

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).

ACKNOWLEDGMENTS

Special thanks are due to the many individuals who have so kindly communicated their unpublished results for inclusion in this compilation.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 N.I.H. (GM40537).

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TABLE 1

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³				References	
				λ	Ad2	SV40	Φ X pBR		
<i>Acidiphilium cryptum</i> 25H	K. Inagaki	<i>AcpI</i> (<i>AsuII</i>)	TT \uparrow CGAA	7	1	0	0	0	3
<i>Acidiphilium organovorum</i> 51H	Takara	<i>AcpII</i> (<i>PfIMI</i>)	CCANNNN \uparrow NTGG	14	18	2	2	2	4
<i>Acidiphilium</i> species 10H	K. Inagaki	<i>Aor51HI</i> (<i>Eco47III</i>)	AGC \uparrow GCT	2	13	1	0	4	5
		<i>Asp10HI</i> (<i>AsuII</i>)	TT \uparrow CGAA	7	1	0	0	0	4
		<i>Asp10HII</i> (<i>PfIMI</i>)	CCANNNN \uparrow NTGG	14	18	2	2	2	4
<i>Acidobacterium capsulatum</i> 1371	K. Inagaki	<i>Acs1371I</i> (<i>SaII</i>)	GTCGAC	2	3	0	0	1	6
<i>Acidobacterium capsulatum</i> 1372	K. Inagaki	<i>Acs1372I</i> (<i>SaII</i>)	GTCGAC	2	3	0	0	1	6
<i>Acidobacterium capsulatum</i> 1373	K. Inagaki	<i>Acs1373I</i> (<i>SaII</i>)	GTCGAC	2	3	0	0	1	6
<i>Acidobacterium capsulatum</i> 1421	K. Inagaki	<i>Acs1421I</i> (<i>SaII</i>)	GTCGAC	2	3	0	0	1	6
<i>Acidobacterium capsulatum</i> 1422	K. Inagaki	<i>Acs1422I</i> (<i>SaII</i>)	GTCGAC	2	3	0	0	1	6
<i>Actinoplanes teohomyceticus</i>	Glaxo 2523C	<i>AreI</i> (<i>NcoI</i>)	CCATGG	4	20	3	0	0	7
<i>Aeromonas hydrophila</i>	NEB #724	<i>AhdI</i> (<i>Eam1105I</i>)	GACNNNNNGTC	9	9	0	1	1	8
<i>Anabaena flos-aquae</i>	J.P. Schouten	<i>AfIV</i> (<i>ScaI</i>)	AGTACT	5	5	1	0	0	9
<i>Arthrobacter protophormiae</i>	NEB #723	<i>ApoI</i> (<i>FsiI</i>)	R \uparrow AATTY	58	0	7	7	2	10
<i>Arthrobacter variabilis</i>	M.M. Wijdenbosch	<i>AvrBI</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	11
		<i>AvrBII</i> (<i>AvrII</i>)	C \uparrow CTAGG	2	2	2	0	0	11
Artificial construct	T.A. Bickle	<i>EcoDR2I</i>	TCANNNNNGTCG	Type I Enzyme				12	
Artificial construct	T.A. Bickle	<i>EcoDR3I</i>	TCANNNNNNNATCG	Type I Enzyme				12	
Artificial construct	T.A. Bickle	<i>EcoRD2I</i>	GAANNNNNR \uparrow TTC	Type I Enzyme				12	
Artificial construct	T.A. Bickle	<i>EcoRD3I</i>	GAANNNNNNNR \uparrow TTC	Type I Enzyme				12	
<i>Bacillus amyloliquefaciens</i> H	ATCC 49763	<i>M.BamHII</i>	GGATCC	Specific methylase				17	
<i>Bacillus caldolyticus</i>	Promega 77	<i>Bca77I</i> (<i>BeI</i>)	W \uparrow CCGGW	81	28	0	3	5	14
<i>Bacillus cereus</i> A	N.N. Sokolov	<i>BcuAI</i>	?	>20	?	>4	1	>6	15
<i>Bacillus cereus</i> RFL1247	A.A. Janulaitis	<i>Bce1247I</i> (<i>MwoI</i>)	GCNNNNNNNGC	347	391	25	21	34	16
<i>Bacillus polymyxa</i> A	N.N. Sokolov	<i>BpoAI</i>	?	>14	3	>2	2	1	17

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³						References
				λ	Ad2	SV40	ΦX	pBR		
<i>Bacillus pumilus</i>	NEB #711	<i>BpmI</i> (<i>GsuI</i>)	CTGGAG (16/14)	25	32	6	3	4	18	
<i>Bacillus pumilus</i> RFL1268	A.A. Janulaitis	<i>BpuI</i> 268I (<i>EcoNI</i>)	CCTNNNNNAGG	9	10	2	0	1	19	
<i>Bacillus</i> species 118	V.E. Repin	<i>BseI</i> 18I (<i>Cfr</i> 10I)	RCCGGY	61	40	1	0	7	20	
<i>Bacillus</i> species A11	D. Clark	<i>BscBI</i> (<i>NlaIV</i>)	GGN↑NCC	82	178	16	6	24	21	
<i>Bacillus</i> species APR91	D. Clark	<i>BscEI</i> (<i>BsePI</i>)	GCGCGC	6	52	0	1	0	21	
<i>Bacillus</i> species B21	S.K. Degtyarev	<i>BspB</i> 21	?	0	0	0	0	0	22	
<i>Bacillus</i> species JY391	D. Clark	<i>BscFI</i> (<i>MboI</i>)	GATC	116	87	8	0	22	21	
<i>Bacillus</i> species RFL143	A.A. Janulaitis	<i>Bsp</i> 143II (<i>HaeII</i>)	RGCGC↑Y	48	76	1	8	11	16	
<i>Bacillus</i> species RFL144	A.A. Janulaitis	<i>Bsp</i> 144I (<i>BamHI</i>)	GGATCC	5	3	1	0	1	16	
<i>Bacillus</i> species RFL146	A.A. Janulaitis	<i>Bsp</i> 146I (<i>ApaLI</i>)	GTGCAC	4	7	0	1	3	16	
<i>Bacillus</i> species RFL147	A.A. Janulaitis	<i>Bsp</i> 147I (<i>MboI</i>)	GATC	116	87	8	0	22	16	
<i>Bacillus</i> species RFL148	A.A. Janulaitis	<i>Bsp</i> 148I (<i>AsuII</i>)	TTCGAA	7	1	0	0	0	16	
<i>Bacillus sphaericus</i> 45	V.E. Repin	<i>Bsh</i> 45I (<i>HgiAI</i>)	GWGCW↑C	28	38	0	3	8	23	
<i>Bacillus sphaericus</i> RFL1260	A.A. Janulaitis	<i>Bsp</i> 1260I (<i>AvaII</i>)	GGWCC	35	73	6	1	8	16	
<i>Bacillus sphaericus</i> RFL1261	A.A. Janulaitis	<i>Bsp</i> 1261I (<i>HaeIII</i>)	GGCC	149	216	18	11	22	16	
<i>Bacillus stearothermophilus</i>	NEB 547	<i>BssKI</i> (<i>ScrFI</i>)	↑CCNGG	185	233	17	3	16	24	
<i>Bacillus stearothermophilus</i> 71	Promega #71	<i>Bst</i> 71I (<i>BbvI</i>)	GCAGC (8/12)	199	179	22	14	21	25	
<i>Bacillus stearothermophilus</i> AU891	D. Clark	<i>BsoCI</i> (<i>SaiI</i>)	GDGCHC	38	105	4	3	10	21	
<i>Bacillus stearothermophilus</i> BS	N.I. Matvienko	<i>BstBSI</i> (<i>SnaI</i>)	GTA↑TAC	3	3	0	0	1	26	
<i>Bacillus stearothermophilus</i> CP114	Z. Chen	<i>BsmSI</i> (<i>SpyI</i>)	CCWWGG	10	44	8	0	1	27	
<i>Bacillus stearothermophilus</i> CPW193	Z. Chen	<i>BsrBI</i>	GAGCGG (-3/-3)	0	0	0	0	0	27	
<i>Bacillus stearothermophilus</i> CPW5	Z. Chen	<i>BseHI</i> (<i>HindIII</i>)	AAGCTT	6	12	6	0	1	27	
<i>Bacillus stearothermophilus</i> H426	Z. Chen	<i>BsmHI</i> (<i>HaeII</i>)	RGCGCY	48	76	1	8	11	27	
<i>Bacillus stearothermophilus</i> JN1891	D. Clark	<i>BsoAI</i> (<i>EcoRV</i>)	GATATC	21	9	1	0	1	21	
<i>Bacillus stearothermophilus</i> JN2091	D. Clark	<i>BsoBI</i> (<i>AvaI</i>)	CYCGRG	8	40	0	1	1	21	
<i>Bacillus stearothermophilus</i> JN791	D. Clark	<i>BsoI</i> (<i>ScrFI</i>)	CCNGG	185	233	17	3	16	21	
<i>Bacillus stearothermophilus</i> OC391	D. Clark	<i>BsoEI</i> (<i>EcoNI</i>)	CCTNNNNNAGG	9	10	2	0	1	21	

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

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³				References	
				λ	Ad2	SV40	ΦX pBR		
<i>Micrococcus</i> species 23	V.E. Repin	<i>Msp23I</i> (<i>XbaI</i>)	TCTAGA	1	5	0	0	0	40
<i>Moraxella osloensis</i>	NEB #722	<i>Msp23II</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	40
<i>Moraxella</i> species B6	S.K. Degtyarev	<i>MspB6I</i>	?	62	35	5	7	7	41
<i>Mycoplasma</i> species	A.A. Janulaitis	<i>MunI</i> (<i>MfeI</i>)	C [†] AAITG	0	0	0	0	0	22
<i>Myxococcus xanthus</i> F18E	K. Izaki	<i>MxaI</i> (<i>SacI</i>)	GAG [†] CTC	8	4	4	1	0	42
<i>Nostoc linckia</i>	A.I. Melnik	<i>Nit387/II</i> (<i>AvaI</i>)	CYCGR [†] G	2	16	0	0	0	43
<i>Nostoc</i> species	PCC 7121	<i>Nit387/II</i> (<i>AvaII</i>)	GGWCC	8	40	0	1	1	44
<i>Phormidium ambiguum</i>	A. Podhajska	<i>Msp7121I</i> (<i>AsuI</i>)	GGNCC	35	73	6	1	8	44
<i>Porphyromonas gingivalis</i>	A. Progulsk-Fox	<i>PamI</i> (<i>MstI</i>)	TGC [†] GCA	74	164	11	2	15	45
<i>Pseudomonas aeruginosa</i> 4148	A. Solonin	<i>PamII</i> (<i>AcylI</i>)	GR [†] CGYC	15	17	0	1	4	46
<i>Pseudomonas aeruginosa</i> Q2	CAMB 2637	<i>M.P.gil</i>	*GATC	40	44	0	7	6	46
<i>Pseudomonas inequalis</i>	M.M. Wijdenbosch	<i>PaeHI</i> (<i>HgiIII</i>)	GRGCY [†] C	7	57	2	0	2	48
<i>Pseudomonas mendocini</i>	NEB 698	<i>PaePI</i> (<i>PstI</i>)	CTGCA [†] G	28	30	2	1	1	48
<i>Pseudomonas putida</i> RFL1253	A.A. Janulaitis	<i>PaeQI</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	49
<i>Rhizobium leguminosarum</i> 69	V.E. Repin	<i>PinAI</i> (<i>AgeI</i>)	A [†] CCGGT	13	5	0	0	0	50
<i>Rhizobium meliloti</i>	I.S. Andreeva	<i>PmeI</i>	GTTT [†] AAAC	2	1	0	0	0	51
<i>Rhizobium trifolii</i>	L.R. Lebedev	<i>Ppu1253I</i> (<i>AatII</i>)	GACGTC	10	3	0	1	1	16
<i>Rhodococcus</i> species SE1991	D. Clark	<i>Rte69I</i> (<i>Eco31I</i>)	GGTCTC	2	18	0	0	1	52
<i>Staphylococcus epidermidis</i>	CAMB 2635	<i>Rme21I</i> (<i>ClaI</i>)	ATCGAT	15	2	0	0	1	53
<i>Streptococcus salivarius</i> ssp thermophilus	L. Benbadis	<i>RtrI</i> (<i>SalI</i>)	G [†] TCGAC	2	3	0	0	1	54
<i>Streptococcus thermophilus</i> ST117	G.A. Somkuti	<i>RhcI</i> (<i>BspHI</i>)	TCATGA	8	3	2	3	4	21
<i>Streptomyces albus</i> 13	V.E. Repin	<i>SepI</i> (<i>AvaIII</i>)	ATGCA [†] T	14	9	3	0	0	55
		<i>SsII</i> (<i>EcoRII</i>)	CC [†] WGG	71	136	17	2	6	56
		<i>Stt117I</i> (<i>EcoRII</i>)	CC [†] WGG	71	136	17	2	6	57
		<i>Sat13I</i> (<i>PstI</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
<i>Streptomyces aureofaciens</i> 13	J. Muchova	<i>Sau</i> HI (<i>Sau</i> I)	CCTNAGG	2	7	0	0	0	59
<i>Streptomyces griseus</i>	V. Bouriotis	<i>Sgr</i> BI (<i>Sac</i> II)	CCGC↑GG	4	33	0	1	0	60
<i>Streptomyces lipmanii</i>	R.H. Baltz	<i>Sli</i> I	?	?	?	?	?	?	61
		<i>Sli</i> II	?	?	?	?	?	?	61
<i>Streptomyces niveus</i>	ATCC 19793	<i>Sni</i> I (<i>Eco</i> RII)	CC↑WGG	71	136	17	2	6	62
<i>Streptomyces scabies</i>	J.L. Schottel	<i>Ssb</i> I (<i>Hind</i> III)	A↑AGCTT	6	12	6	0	1	63
<i>Streptomyces species</i>	T.G. Simcox	<i>Srf</i> I	GCCC↑GGGC	0	1	0	0	0	64
<i>Streptomyces species</i>	V. Bouriotis	<i>Sse</i> AI (<i>Nar</i> I)	GG↑CGCC	1	20	0	2	4	65
<i>Streptovorticillium cinnamomeum</i>	Glaxo 2566C	<i>Sci</i> BI (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	66
<i>Synechococcus species</i> RF-1	J. Tu	<i>Ssp</i> RFI (<i>Asu</i> II)	TT↑CGAA	7	1	0	0	0	67
Unidentified bacterium RFL1243	A.A. Janulaitis	<i>Uba</i> 1243I (<i>Eco</i> RII)	CCWGG	71	136	17	2	6	16
Unidentified bacterium RFL1244	A.A. Janulaitis	<i>Uba</i> 1244I (<i>Sac</i> II)	CCGCGG	4	33	0	1	0	16
Unidentified bacterium RFL1245	A.A. Janulaitis	<i>Uba</i> 1245I (<i>Pvu</i> II)	CAGCTG	15	24	3	0	1	16
Unidentified bacterium RFL1246	A.A. Janulaitis	<i>Uba</i> 1246I (<i>Cla</i> I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1248	A.A. Janulaitis	<i>Uba</i> 1248I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1249	A.A. Janulaitis	<i>Uba</i> 1249I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1250	A.A. Janulaitis	<i>Uba</i> 1250I (<i>Bam</i> HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1256	A.A. Janulaitis	<i>Uba</i> 1256I (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1257	A.A. Janulaitis	<i>Uba</i> 1257I (<i>Cla</i> I)	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1258	A.A. Janulaitis	<i>Uba</i> 1258I (<i>Bam</i> HI)	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1259	A.A. Janulaitis	<i>Uba</i> 1259I (<i>Mbo</i> I)	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1262	A.A. Janulaitis	<i>Uba</i> 1262I (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1263	A.A. Janulaitis	<i>Uba</i> 1263I (<i>Hgi</i> JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1264	A.A. Janulaitis	<i>Uba</i> 1264I (<i>Hgi</i> JII)	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1265	A.A. Janulaitis	<i>Uba</i> 1265I (<i>Afl</i> II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1266	A.A. Janulaitis	<i>Uba</i> 1266I (<i>Afl</i> II)	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1267	A.A. Janulaitis	<i>Uba</i> 1267I (<i>Hpa</i> 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	<i>Uba1269I (BsmI)</i>	GAATGC	46	10	4	4	1	16
Unidentified bacterium RFL1271	A.A. Janulaitis	<i>Uba1271I (XhoI)</i>	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1272	A.A. Janulaitis	<i>Uba1272I (AvaII)</i>	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1275	A.A. Janulaitis	<i>Uba1275I (ClnI)</i>	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1276	A.A. Janulaitis	<i>Uba1276I (Ksp632I)</i>	CTCTTC	34	29	1	2	2	16
Unidentified bacterium RFL1278	A.A. Janulaitis	<i>Uba1278I (AvaII)</i>	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1279	A.A. Janulaitis	<i>Uba1279I (BspMII)</i>	TCCGGA	24	8	0	0	1	16
Unidentified bacterium RFL1280	A.A. Janulaitis	<i>Uba1280I (CauII)</i>	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1282	A.A. Janulaitis	<i>Uba1282I (BclI)</i>	TGATCA	8	5	1	0	0	16
Unidentified bacterium RFL1283	A.A. Janulaitis	<i>Uba1283I (BclI)</i>	TGATCA	8	5	1	0	0	16
Unidentified bacterium RFL1284	A.A. Janulaitis	<i>Uba1284I (EspI)</i>	GCTNAGC	6	8	1	0	0	16
Unidentified bacterium RFL1285	A.A. Janulaitis	<i>Uba1285I (McrI)</i>	CGRYCG	22	50	0	1	7	16
Unidentified bacterium RFL1286	A.A. Janulaitis	<i>Uba1286I (ClnI)</i>	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1287	A.A. Janulaitis	<i>Uba1287I (PstI)</i>	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1288	A.A. Janulaitis	<i>Uba1288I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1289	A.A. Janulaitis	<i>Uba1289I (EcoNI)</i>	CCTNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1290	A.A. Janulaitis	<i>Uba1290I (EcoNI)</i>	CCTNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1291	A.A. Janulaitis	<i>Uba1291I (BstEII)</i>	GGTNACC	13	10	0	0	0	16
Unidentified bacterium RFL1292	A.A. Janulaitis	<i>Uba1292I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1293	A.A. Janulaitis	<i>Uba1293I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1294	A.A. Janulaitis	<i>Uba1294I (SauI)</i>	CCTNAGG	2	7	0	0	0	16
		<i>Uba1294II (PstI)</i>	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1295	A.A. Janulaitis	<i>Uba1295I (ClnI)</i>	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1296	A.A. Janulaitis	<i>Uba1296I (PstI)</i>	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1297	A.A. Janulaitis	<i>Uba1297I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1298	A.A. Janulaitis	<i>Uba1298I (XhoI)</i>	CTGCAG	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	<i>Uba1299I (AflII)</i>	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1302	A.A. Janulaitis	<i>Uba1302I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1303	A.A. Janulaitis	<i>Uba1303I (McrI)</i>	CGRYCG	22	50	0	1	7	16
Unidentified bacterium RFL1304	A.A. Janulaitis	<i>Uba1304I (AvaII)</i>	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1305	A.A. Janulaitis	<i>Uba1305I (NotI)</i>	GGNNCC	82	178	16	6	24	16
Unidentified bacterium RFL1306	A.A. Janulaitis	<i>Uba1306I (SacI)</i>	CCGCGG	4	33	0	1	0	16
Unidentified bacterium RFL1307	A.A. Janulaitis	<i>Uba1307I (HgiII)</i>	GRGICY	7	57	2	0	2	16
Unidentified bacterium RFL1308	A.A. Janulaitis	<i>Uba1308I (EcoNI)</i>	CCTNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1309	A.A. Janulaitis	<i>Uba1309I (EcoNI)</i>	CCTNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1310	A.A. Janulaitis	<i>Uba1310I (EcoNI)</i>	CCTNNNNAGG	9	10	2	0	1	16
Unidentified bacterium RFL1311	A.A. Janulaitis	<i>Uba1311I (SylI)</i>	CCWWGG	10	44	8	0	1	16
Unidentified bacterium RFL1312	A.A. Janulaitis	<i>Uba1312I (AflII)</i>	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1313	A.A. Janulaitis	<i>Uba1313I (AflII)</i>	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1314	A.A. Janulaitis	<i>Uba1314I (AvaII)</i>	GGWCC	35	73	6	1	8	16
Unidentified bacterium RFL1315	A.A. Janulaitis	<i>Uba1315I (CtaI)</i>	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1316	A.A. Janulaitis	<i>Uba1316I (Eco31I)</i>	GGTCTC	2	18	0	0	1	16
Unidentified bacterium RFL1317	A.A. Janulaitis	<i>Uba1317I (MboI)</i>	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1318	A.A. Janulaitis	<i>Uba1318I (CauII)</i>	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1319	A.A. Janulaitis	<i>Uba1319I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1320	A.A. Janulaitis	<i>Uba1320I (EspI)</i>	GCTNAGC	6	8	1	0	0	16
Unidentified bacterium RFL1321	A.A. Janulaitis	<i>Uba1321I (FnuDII)</i>	CGCG	157	303	0	14	23	16
Unidentified bacterium RFL1322	A.A. Janulaitis	<i>Uba1322I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1323	A.A. Janulaitis	<i>Uba1323I (MboI)</i>	GATC	116	87	8	0	22	16
Unidentified bacterium RFL1324	A.A. Janulaitis	<i>Uba1324I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1325	A.A. Janulaitis	<i>Uba1325I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1326	A.A. Janulaitis	<i>Uba1326I (DraII)</i>	RGGNCCY	3	44	3	0	4	16
Unidentified bacterium RFL1327	A.A. Janulaitis	<i>Uba1327I (CfrI)</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	<i>Uba1328I (PstI)</i>	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1329	A.A. Janulaitis	<i>Uba1329I (HgiII)</i>	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1330	A.A. Janulaitis	<i>Uba1330I (HgiII)</i>	GRGCYC	7	57	2	0	2	16
Unidentified bacterium RFL1331	A.A. Janulaitis	<i>Uba1331I (AflI)</i>	CTTAAG	3	4	1	2	0	16
Unidentified bacterium RFL1332	A.A. Janulaitis	<i>Uba1332I (SauI)</i>	CCTNAGG	2	7	0	0	0	16
Unidentified bacterium RFL1333	A.A. Janulaitis	<i>Uba1333I (SauI)</i>	CCTNAGG	2	7	0	0	0	16
Unidentified bacterium RFL1334	A.A. Janulaitis	<i>Uba1334I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1335	A.A. Janulaitis	<i>Uba1335I (XhoI)</i>	CTCGAG	1	6	0	1	0	16
Unidentified bacterium RFL1336	A.A. Janulaitis	<i>Uba1336I (HaeIII)</i>	GGCC	149	216	18	11	22	16
Unidentified bacterium RFL1337	A.A. Janulaitis	<i>Uba1337I (PstI)</i>	CTGCAG	28	30	2	1	1	16
Unidentified bacterium RFL1338	A.A. Janulaitis	<i>Uba1338I (HpaII)</i>	CCGG	328	171	1	5	26	16
Unidentified bacterium RFL1339	A.A. Janulaitis	<i>Uba1339I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1342	A.A. Janulaitis	<i>Uba1342I (ClnI)</i>	ATCGAT	15	2	0	0	1	16
Unidentified bacterium RFL1343	A.A. Janulaitis	<i>Uba1343I (Eco31I)</i>	GGTCTC	2	18	0	0	1	16
Unidentified bacterium RFL1346	A.A. Janulaitis	<i>Uba1346I (BamHI)</i>	GGATCC	5	3	1	0	1	16
Unidentified bacterium RFL1347	A.A. Janulaitis	<i>Uba1347I (CauII)</i>	CCSGG	114	97	0	1	10	16
Unidentified bacterium RFL1353	A.A. Janulaitis	<i>Uba1353I (AvaIII)</i>	ATGCAT	14	9	3	0	0	16
<i>Vibrio parahaemolyticus</i> 1307	T. Shimada	<i>VpaK11I (AvaII)</i>	GGWCC	35	73	6	1	8	68
<i>Vibrio parahaemolyticus</i> 4387-61	T. Shimada	<i>VpaK32I (SapI)</i>	GCTCTTC	10	7	0	1	1	69
<i>Vibrio parahaemolyticus</i> Takikawa 13	T. Shimada	<i>VpaK15I (AsuI)</i>	GGNCC	74	164	11	2	15	68

FOOTNOTES

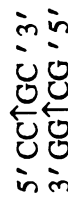
1. When two enzymes recognize the same sequence, i.e., are isoschizomers, the prototype (i.e., the first example isolated) is indicated in parentheses.
2. Recognition sequences are written from 5' → 3', only one strand being given, and the point of cleavage is indicated by an arrow (↑). When no arrow appears, the precise cleavage site has not been determined. For example, C↑GATCG is an abbreviation for

$$\begin{array}{l} 5' \text{ C}\uparrow\text{G A T C G } 3' \\ 3' \text{ G C T A G}\uparrow\text{C } 5' \end{array}$$

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



AcI CCGC(-2/-2) indicates cleavage as shown below



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

* A is N⁶-methyladenosine. C is C⁵-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 ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
Enzyme	Recognition sequence ²	Me site ³							
<i>Cfr</i> AI	GCANNNNNNNGTGG			<i>Ava</i> I		CTYCGRG		ABEIKLMNOPRSUVX	
<i>Eco</i> AI	GAGNNNNNNGTCA	2(6),-3(6)			<i>Eco</i> 88I	CTYCGRG		AW	
<i>Eco</i> BI	TGANNNNNNNGTCT	3(6),-4(6)			<i>Nsp</i> III	CTYCGRG		F	
<i>Eco</i> DI	TTANNNNNNNGTCY			<i>Ava</i> II		GTGWCC		P	
<i>Eco</i> DR2I	TCANNNNNNNGTCG				<i>Eco</i> 47I	GTGWCC		ABEIKMNPRESX	
<i>Eco</i> DR3I	TCANNNNNNNGTATCG				<i>Sin</i> I	GTGWCC	4(5)	FOU	
<i>Eco</i> DXXI	TCANNNNNNNGRTTC			<i>Ava</i> III		ATGCAT		LRSV	
<i>Eco</i> EI	GAGNNNNNNGTATGC				<i>Eco</i> T22I	ATGCA \uparrow T		KOU	
<i>Eco</i> KI	AACNNNNNNGTGC	2(6),-3(6)			<i>Mph</i> 1103I	ATGCA \uparrow T		F	
<i>Eco</i> R124I	GAANNNNNNNGTTCG				<i>Nsi</i> I	ATGCA \uparrow T		BELMNRSVX	
<i>Eco</i> R124/3I	GAANNNNNNNGTTCG	-3(6)		<i>Avr</i> II		A \uparrow TGCAT		F	
<i>Eco</i> RD2I	GAANNNNNNNGRTTC				<i>Ppu</i> 10I	CTCTAGG		N	
<i>Eco</i> RD3I	GAANNNNNNNGRTTC				<i>Bln</i> I	CTCTAGG		AK	
<i>Sty</i> SBI	GAGNNNNNNGRTAYG	2(6),-4(6)		<i>Bae</i> I		ACNNNNNGTAYC			
<i>Sty</i> SJI	GAGNNNNNNGTRC			<i>Bal</i> I		TGG \uparrow CCA	4(5)	AIKRSVX	
<i>Sty</i> SPI	AACNNNNNNGTRC	2(6),-3(6)			<i>Msc</i> I	TGG \uparrow CCA		BNU	
<i>Sty</i> SQI	AACNNNNNNGRTAYG			<i>Bam</i> HI		G \uparrow TATCC	5(4)	ABEFHIKLMNOPQRSUVWX	
					<i>Bst</i> I	G \uparrow TATCC		P	
				<i>Bbu</i> I		GCAGC(8/12)	2(5),-2(5)	EINX	
					<i>Bst</i> 71I	GCAGC(8/12)		R	
				<i>Bbu</i> II		GAAGAC(2/6)			
					<i>Bbs</i> I	GAAGAC(2/6)		N	
				<i>Bcc</i> I		CCATC			
				<i>Bce</i> II		ACGGC(12/13)			
				<i>Bcg</i> I ⁶		GCANNNNNNTCG(12/10)		N	
				<i>Bcl</i> I		T \uparrow GATCA		ABEFILMNOPRSUVX	
					<i>Bsi</i> QI	T \uparrow GATCA		AW	
					<i>Fba</i> I	T \uparrow GATCA		K	
				<i>Bet</i> I		WTCCGGW			
				<i>Bgl</i> I		GCCNNNN \uparrow NGGC		ABEFHILMNOPQRSUVWX	
				<i>Bgl</i> II		A \uparrow GATCT		ABEFHIKLMNOPQRSUVWX	
				<i>Bin</i> I		GGATC(4/5)			
					<i>Alu</i> I	GGATC(4/5)		NSU	
				<i>Bpu</i> 10I		CCTNAGC(-5/-2)			
				<i>Bsa</i> AI		YAC \uparrow GTR		N	
				<i>Bsa</i> BI		GATNN \uparrow NNATC		N	
					<i>Bsi</i> BI	GATNN \uparrow NNATC		AW	
					<i>Mam</i> I	GATNN \uparrow NNATC		M	
<i>Aat</i> II	GACGT \uparrow C			<i>Bse</i> PI		GCGCGC			
<i>Acc</i> I	CT \uparrow MKAC				<i>Bss</i> III	G \uparrow CGCGC		BELMNOQRUVX	
<i>Acc</i> II	CCGC(-3/-1)			<i>Bsg</i> I		GTGCAG(16/14)		N	
<i>Acy</i> I	GR \uparrow CGYC			<i>Bsi</i> I		CTCGTG(-5/-1)			
	<i>Bbi</i> II			<i>Bsi</i> YI		CCNNNN \uparrow NNGG		AMUW	
	<i>Bsa</i> HI				<i>Bsl</i> I	CCNNNN \uparrow NNGG		N	
	<i>Hin</i> II			<i>Bsm</i> I		GAATGC(1/-1)		ELMNOSUVX	
<i>Afl</i> II	C \uparrow TAAAG				<i>Bac</i> CI	GAATGC(1/-1)		W	
	<i>Bfr</i> I			<i>Bam</i> AI		GTCTC(1/5)		NU	
	<i>Esp</i> 4I				<i>Alu</i> 26I	GTCTC(1/5)		FR	
<i>Afl</i> III	A \uparrow CRYGT			<i>Bsp</i> GI		CTGGAC			
<i>Age</i> I	A \uparrow CCGGT			<i>Bsp</i> HI		T \uparrow CATGA		NSU	
<i>Aha</i> III	TTT \uparrow AAA			<i>Bsp</i> MI		ACTGC(4/8)		NU	
	<i>Dra</i> I			<i>Bsp</i> MII		T \uparrow CCGGA			
<i>Alu</i> I	AG \uparrow CT	3(5)			<i>Acc</i> III	T \uparrow CCGGA		AEKQRV	
<i>Alu</i> NI	CAGNN \uparrow CTG			<i>Bse</i> AI		T \uparrow CCGGA		M	
<i>Apa</i> I	GGGCC \uparrow C	4(5)		<i>Bsi</i> MI		T \uparrow CCGGA		AW	
	<i>Bsp</i> 120I			<i>Bsp</i> EI		T \uparrow CCGGA		NS	
<i>Apa</i> BI	GCANNNNN \uparrow TGC			<i>Kpn</i> 2I		T \uparrow CCGGA		F	
<i>Apa</i> LI	G \uparrow TGCAC			<i>Mro</i> I		T \uparrow CCGGA		MOU	
	<i>Alu</i> 44I				<i>Bsr</i> I	ACTGG(1/-1)		N	
	<i>Sno</i> I			<i>Bsr</i> BI		GAGCGG(-3/-3)			
<i>Asc</i> I	GG \uparrow CGCGCC			<i>Bst</i> EII		G \uparrow TNACC		BEHLMNOPRSUVX	
<i>Asu</i> I	G \uparrow GNCC				<i>Bst</i> PI	G \uparrow TNACC		K	
	<i>Bsi</i> ZI			<i>Eco</i> 91I		G \uparrow TNACC		F	
	<i>Cfr</i> 13I			<i>Eco</i> 65I		G \uparrow TNACC		AK	
	<i>Sau</i> 96I					CCANNNNN \uparrow TGG		BEKLMNOQRSUVX	
<i>Asu</i> II	TT \uparrow CGAA			<i>Bst</i> XI		GCN \uparrow NGC			
	<i>Bsi</i> CI			<i>Cac</i> 8I		CC \uparrow SGG			
	<i>Bsp</i> 119I			<i>Cau</i> II		CC \uparrow SGG			
	<i>Bst</i> BI				<i>Bcn</i> I	CC \uparrow SGG	2(4)	AFK	
	<i>Csp</i> 45I				<i>Nci</i> I	CC \uparrow SGG		BELMNOSUVWX	
	<i>Lsp</i> I			<i>Cfr</i> I		Y \uparrow GGCCR	4(5)		
	<i>Nsp</i> V				<i>Eae</i> I	Y \uparrow GGCCR	4(5)	EKLMNSUVX	
	<i>Sfu</i> I			<i>Cfr</i> 10I		R \uparrow CCGGY	2(5)	AFKMNOU	

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source	Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Cla</i> I	<i>Bsr</i> FI	R↑CCGGY		N	<i>Hha</i> I		GCG↑C	2(5)	ABEKNOPRSUX
		AT↑CGAT	5(6)	ABKMNPPQRSVX		<i>Cfo</i> I	GCG↑C		BILMRSV
	<i>Ban</i> III	AT↑CGAT		OU		<i>Hin</i> 6I	G↑CCG		F
	<i>Bse</i> I	AT↑CGAT		L		<i>Hin</i> P11	G↑CCG		NSX
	<i>Bsi</i> XI	AT↑CGAT		AW		<i>Hind</i> II	GTY↑RAC	5(6)	EM
	<i>Bsp</i> 106I	AT↑CGAT		E			<i>Hinc</i> II	GTY↑RAC	
	<i>Bsp</i> DI	AT↑CGAT		N	<i>Hind</i> III	ATAGCTT	1(6)	ABEFHIKLNOPQRSUVWX	
	<i>Bsu</i> 15I	AT↑CGAT		F	<i>Hinf</i> I	G↑ANTC		ABEFHIKLNOPQRSUVWX	
<i>Cvi</i> JI		RG↑CY	3(5)		<i>Hpa</i> I	GTT↑AAC	5(6)	ABEFHIKLNOPQRSUVX	
<i>Cvi</i> RI		TG↑CA	4(6)		<i>Hpa</i> II	C↑CCG	2(5)	ABEFLMNOPQRSUVX	
<i>Dde</i> I		CT↑NAG	1(5)	BEILMNOPRUVX	<i>Hap</i> II	C↑CCG	2(5)	IK	
<i>Dpn</i> I*		GA↑TC		ABEILMNRSUVX		<i>Msp</i> I	C↑CCG	1(5)	ABEFHIKLNOPQRSUVWX
<i>Dra</i> II		RG↑GNCCY		M	<i>Hph</i> I	GGTGA(8/7)	-2(5)	NSUVX	
	<i>Eco</i> O109I	RG↑GNCCY		AEFKLNOSUVX	<i>Kpn</i> I	GGTAC↑C	4(6)	ABEFHIKLNOPQRSUVX	
	<i>Pas</i> I	RGGNCT↑CY		I	<i>Acc</i> 65I	G↑GTACC		FNR	
<i>Dra</i> III		CACNNN↑GTG		EMNSUX	<i>Asp</i> 718I	G↑GTACC		M	
<i>Drd</i> I		GACNNNN↑NNGTC		N	<i>Kap</i> 632I	CTCTTC(1/4)		M	
<i>Drd</i> II		GAACCA				<i>Eam</i> 1104I	CTCTTC(1/4)		F
<i>Dsa</i> I		CTCRYGG		M	<i>Ear</i> I	CTCTTC(1/4)		N	
<i>Eam</i> 1105I		GACNNN↑NNGTC		FN	<i>Mae</i> I	C↑TAG		M	
<i>Eci</i> I		TCCGCC				<i>Bfa</i> I	C↑TAG		N
<i>Eco</i> 31I		GGTCTC(1/5)		F	<i>Rma</i> I	C↑TAG		N	
	<i>Bsa</i> I	GGTCTC(1/5)		N	<i>Mae</i> II	A↑CCGT		M	
<i>Eco</i> 47III			ABFKLMNORU	<i>Mae</i> III		↑GTNAC		M	
<i>Eco</i> 57I		CTGAAG(16/14)	5(6),5(6)	FN	<i>Mbo</i> I ⁷	↑GATC		BEFIKNPQRSVX	
<i>Eco</i> NI		CCTNN↑NNGG		NSU	+	<i>Bsp</i> 143I	↑GATC	F	
<i>Eco</i> RI		G↑AATC	3(6)	ABEFHIKLNOPQRSUVWX	<i>Dpn</i> II	↑GATC	2(6)	NU	
<i>Eco</i> RII ⁶		↑CCWGG	2(5)	BEOSUV	<i>Nde</i> II	↑GATC		BM	
+	<i>Apy</i> I	CCTWGG		M	+	<i>Sau</i> 3AI	↑GATC	4(5)	ABEIKLNOPQRSUVX
+	<i>Bsi</i> LI	CCTWGG		AW	<i>Mbo</i> II	GAAGA(8/7)	5(6)	BFIKNOPQRSUVX	
+	<i>Bst</i> NI	CCTWGG	2(4)	ENXS		<i>Mcr</i> I	CGRY↑CG		M
+	<i>Bst</i> OI	CCTWGG		R	<i>Bsi</i> EI	CGRY↑CG		ANW	
+	<i>Mva</i> I	CCTWGG	2(4)	AFKMOU		<i>Mfe</i> I	C↑AATTG		
<i>Eco</i> RV		GAT↑ATC	2(6)	ABEHKLNOPQRSUVWX	<i>Mun</i> I	C↑AATTG	3(6)	FN	
	<i>Eco</i> 32I	GAT↑ATC		F		<i>Mlu</i> I	A↑CCGCT		ABEFHIKLNOPQRSUVX
<i>Esp</i> I		GC↑TNAGC		U	<i>Mly</i> I	GACTC(5/5)			
	<i>Bpu</i> 1102I	GC↑TNAGC		EFN	<i>Mme</i> I	TCCRAC(20/18)			
	<i>Cei</i> II	GC↑TNAGC		ALM	<i>Mni</i> I	CCTC(7/6)		ENSUX	
<i>Esp</i> 3I		CCTCTC(1/5)		FN	<i>Mse</i> I	T↑TAA		NSU	
<i>Fau</i> I		CCCGC(4/6)			<i>Msi</i> I	CAYNNNNRTG			
<i>Fin</i> I		GTCCC				TGCTGCA		X	
<i>Fnu</i> DII		CG↑CG			<i>Avi</i> II	TGCTGCA		M	
	<i>Acc</i> II	CG↑CG		AKQVX		<i>Fdi</i> II	TGCTGCA		U
	<i>Bsp</i> 50I	CG↑CG		EF	<i>Fsp</i> I	TGCTGCA		NSU	
	<i>Bst</i> UI	CG↑CG		NSU	<i>Mwo</i> I	GCNNNNN↑NNGC			
	<i>Mun</i> I	CG↑CG		M		<i>Bsp</i> WI	GCNNNNN↑NNGC		M
	<i>Tha</i> I	CG↑CG		BI	<i>Nae</i> I	GCC↑GGC		AEKLMNOUVX	
<i>Fnu</i> 4HI		GC↑NGC		N		<i>Ngo</i> MI	G↑CCGGC		N
<i>Fok</i> I		GGATG(9/13)	3(6),-2(6)	AEFIKMNURVX	<i>Nar</i> I	GG↑CCGC		BEMNOPRSUVX	
<i>Fse</i> I		GGCCGG↑CC				<i>Bbe</i> I	GGCG↑C		AK
<i>Fsi</i> I		R↑AATTY			<i>Ehe</i> I	GGCG↑CC		FOU	
	<i>Apo</i> I	R↑AATTY		N	<i>Kas</i> I	G↑CCGCC		N	
<i>Gdi</i> II		YGGCCG(-5/-1)			<i>Nco</i> I	C↑CATGG		ABEFHIKLNOPQRSUVWX	
<i>Gsu</i> I		CTGGAG(16/14)		FN		<i>Nde</i> I	CA↑TATG	4(6)	BEFKLMNPSUVX
	<i>Bpm</i> I	CTGGAG(16/14)		N	<i>Nhe</i> I	G↑CTAGC		ABEKLMPQRSUVX	
<i>Hae</i> I		WGG↑CCW			<i>Nla</i> III	CATG↑		NSU	
<i>Hae</i> II		RGCGC↑Y		ABEIKLNOPRSUVX	<i>Nla</i> IV	GGN↑NCC		NSU	
	<i>Bsp</i> 143II	RGCGC↑Y		F	<i>Bsc</i> BI	GGN↑NCC		AI	
<i>Hae</i> III		GG↑CC	3(5)	ABHIKLNOPQRSUVX		<i>Not</i> I	GC↑GGCCGC		ABEFHIKLNOPQRSUVWX
	<i>Bsh</i> I	GG↑CC		W	<i>Nru</i> I	TG↑TCGA		ABEIKLNOPQRSUVX	
	<i>Bsu</i> RI	GG↑CC	3(5)	F	<i>Bsp</i> 68I	TG↑TCGA		F	
	<i>Pal</i> I	GG↑CC		EPV		<i>Spo</i> I	TG↑TCGA		R
<i>Hga</i> I		GACGC(5/10)		NSUX	<i>Nsp</i> I	RCATG↑Y		AKMU	
<i>Hgi</i> AI		GWGCW↑C		NX		<i>Nsp</i> BII	CMG↑CKG		U
	<i>Alw</i> 21I	GWGCW↑C		F	<i>Pac</i> I	T↑AAT↑TAA		N	
	<i>Asp</i> HI	GWGCW↑C		M	<i>Pfl</i> 1108I	TG↑TAG			
<i>Hgi</i> CI		G↑GYRCC			<i>Pfl</i> MI	CCANNNN↑NTGG		NSU	
	<i>Ban</i> I	G↑GYRCC		EIMNOPRSUVX	<i>Van</i> 91I	CCANNNN↑NTGG		FM	
	<i>Eco</i> 64I	G↑GYRCC		F		<i>Ple</i> I	GAGTC(4/5)		NU
<i>Hgi</i> EII		ACCNNNNNNGGT			<i>Pma</i> CI	CAC↑GTG		AK	
<i>Hgi</i> JII		GRGCY↑C				<i>Bbr</i> PI	CAC↑GTG		M
	<i>Ban</i> II	GRGCY↑C		BEIKLNOPRSUVX	<i>Eco</i> 72I	CAC↑GTG		F	
	<i>Eco</i> 24I	GRGCY↑C		F	<i>Pml</i> I	CAC↑GTG		NU	

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source	Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>PmeI</i>		GTTTAAAC		N	<i>TfiI</i>		GTAWTC		N
<i>PvuMI</i>		RG ⁺ GWCCY		NSU	<i>Tsp45I</i>		GTSAC		
	<i>Psp5II</i>	RG ⁺ GWCCY		F	<i>TspEI</i>		AATT		
<i>PshAI</i>		GACNN ⁺ NNGTC		K	<i>Tth111I</i>		GACN ⁺ NNGTC		AEIKNPRUVX
<i>PstI</i>		CTGCA ⁺ TG	5(6)	ABEFHIKLMNOPQRSUVWX		<i>AspI</i>	GACN ⁺ NNGTC		M
<i>PvuI</i>		CGAT ⁺ TCG		ABEFKLMNOPQRSUVX	<i>Tth111II</i>		CAARCA(11/9)		
	<i>BspCI</i>	CGAT ⁺ TCG		E	<i>VspI</i>		AT ⁺ TAAT		FKR
	<i>XorII</i>	CGAT ⁺ TCG		BS		<i>AseI</i>	AT ⁺ TAAT		NSU
<i>PvuII</i>		CAG ⁺ CTG	4(4)	ABEFKLMNOPQRSUVWX		<i>AsnI</i>	AT ⁺ TAAT		M
<i>RleAI</i>		CCACA(12/9)			<i>XbaI</i>		T ⁺ CTAGA	6(6)	ABEFHIKLMNOPQRSUVWX
<i>RsaI</i>		GT ⁺ AC		ABEILMNOPQRSUVWX	<i>XcmI</i>		CCANN ⁺ NN ⁺ NNNTGG		NU
	<i>AfaI</i>	GT ⁺ AC		K	<i>XhoI</i>		C ⁺ TCGAG		ABEFHIKLMNOPQRSUVX
	<i>Csp6I</i>	GT ⁺ AC		F		<i>CcrI</i>	C ⁺ TCGAG		X
<i>RarII</i>		CG ⁺ GWCCG		ABMNSUX		<i>PaeR7I</i>	C ⁺ TCGAG	5(6)	NSX
	<i>CpoI</i>	CG ⁺ GWCCG		AFK	<i>XhoII</i>		R ⁺ GATCY		EMRVX
	<i>CspI</i>	CG ⁺ GWCCG		EORV		<i>BstYI</i>	R ⁺ GATCY		BNU
<i>SacI</i>		GAGCT ⁺ T		AEIKLMNOPQRSUVWX		<i>MflI</i>	R ⁺ GATCY		AK
	<i>Ecl136II</i>	GAG ⁺ TCT		FN	<i>XmaIII</i>		C ⁺ TGCCG	4(5)	BE
	<i>SstI</i>	GAGCT ⁺ T		BS		<i>BstZI</i>	C ⁺ TGCCG		R
<i>SacII</i>		CCGCTGG		EILNOPRSUVX		<i>EagI</i>	C ⁺ TGCCG		NS
	<i>Cfr42I</i>	CCGCTGG		F		<i>EcoXI</i>	C ⁺ TGCCG		M
	<i>KspI</i>	CCGCTGG		M		<i>Eco52I</i>	C ⁺ TGCCG		AFKORU
	<i>SstII</i>	CCGCTGG		BS	<i>XmnI</i>		GAANN ⁺ TNNTTC		ENUX
<i>SalI</i>		G ⁺ TTCGAC		ABEFHIKLMNOPQRSUVX		<i>Asp700I</i>	GAANN ⁺ TNNTTC		M
<i>SapI</i>		GCTCTTC(1/4)							
<i>SauI</i>		CC ⁺ TNAGG		M					
	<i>AxyI</i>	CC ⁺ TNAGG		V					
	<i>Bau36I</i>	CC ⁺ TNAGG		NRS					
	<i>CunI</i>	CC ⁺ TNAGG		BS					
	<i>Eco81I</i>	CC ⁺ TNAGG		AFKOU					
	<i>MstII</i>	CC ⁺ TNAGG		EX					
<i>Scal</i>		AGT ⁺ ACT		ABEFIKLMNOPRSUVX					
<i>ScrFI</i>		CC ⁺ TGG		EMNOSUVX					
	<i>DeaV</i>	TCCNGG		M					
<i>SduI</i>		GDGCH ⁺ T		F					
	<i>BmyI</i>	GDGCH ⁺ T		M					
	<i>Bsp1286I</i>	GDGCH ⁺ T		AKNRUX					
<i>SecI</i>		C ⁺ TNNGG							
	<i>BsaJI</i>	C ⁺ TNNGG		N					
<i>SfaNI</i>		GCATC(5/9)		NSUX					
<i>SfeI</i>		C ⁺ TRYAG							
	<i>SfcI</i>	C ⁺ TRYAG		N					
<i>SfiI</i>		GGCCN ⁺ NN ⁺ TGGCC		ABEILMNOPQRSUVX					
<i>SgrAI</i>		CR ⁺ TCCGGYG		M					
<i>SmaI</i>		CCC ⁺ TGGG	2(4)	ABEFIKLMNOPQRSUVWX					
	<i>Cfr9I</i>	C ⁺ TCCGGG	2(4)	FOU					
	<i>PspAI</i>	C ⁺ TCCGGG		E					
	<i>XmaI</i>	C ⁺ TCCGGG		EINRSUVX					
<i>SnaI</i>		GTATAC							
	<i>Bst1107I</i>	GTA ⁺ TAC		FMN					
<i>SnaBI</i>		TACTGTA		AEIKLMNRSVX					
	<i>Eco106I</i>	TACTGTA		FOU					
<i>SpeI</i>		A ⁺ CTAGT		ABEIKLMNORSUVWX					
<i>SphI</i>		GCATG ⁺ T		ABEHIKLMNOPQRSUX					
	<i>BbuI</i>	GCATG ⁺ T		RV					
	<i>PaeI</i>	GCATG ⁺ T		F					
<i>SplI</i>		C ⁺ TGTACG		AK					
	<i>BsiWI</i>	C ⁺ TGTACG		AMNUW					
	<i>PfI23II</i>	C ⁺ TGTACG		F					
<i>SrfI</i>		GCCCTGGGC		E					
<i>Sse8387I</i>		CCTGCA ⁺ TGG		AK					
<i>SspI</i>		AAT ⁺ ATT		ABEFKLMNORUVX					
<i>StuI</i>		AGG ⁺ TCT		ABEIKLMNPRSVX					
	<i>AatI</i>	AGG ⁺ TCT		OU					
	<i>Eco147I</i>	AGG ⁺ TCT		F					
<i>StyI</i>		C ⁺ TWWGG		BEMNRSUVX					
	<i>Eco130I</i>	C ⁺ TWWGG		FU					
	<i>EcoT14I</i>	C ⁺ TWWGG		AK					
<i>SwaI</i>		ATTT ⁺ TAAAT		M					
<i>TaqI</i>		TTCGA	4(6)	ABEFILMNOPQRSUVWX					
	<i>TthHB8I</i>	TTCGA	4(6)	AK					
<i>TaqII⁸</i>		GACCGA(11/9) CACCCA(11/9)							

FOOTNOTES

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

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 CACCA.