWCC		FOU
	*Sin*I	G↑GWCC	4(5)	LRSV
*Ava*III		ATGCAT		
	*Eco*T22I	ATGCA↑T		KOU
	*Mph*1103I	ATGCA↑T		F
	*Nsi*I	ATGCA↑T		BELMNRSVX
	*Ppu*10I	A↑TGCAT		F
*Avr*II		C↑CTAGG		N
	*Bln*I	C↑CTAGG		AK
*Bae*I		ACNNNNGTAYC		
*Bal*I		TGG↑CCA	4(5)	AIKRSVX
	*Msc*I	TGG↑CCA		BNU
*Bam*HI		G↑GATCC	5(4)	ABEFHIKLMNOPQRSUVWX
	*Bst*I	G↑GATCC		P
*Bbv*I		GCAGC(8/12)	2(5),-2(5)	EINX
	*Bst*71I	GCAGC(8/12)		R
*Bbv*II		GAAGAC(2/6)		
	*Bbs*I	GAAGAC(2/6)		N
*Bcc*I		CCATC		
*Bcef*I		ACGGC(12/13)		
*Bcg*I[5]		GCANNNNNNTCG(12/10)		N
*Bcl*I		T↑GATCA		ABEFILMNOPRSUVX
	*Bsi*QI	T↑GATCA		AW
	*Fba*I	T↑GATCA		K
*Bet*I		W↑CCGGW		
*Bgl*I		GCCNNNN↑NGGC		ABEFHILMNOPQRSUVWX
*Bgl*II		A↑GATCT		ABEFHIKLMNOPQRSUVWX
*Bin*I		GGATC(4/5)		
	*Alw*I	GGATC(4/5)		NSU
*Bpu*10I		CCTNAGC(-5/-2)		
*Bsa*AI		YAC↑GTR		N
*Bsa*BI		GATNN↑NNATC		N
	*Bsi*BI	GATNN↑NNATC		AW
	*Mam*I	GATNN↑NNATC		M
*Bse*PI		GCGCGC		
	*Bss*HII	G↑CGCGC		BELMNOQRUVX
*Bsg*I		GTGCAG(16/14)		N
*Bsi*I		CTCGTG(-5/-1)		
*Bsi*YI		CCNNNNN↑NNGG		AMUW
	*Bsl*I	CCNNNNN↑NNGG		N
*Bsm*I		GAATGC(1/-1)		ELMNOSUVX
	*Bsc*CI	GAATGC(1/-1)		W
*Bsm*AI		GTCTC(1/5)		NU
	*Alw*26I	GTCTC(1/5)		FR
*Bsp*GI		CTGGAC		
*Bsp*HI		T↑CATGA		NSU
*Bsp*MI		ACCTGC(4/8)		NU
*Bsp*MII		T↑CCGGA		
	*Acc*III	T↑CCGGA		AEKQRV
	*Bse*AI	T↑CCGGA		M
	*Bsi*MI	T↑CCGGA		AW
	*Bsp*EI	T↑CCGGA		NS
	*Kpn*2I	T↑CCGGA		F
	*Mro*I	T↑CCGGA		MOU
*Bsr*I		ACTGG(1/-1)		N
*Bsr*BI		GAGCGG(-3/-3)		
*Bst*EII		G↑GTNACC		BEHLMNOPRSUVX
	*Bst*PI	G↑GTNACC		K
	*Eco*91I	G↑GTNACC		F
	*Eco*O65I	G↑GTNACC		AK
*Bst*XI		CCANNNNN↑NTGG		BEKLMNOQRSUVX
*Cac*8I		GCN↑NGC		
*Cau*II		CC↑SGG		
	*Bcn*I	CC↑SGG	2(4)	AFK
	*Nci*I	CC↑SGG		BELMNOSUVWX
*Cfr*I		Y↑GGCCR	4(5)	
	*Eae*I	Y↑GGCCR	4(5)	EKLMNSUVX
*Cfr*10I		R↑CCGGY	2(5)	AFKMNOU

Enzyme[1]	Isoschizomers	Recognition[2] Sequence	Me[3] site	Commercial[4] source
	*Bsr*FI	R↑CCGGY		N
*Cla*I		AT↑CGAT	5(6)	ABKMNPQRSVX
	*Ban*III	AT↑CGAT		OU
	*Bsc*I	AT↑CGAT		L
	*Bsi*XI	AT↑CGAT		AW
	*Bsp*106I	AT↑CGAT		E
	*Bsp*DI	AT↑CGAT		N
	*Bsu*15I	AT↑CGAT		F
*Cvi*JI		RG↑CY	3(5)	
*Cvi*RI		TG↑CA	4(6)	
*Dde*I		C↑TNAG	1(5)	BEILMNOPRUVX
*Dpn*I*		GA↑TC		ABEILMNRSUVX
*Dra*II		RG↑GNCCY		M
	*Eco*O109I	RG↑GNCCY		AEFKLNOSUVX
	*Pss*I	RGGNC↑CY		I
*Dra*III		CACNNN↑GTG		EMNSUX
*Drd*I		GACNNNN↑NNGTC		N
*Drd*II		GAACCA		
*Dsa*I		C↑CRYGG		M
*Eam*1105I		GACNNN↑NNGTC		FN
*Eci*I		TCCGCC		
*Eco*31I		GGTCTC(1/5)		F
	*Bsa*I	GGTCTC(1/5)		N
*Eco*47III		AGC↑GCT		ABFKLMNORU
*Eco*57I		CTGAAG(16/14)	5(6),5(6)	FN
*Eco*NI		CCTNN↑NNNAGG		NSU
*Eco*RI		G↑AATTC	3(6)	ABEFHIKLMNOPQRSUVWX
*Eco*RII[6]		↑CCWGG	2(5)	BEOSUV
+	*Apy*I	CC↑WGG		M
+	*Bsi*LI	CC↑WGG		AW
+	*Bst*NI	CC↑WGG	2(4)	ENSX
+	*Bst*OI	CC↑WGG		R
+	*Mva*I	CC↑WGG	2(4)	AFKMOU
*Eco*RV		GAT↑ATC	2(6)	ABEHIKLMNOPQRSUVWX
	*Eco*32I	GAT↑ATC		F
*Esp*I		GC↑TNAGC		U
	*Bpu*1102I	GC↑TNAGC		EFN
	*Cel*II	GC↑TNAGC		ALM
*Esp*3I		CGTCTC(1/5)		FN
*Fau*I		CCCGC(4/6)		
*Fin*I		GTCCC		
*Fnu*DII		CG↑CG		
	*Acc*II	CG↑CG		AKQVX
	*Bsp*50I	CG↑CG		EF
	*Bst*UI	CG↑CG		NSU
	*Mvn*I	CG↑CG		M
	*Tha*I	CG↑CG		BI
*Fnu*4HI		GC↑NGC		N
*Fok*I		GGATG(9/13)	3(6),-2(6)	AEFIKMNRUVX
*Fse*I		GGCCGG↑CC		
*Fsi*I		R↑AATTY		
	*Apo*I	R↑AATTY		N
*Gdi*II		YGGCCG(-5/-1)		
*Gsu*I		CTGGAG(16/14)		FN
	*Bpm*I	CTGGAG(16/14)		N
*Hae*I		WGG↑CCW		
*Hae*II		RGCGC↑Y		ABEIKLMNOPRSUVX
	*Bsp*143II	RGCGC↑Y		F
*Hae*III		GG↑CC	3(5)	ABHIKLMNOPQRSUVX
	*Bsh*I	GG↑CC		W
	*Bsu*RI	GG↑CC	3(5)	F
	*Pal*I	GG↑CC		EPV
*Hga*I		GACGC(5/10)		NSUX
*Hgi*AI		GWGCW↑C		NX
	*Alw*21I	GWGCW↑C		F
	*Asp*HI	GWGCW↑C		M
*Hgi*CI		G↑GYRCC		
	*Ban*I	G↑GYRCC		EIMNOPRSUVX
	*Eco*64I	G↑GYRCC		F
*Hgi*EII		ACCNNNNNNGGT		
*Hgi*JII		GRGCY↑C		
	*Ban*II	GRGCY↑C		BEIKLMNOPRSUVX
	*Eco*24I	GRGCY↑C		F

Enzyme[1]	Isoschizomers	Recognition[2] Sequence	Me[3] site	Commercial[4] source
*Hha*I		GCG↑C	2(5)	ABEKNOPRSUX
	*Cfo*I	GCG↑C		BILMRSV
	*Hin*6I	G↑CGC		F
	*Hin*P1I	G↑CGC		NSX
*Hind*II		GTY↑RAC	5(6)	EM
	*Hinc*II	GTY↑RAC		ABFHIKLNOPQRSUVX
*Hind*III		A↑AGCTT	1(6)	ABEFHIKLMNOPQRSUVWX
*Hinf*I		G↑ANTC		ABEFHIKLMNOPQRSUVWX
*Hpa*I		GTT↑AAC	5(6)	ABEFHIKLMNOPQRSUVX
*Hpa*II		C↑CGG	2(5)	ABEFLMNOPQRSUVX
	*Hap*II	C↑CGG	2(5)	IK
	*Msp*I	C↑CGG	1(5)	ABEFHIKLMNOPQRSUVWX
*Hph*I		GGTGA(8/7)	-2(5)	NSUVX
*Kpn*I		GGTAC↑C	4(6)	ABEFIKLMNOPQRSUVX
	*Acc*65I	G↑GTACC		FNR
	*Asp*718I	G↑GTACC		M
*Ksp*632I		CTCTTC(1/4)		M
	*Eam*1104I	CTCTTC(1/4)		F
	*Ear*I	CTCTTC(1/4)		N
*Mae*I		C↑TAG		M
	*Bfa*I	C↑TAG		N
	*Rma*I	C↑TAG		N
*Mae*II		A↑CGT		M
*Mae*III		↑GTNAC		M
*Mbo*I[7]		↑GATC		BEFIKNPQRSVX
+	*Bsp*143I	↑GATC		F
	*Dpn*II	↑GATC	2(6)	NU
	*Nde*II	↑GATC		BM
+	*Sau*3AI	↑GATC	4(5)	ABEIKLMNOPQRSUVX
*Mbo*II		GAAGA(8/7)	5(6)	BFIKNOPQRSUVX
*Mcr*I		CGRY↑CG		M
	*Bsi*EI	CGRY↑CG		ANW
*Mfe*I		C↑AATTG		
	*Mun*I	C↑AATTG	3(6)	FN
*Mlu*I		A↑CGCGT		ABEFIKLMNOPQRSUVX
*Mly*I		GACTC(5/5)		
*Mme*I		TCCRAC(20/18)		
*Mnl*I		CCTC(7/6)		ENSUX
*Mse*I		T↑TAA		NSU
*Msl*I		CAYNNNNRTG		
*Mst*I		TGC↑GCA		X
	*Avi*II	TGC↑GCA		M
	*Fdi*II	TGC↑GCA		U
	*Fsp*I	TGC↑GCA		NSU
*Mwo*I		GCNNNNN↑NNGC		
	*Bsp*WI	GCNNNNN↑NNGC		M
*Nae*I		GCC↑GGC		AEKLMNOUVX
	*Ngo*MI	G↑CCGGC		N
*Nar*I		GG↑CGCC		BEMNOPRSUVX
	*Bbe*I	GGCGC↑C		AK
	*Ehe*I	GGC↑GCC		FOU
	*Kas*I	G↑GCGCC		N
*Nco*I		C↑CATGG		ABEFHIKLMNOPQRSUVWX
*Nde*I		CA↑TATG	4(6)	BEFKLMNPSUVX
*Nhe*I		G↑CTAGC		ABEKLMNOPRSUVX
*Nla*III		CATG↑		NSU
*Nla*IV		GGN↑NCC		NSU
	*Bsc*BI	GGN↑NCC		AI
*Not*I		GC↑GGCCGC		ABEFIKLMNOPQRSUVWX
*Nru*I		TCG↑CGA		ABEIKLMNOPQSUVWX
	*Bsp*68I	TCG↑CGA		F
	*Spo*I	TCG↑CGA		R
*Nsp*I		RCATG↑Y		AKMU
*Nsp*BII		CMG↑CKG		U
*Pac*I		TTAAT↑TAA		N
*Pfl*1108I		TCGTAG		
*Pfl*MI		CCANNNN↑NTGG		NSU
	*Van*91I	CCANNNN↑NTGG		FM
*Ple*I		GAGTC(4/5)		NU
*Pma*CI		CAC↑GTG		AK
	*Bbr*PI	CAC↑GTG		M
	*Eco*72I	CAC↑GTG		F
	*Pml*I	CAC↑GTG		NU

Enzyme[1]	Isoschizomers	Recognition[2] Sequence	Me[3] site	Commercial[4] source
*Pme*I		GTTT↑AAAC		N
*Ppu*MI		RG↑GWCCY		NSU
	*Psp*5II	RG↑GWCCY		F
*Psh*AI		GACNN↑NNGTC		K
*Pst*I		CTGCA↑G	5(6)	ABEFHIKLMNOPQRSUVWX
*Pvu*I		CGAT↑CG		ABEFKLMNOPQRSUVX
	*Bsp*CI	CGAT↑CG		E
	*Xor*II	CGAT↑CG		BS
*Pvu*II		CAG↑CTG	4(4)	ABEFIKLMNOPQRSUVWX
*Rle*AI		CCCACA(12/9)		
*Rsa*I		GT↑AC		ABEILMNOPQRSUVWX
	*Afa*I	GT↑AC		K
	*Csp*6I	G↑TAC		F
*Rsr*II		CG↑GWCCG		ABMNSUX
	*Cpo*I	CG↑GWCCG		AFK
	*Csp*I	CG↑GWCCG		EORV
*Sac*I		GAGCT↑C		AEIKLMNOPQRSUVWX
	*Ecl*136II	GAG↑CTC		FN
	*Sst*I	GAGCT↑C		BS
*Sac*II		CCGC↑GG		EILNOPRSUVX
	*Cfr*42I	CCGC↑GG		F
	*Ksp*I	CCGC↑GG		M
	*Sst*II	CCGC↑GG		BS
*Sal*I		G↑TCGAC		ABEFHIKLMNOPQRSUVX
*Sap*I		GCTCTTC(1/4)		
*Sau*I		CC↑TNAGG		M
	*Axy*I	CC↑TNAGG		V
	*Bsu*36I	CC↑TNAGG		NRS
	*Cvn*I	CC↑TNAGG		BS
	*Eco*81I	CC↑TNAGG		AFKOU
	*Mst*II	CC↑TNAGG		EX
*Sca*I		AGT↑ACT		ABEFIKLMNOPRSUVX
*Scr*FI		CC↑NGG		EMNOSUVX
	*Dsa*V	↑CCNGG		M
*Sdu*I		GDGCH↑C		F
	*Bmy*I	GDGCH↑C		M
	*Bsp*1286I	GDGCH↑C		AKNRUX
*Sec*I		C↑CNNGG		
	*Bsa*JI	C↑CNNGG		N
*Sfa*NI		GCATC(5/9)		NSUX
*Sfe*I		C↑TRYAG		
	*Sfc*I	C↑TRYAG		N
*Sfi*I		GGCCNNNN↑NGGCC		ABEILMNOPQRSUVX
*Sgr*AI		CR↑CCGGYG		M
*Sma*I		CCC↑GGG	2(4)	ABEFIKLMNOPQRSUVWX
	*Cfr*9I	C↑CCGGG	2(4)	FOU
	*Psp*AI	C↑CCGGG		E
	*Xma*I	C↑CCGGG		EINRSUVX
*Sna*I		GTATAC		
	*Bst*1107I	GTA↑TAC		FMN
*Sna*BI		TAC↑GTA		AEKLMNRSVX
	*Eco*105I	TAC↑GTA		FOU
*Spe*I		A↑CTAGT		ABEKLMNORSUVWX
*Sph*I		GCATG↑C		ABEHIKLMNOPQRSUX
	*Bbu*I	GCATG↑C		RV
	*Pae*I	GCATG↑C		F
*Spl*I		C↑GTACG		AK
	*Bsi*WI	C↑GTACG		AMNUW
	*Pfl*23II	C↑GTACG		F
*Srf*I		GCCC↑GGGC		E
*Sse*8387I		CCTGCA↑GG		AK
*Ssp*I		AAT↑ATT		ABEFKLMNORUVX
*Stu*I		AGG↑CCT		ABEIKLMNPRSVX
	*Aat*I	AGG↑CCT		OU
	*Eco*147I	AGG↑CCT		F
*Sty*I		C↑CWWGG		BEMNRSUVX
	*Eco*130I	C↑CWWGG		FU
	*Eco*T14I	C↑CWWGG		AK
*Swa*I		ATTT↑AAAT		M
*Taq*I		T↑CGA	4(6)	ABEFILMNOPQRSUVWX
	*Tth*HB8I	T↑CGA	4(6)	AK
*Taq*II[8]		GACCGA(11/9) CACCCA(11/9)		
*Tfi*I		G↑AWTC		N
*Tsp*45I		GTSAC		
*Tsp*EI		AATT		
*Tth*111I		GACN↑NNGTC		AEIKNPRUVX
	*Asp*I	GACN↑NNGTC		M
*Tth*111II		CAARCA(11/9)		
*Vsp*I		AT↑TAAT		FKR
	*Ase*I	AT↑TAAT		NSU
	*Asn*I	AT↑TAAT		M
*Xba*I		T↑CTAGA	6(6)	ABEFHIKLMNOPQRSUVWX
*Xcm*I		CCANNNNN↑NNNNTGG		NU
*Xho*I		C↑TCGAG		ABEFHIKLMNOPQRSUVX
	*Ccr*I	C↑TCGAG		X
	*Pae*R7I	C↑TCGAG	5(6)	NSX
*Xho*II		R↑GATCY		EMRVX
	*Bst*YI	R↑GATCY		BNU
	*Mfl*I	R↑GATCY		AK
*Xma*III		C↑GGCCG	4(5)	BE
	*Bst*ZI	C↑GGCCG		R
	*Eag*I	C↑GGCCG		NS
	*Ecl*XI	C↑GGCCG		M
	*Eco*52I	C↑GGCCG		AFKORU
*Xmn*I		GAANN↑NNTTC		ENUX
	*Asp*700I	GAANN↑NNTTC		M

FOOTNOTES

1. * signifies that *Dpn*I and its isoschizomers require the presence of 6-methyladenosine within the recognition sequence GATC.

2. Recognition sequences are given using 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
H = A or C or T
B = G or T or C
V = G or C or A
D = G or A or T
N = A or C or G or T

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 (2/92)
B	BRL (1/92)
E	Stratagene (1/92)
F	Fermentas (6/91)
H	American Allied (1/92)
I	IBI (6/91)
K	Takara (10/91)
L	Northumbria Biologicals Ltd. (10/91)
M	Boehringer Mannheim (9/91)
N	New England Biolabs (2/92)
O	Toyobo (6/91)
P	PL-Pharmacia-LKB (9/91)
Q	Molecular Biology Resources (10/91)
R	Promega Corporation (10/91)
S	Sigma (1/92)
U	USB (10/91)
V	Serva (2/91)
W	ILS (5/91)
X	New York Biolabs (4/91)

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

7. *Mbo*I isoschizomers fall into two classes based upon their sensitivity to methylation. *Mbo*I will not cleave when the recognition sequence contains 6-methyladenosine whereas *Sau*3AI will not cleave when its recognition sequence contains 5-methylcytosine. Isoschizomers of *Mbo*I that are like *Sau*3AI are indicated by +.

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