

Restriction enzymes and their isoschizomers

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INTRODUCTION

Since the last compilation of restriction enzymes, (1) 442 new entries have been added including 13 new specificities. A complete list of these new enzymes can be found in Table I. With the growing size of the restriction enzyme database and the recognition that the most widespread use of the information is as a database for computer programs predicting restriction enzyme cleavage patterns, Table II contains a listing of all prototype restriction enzymes (Types I, II and III) together with their commercially available isoschizomers. It should be noted that an alternative compilation of these enzymes has recently been produced (3).

During the previous year the names of several restriction enzymes have been changed by the original authors.

Old Name	Prototype	Recognition Sequence	New Name
<i>HalB6I</i>	<i>EcoRI</i>	GIAATTC	<i>HalI</i>
<i>HalB6II</i>	<i>PstI</i>	CTGCAIG	<i>HalII</i>
<i>NgoAIII</i>	<i>SacII</i>	CCGCIGG	<i>NgoFIII</i>
<i>NgoAIV</i>	<i>NaeI</i>	GICCGGC	<i>NgoFIV</i>
<i>PglB4I</i>	<i>Clal</i>	ATICGAT	<i>PglI</i>
<i>Spil</i>		CCGC	<i>AcI</i>
<i>SsrB6I</i>	<i>HpaI</i>	GTTIAAC	<i>SsrI</i>
<i>Uba1102I</i>	<i>EspI</i>	GCITNAGC	<i>Bpu1102I</i>
<i>Uba1103I</i>	<i>AvaIII</i>	ATGCAIT	<i>Mph1103I</i>
<i>Uba1103II</i>	<i>DpnI</i>	GATC	<i>Mph1103II</i>
<i>Uba1104I</i>	<i>Ksp632I</i>	CTCTTC (1/5)	<i>Eam1104I</i>
<i>Uba1105I</i>		GACNNNINNGTC	<i>Eam1105I</i>
<i>Uba1106I</i>	<i>PpuMI</i>	RGGWCCY	<i>Mlu1106I</i>
<i>Uba1108I</i>		TCGTAG	<i>Pfl1108I</i>
<i>Uba1I</i>	<i>PpuMI</i>	RGIGWCCY	<i>Pfl27I</i>

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. 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.

In forming Table I 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 (4).

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TABLE 1

Microorganism

Source

Enzyme¹Sequence²

Number of Cleavage Sites³

λ Ad2 SV40 φX pBR

References

Acetobacter pasteurianus	IFO 13752	<i>ApaORI (EcoRII)</i>	CC↑WGG	71	136	17	2	6	26	
Acetobacter pasteurianus B	J. Grones	<i>ApaBI</i>	GCANNNNNTTGC	34	20	5	2	2	19	
Acetobacter pasteurianus C	J. Grones	<i>ApaCI (BamHI)</i>	GGATCC	5	3	1	0	1	18	
Acetobacter pasteurianus D	J. Grones	<i>ApaDI</i>	?	>20	?	?	?	?	19	
Acidiphilium species 15	K. Inagaki	<i>Asp15I (XhoI)</i>	CTCGAG	1	6	0	1	0	21	
Acidiphilium species 17	K. Inagaki	<i>Asp17I (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 22	K. Inagaki	<i>Asp22I (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 1H	K. Inagaki	<i>Asp1HI (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 2H	K. Inagaki	<i>Asp2HI (EcoRII)</i>	CCWGG	71	136	17	2	6	21	
Acidiphilium species 5H	K. Inagaki	<i>Asp5HI (SphI)</i>	GCAATGC	6	8	2	0	1	21	
Acidiphilium species 6H	K. Inagaki	<i>Asp6HI (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 8H	K. Inagaki	<i>Asp8HI (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 14H	K. Inagaki	<i>Asp14HI (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 16H	K. Inagaki	<i>Asp16HI (RsaI)</i>	GTAC	113	83	12	11	3	21	
Acidiphilium species 17H	K. Inagaki	<i>Asp17HI (RsaI)</i>	GTAC	113	83	12	11	3	21	
Acidiphilium species 18H	K. Inagaki	<i>Asp18HI (RsaI)</i>	GTAC	113	83	12	11	3	21	
Acidiphilium species 21H	K. Inagaki	<i>Asp21HI (XhoII)</i>	RGATCY	21	22	3	0	8	21	
Acidiphilium species 26H	K. Inagaki	<i>Asp26HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	22	
Acidiphilium species 27H	K. Inagaki	<i>Asp27HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	22	
Acidiphilium species 29H	K. Inagaki	<i>Asp29HI (RsaI)</i>	GTAC	113	83	12	11	3	21	
Acidiphilium species 32H	K. Inagaki	<i>Asp32HI (SacI)</i>	CCGGGG	4	33	0	1	0	21	
Acidiphilium species 35H	K. Inagaki	<i>Asp35HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	23	
Acidiphilium species 36H	K. Inagaki	<i>Asp36HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	22	
Acidiphilium species 40H	K. Inagaki	<i>Asp40HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	22	
Acidiphilium species 50H	K. Inagaki	<i>Asp50HI (BsmI)</i>	GAATGC (1/-1)	46	10	4	4	1	22	

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	Φ X	pBR			
Acidiphilium species 22M	K. Inagaki	Afa22MI (PvuII)	CGA↑TCG	3	7	0	0	1	1	20	
Acidiphilium species 16R	K. Inagaki	Afa16RI (PvuII)	CGA↑TCG	3	7	0	0	1	1	20	
Acidiphilium facilis 24R	K. Inagaki	Afa24RI (NaeI)	GCCGGC	1	13	1	0	4	4	21	
Agrobacterium tumefaciens RFL1	A.A. Janulaitis	Aru1II (BamHI)	GGATCC	5	3	1	0	1	1	28	
Arthrobacter citreus	NEB 577	AccI	CCGC (-2/-2)	516	582	11	36	67	67	54	
Arthrobacter species	NEB #688	AscI	GG↑CGCGCC	2	2	0	0	0	0	45	
Bacillus alvei B	N.N. Sokolov	BavBI (PvuII)	CAG↑CTG	15	24	3	0	1	1	74	
Bacillus alvei C	N.N. Sokolov	BavBII (AsuI)	G↑GNCC	74	164	11	2	15	15	65	
Bacillus brevis B	N.N. Sokolov	BavCI (ClaI)	ATCGAT	15	2	0	0	1	1	71	
Bacillus circulans A	N.N. Sokolov	BbvBI (HgiCI)	G↑GYRCC	25	57	1	3	9	9	64	
Bacillus circulans B	N.N. Sokolov	BcIAI	?	>18	?	?	?	?	?	69	
		BcIBI (ClaI)	ATCGAT	15	2	0	0	1	1	73	
		BcIBII	?	>20	?	?	?	>5	>5	70	
Bacillus megaterium B78	Z. Chen	BmeBI (PstI)	CTGCAG	28	30	2	1	1	1	7	
Bacillus species	V. Bourtois	BssAI (Cfr10I)	R↑CCGGY	61	40	1	0	7	7	59	
Bacillus species	D. Clark	BsrWI (SphI)	C↑GTACG	1	4	0	2	0	0	9,10	
Bacillus species	D. Clark	BsrXI (ClaI)	AT↑CGAT	15	2	0	0	1	1	9	
Bacillus species	D. Clark	BsrZI (AsuI)	G↑GNCC	74	164	11	2	15	15	9	
Bacillus species	NEB 606	BsII (BsrYI)	CCNNNNN↑NNGG	176	216	10	19	20	20	11	
Bacillus species	N.N. Sokolov	BspFI (MboI)	↑GATC	116	87	8	0	22	22	66	
Bacillus species	N.N. Sokolov	BspJI (MboI)	↑GATC	116	87	8	0	22	22	72	
Bacillus species		BspJII (ClaI)	AT↑CGAT	15	2	0	0	1	1	68	
Bacillus species	G. Elgar	BssXI (Fnu4HI)	GCNGC	380	411	24	31	42	42	14	
Bacillus species 1720	S.K. Degtyarev	Bsp1720I (EspI)	GC↑TNAGC	6	8	1	0	0	0	12	
Bacillus species 2G	D. Clark	BscCI (BsmI)	GAATGC	46	10	4	4	1	1	9	

Microorganism	Source	Enzyme ¹	Sequence ²	λ	Ad2	SV40	Φ X	pBR	References
<i>Bacillus</i> species C1	T.G. Simcox	<i>Bsp</i> CI (<i>Pvu</i> II)	CGAT ⁺ CG	3	7	0	0	1	63
<i>Bacillus</i> species E13	D. Clark	<i>Bsc</i> DI (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	9
<i>Bacillus</i> species RFL71	A.A. Janulaitis	<i>Bsp</i> 71I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	27
<i>Bacillus</i> species RFL125	A.A. Janulaitis	<i>Bsp</i> 125I (<i>Cla</i> II)	ATCGAT	15	2	0	0	1	27
<i>Bacillus</i> species RFL126	A.A. Janulaitis	<i>Bsp</i> 126I (<i>Cla</i> II)	ATCGAT	15	2	0	0	1	27
<i>Bacillus</i> species RFL127	A.A. Janulaitis	<i>Bsp</i> 127I (<i>Cla</i> II)	ATCGAT	15	2	0	0	1	27
<i>Bacillus</i> species RFL128	A.A. Janulaitis	<i>Bsp</i> 128I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	27
<i>Bacillus</i> species RFL129	A.A. Janulaitis	<i>Bsp</i> 129I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	27
<i>Bacillus</i> species RFL130	A.A. Janulaitis	<i>Bsp</i> 130I (<i>Bam</i> HI)	GGATCC	5	3	1	0	1	27
<i>Bacillus</i> species RFL131	A.A. Janulaitis	<i>Bsp</i> 131I (<i>Bam</i> HI)	GGATCC	5	3	1	0	1	27
<i>Bacillus</i> species RFL132	A.A. Janulaitis	<i>Bsp</i> 132I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	27
<i>Bacillus</i> species RFL133	A.A. Janulaitis	<i>Bsp</i> 133I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	27
<i>Bacillus</i> species RFL135	A.A. Janulaitis	<i>Bsp</i> 135I (<i>Mbo</i> I)	GATC	116	87	8	0	22	27
<i>Bacillus</i> species RFL136	A.A. Janulaitis	<i>Bsp</i> 136I (<i>Mbo</i> I)	GATC	116	87	8	0	22	27
<i>Bacillus</i> species RFL137	A.A. Janulaitis	<i>Bsp</i> 137I (<i>Hae</i> III)	GGCC	149	216	18	11	22	27
<i>Bacillus</i> species RFL138	A.A. Janulaitis	<i>Bsp</i> 138I (<i>Mbo</i> I)	GATC	116	87	8	0	22	27
<i>Bacillus</i> species RFL139	A.A. Janulaitis	<i>Bsp</i> 139I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	27
<i>Bacillus</i> species RFL140	A.A. Janulaitis	<i>Bsp</i> 140I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	27
<i>Bacillus</i> species RFL141	A.A. Janulaitis	<i>Bsp</i> 141I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	27
<i>Bacillus</i> species RFL142	A.A. Janulaitis	<i>Bsp</i> 142I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	27
<i>Bacillus</i> species RFL143	A.A. Janulaitis	<i>Bsp</i> 143I (<i>Mbo</i> I)	GATC	116	87	8	0	22	27
<i>Bacillus</i> species cy53	Z. Chen	<i>Bsp</i> F53I (<i>Ava</i> II)	GGWCC	35	73	6	1	8	7
<i>Bacillus</i> species cy105	Z. Chen	<i>Bsp</i> F105I (<i>Cau</i> II)	CCSCG	114	97	0	1	10	7
<i>Bacillus</i> species cy145	Z. Chen	<i>Bsp</i> 145I (<i>Cla</i> II)	ATCGAT	15	2	0	0	1	7
<i>Bacillus</i> species cy268	Z. Chen	<i>Bsp</i> 268I (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	7

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	ϕ X	pBR			
<i>Bacillus species cy317</i>	Z. Chen	<i>Bsp317I (EcoRII)</i>	CCWGG	71	136	17	2	6	7		
<i>Bacillus sphaericus</i>	NEB 659	<i>BaeI</i>	ACNNNGTAYC	10	5	0	1	0	85		
<i>Bacillus sphaericus</i>	P.C. Shaw	<i>BspI (MboI)</i>	GATC	116	87	8	0	22	41		
<i>Bacillus sphaericus</i> 1894	KCTC 1188	<i>Bsp1894I (AvaI)</i>	G \uparrow GNCC	74	164	11	2	15	61		
<i>Bacillus sphaericus</i> DC1	D. Clark	<i>BshII (ScaI)</i>	AGTACT	5	5	0	0	1	9		
<i>Bacillus sphaericus</i> DC2	D. Clark	<i>BshLI (EcoRV)</i>	GATATC	21	9	1	0	1	9		
<i>Bacillus sphaericus</i> DC3	D. Clark	<i>BshMI (HpaII)</i>	CCGG	328	171	1	5	26	9		
<i>Bacillus stearothermophilus</i> 1	V.E. Repin	<i>BsrII (EcoRII)</i>	CCWGG	71	136	17	2	6	58		
<i>Bacillus stearothermophilus</i> 1274	Z. Chen	<i>Bsr1274I (MboI)</i>	GATC	116	87	8	0	22	7		
<i>Bacillus stearothermophilus</i> 28	S.K. Degtyarev	<i>Bsr28I (ClaI)</i>	ATCGAT	15	2	0	0	1	57,83		
<i>Bacillus stearothermophilus</i> 29	V.E. Repin	<i>Bsr29I (SmaI)</i>	CCTNAGG	2	7	0	0	0	62		
<i>Bacillus stearothermophilus</i> 30	V.E. Repin	<i>Bsr30I (SmaI)</i>	CCTNAGG	2	7	0	0	0	62		
<i>Bacillus stearothermophilus</i> 77	V.E. Repin	<i>Bsr77I (BclI)</i>	TGATCA	8	5	1	0	0	56		
<i>Bacillus stearothermophilus</i> C1825	Z. Chen	<i>BsrCI (ClaI)</i>	ATCGAT	15	2	0	0	1	7		
<i>Bacillus stearothermophilus</i> C34	Z. Chen	<i>BsaCI (ScaFI)</i>	CCNCG	185	233	17	3	16	7		
<i>Bacillus stearothermophilus</i> CPW1	Z. Chen	<i>BsaNI (EcoRII)</i>	CCWGG	71	136	17	2	6	6		
<i>Bacillus stearothermophilus</i> CPW7	Z. Chen	<i>BsrAI (AvaII)</i>	GGWCC	35	73	6	1	8	6		
<i>Bacillus stearothermophilus</i> CPW8	Z. Chen	<i>BsaRI (HaeIII)</i>	GGCC	149	216	18	11	22	6		
		<i>BsaRII</i>	?	?	?	?	?	?	6		
<i>Bacillus stearothermophilus</i> CPW9	Z. Chen	<i>BsrEI (Ksp632I)</i>	CTCTTC	34	29	1	2	2	6		
<i>Bacillus stearothermophilus</i> CPW11	Z. Chen	<i>BsaHI (AcyI)</i>	GRCGYC	40	44	0	7	6	6		
<i>Bacillus stearothermophilus</i> CPW13	Z. Chen	<i>BsrMI (MboI)</i>	GATC	116	87	8	0	22	6		
<i>Bacillus stearothermophilus</i> CPW16	Z. Chen	<i>BsrFI (Cfr10I)</i>	RCCGGY	61	40	1	0	7	6		
<i>Bacillus stearothermophilus</i> CPW19	Z. Chen	<i>BsrSI (BsrI)</i>	ACTGG	110	86	11	9	19	7		
<i>Bacillus stearothermophilus</i> CPW59	Z. Chen	<i>BsaQI (PstI)</i>	CTGCAG	28	30	2	1	1	6		

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	ΦX	pBR			
<i>Bacillus stearothermophilus</i> CPWI	Z. Chen	<i>Bsa</i> NI (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	6		
<i>Bacillus stearothermophilus</i> D47	Z. Chen	<i>Bsa</i> SI (<i>Asu</i> I)	GGNCC	74	164	11	2	15	7		
<i>Bacillus stearothermophilus</i> D144	Z. Chen	<i>Bsa</i> DI (<i>Bam</i> HI)	GGATCC	5	3	1	0	1	7		
<i>Bacillus stearothermophilus</i> EJ04	Z. Chen	<i>Bsa</i> EI (<i>Nla</i> IV)	GGNNCC	82	178	16	6	24	7		
<i>Bacillus stearothermophilus</i> F272	Z. Chen	<i>Bsa</i> FI (<i>Afl</i> II)	CTTAAG	3	4	1	2	0	7		
<i>Bacillus stearothermophilus</i> G426	Z. Chen	<i>Bsa</i> GI (<i>Hgi</i> AI)	GWGCWC	28	38	0	3	8	7		
<i>Bacillus stearothermophilus</i> K524	Z. Chen	<i>Bsa</i> KI (<i>Hpa</i> I)	GTTAAC	14	6	4	3	0	7		
<i>Bacillus stearothermophilus</i> L170	Z. Chen	<i>Bsa</i> LI (<i>Alu</i> I)	AGCT	143	158	34	24	16	7		
<i>Bacillus stearothermophilus</i> M293	Z. Chen	<i>Bsa</i> MI (<i>Bsm</i> I)	GAATGC	46	10	4	4	1	7		
<i>Bacillus stearothermophilus</i> O22	Z. Chen	<i>Bsa</i> OI (<i>Mcr</i> I)	CGRYCG	22	50	0	1	7	7		
<i>Bacillus stearothermophilus</i> V018	Z. Chen	<i>Bsa</i> VI (<i>Bbv</i> II)	GAAGAC	24	27	3	3	3	7		
<i>Bacteroides caecae</i>	NEB 669	<i>Bcc</i> I	CCATC	145	62	10	12	9	46		
<i>Bacteroides fragilis</i>	NEB 668	<i>Bfa</i> I (<i>Mae</i> I)	C↑TAG	13	54	12	3	5	46		
<i>Bacteroides fragilis</i>	NCTC 11155	<i>Bfr</i> AI (<i>Cla</i> I)	ATCGAT	15	2	0	0	1	9		
<i>Brevibacterium acetyllicum</i>	NEB 678	<i>Beh</i> I	W↑CCGGW	81	28	0	3	5	85		
<i>Brevibacterium immotum</i>	G.G. Prikhodko	<i>Bim</i> I (<i>Asu</i> II)	TT↑CGAA	7	1	0	0	0	45,55		
<i>Brevibacterium linens</i>	IAM 1902	<i>Bin</i> I (<i>Avr</i> II)	C↑CTAGG	2	2	2	0	0	82		
<i>Caulobacter species</i> RFL2	A.A. Janulaitis	<i>Cas</i> 2I (<i>Pvu</i> I)	CGATCG	3	7	0	0	1	27		
<i>Chlorella</i> strain NC64A (XZ-6E)	J.L. Van Etten	<i>Cvi</i> RI	TG↑CA*	273	206	36	18	21	76,78		
		<i>Cvi</i> RII (<i>Rsa</i> I)	G↑TAC	113	83	12	11	3	78		
<i>Citrobacter freundii</i> RFL55	A.A. Janulaitis	<i>Cjf</i> 55I (<i>Cjf</i> I)	YGGCCR	39	70	0	2	6	27		
<i>Citrobacter freundii</i> RFL56	A.A. Janulaitis	<i>Cjf</i> 56I (<i>Eco</i> 3II)	GGTCTC	2	18	0	0	1	27		
<i>Citrobacter freundii</i> RFL57	A.A. Janulaitis	<i>Cjf</i> 57I (<i>Bsp</i> MI)	TCCGGA	24	8	0	0	1	27		
<i>Citrobacter freundii</i> RFL58	A.A. Janulaitis	<i>Cjf</i> 58I (<i>Eco</i> RII)	CCWGG	71	136	17	2	6	27		
<i>Citrobacter freundii</i> RFL92	A.A. Janulaitis	<i>Cjf</i> 92I (<i>Afl</i> III)	CTTAAG	3	4	1	2	0	32		

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	Φ X	pBR			
Comamonas testosteroni RFL1	A.A. Janulaitis	CteII (SacII)	CCGCCG	4	33	0	1	0	27		
Enterobacter aerogenes RFL2	A.A. Janulaitis	Eae2I (XhoI)	CTCGAG	1	6	0	1	0	27		
Enterobacter cloacae RFL1	A.A. Janulaitis	EclII (SacII)	CCGCCG	4	33	0	1	0	27		
Enterobacter species RFL3	A.A. Janulaitis	Ese3I (SacII)	CCGCCG	4	33	0	1	0	27		
Erwinia species RFL16	A.A. Janulaitis	Esp16I (Esp3I)	CGTCTC	14	21	0	0	1	27		
Erwinia species RFL21	A.A. Janulaitis	Esp21I (HgiCI)	GGYRCC	25	57	1	3	9	27		
Erwinia species RFL23	A.A. Janulaitis	Esp23I (Esp3I)	CGTCTC	14	21	0	0	1	27		
Erwinia species RFL24	A.A. Janulaitis	Esp24I (EcoRII)	CCWGG	71	136	17	2	6	27		
Erwinia species RFL25	A.A. Janulaitis	Esp25I (HgiCI)	GGYRCC	25	57	1	3	9	27		
Escherichia coli H1	L.I. Glaitman	EcoHI (CauII)	CCSGTG	114	97	0	1	10	17		
Escherichia coli O128	H. Matsumoto	EcoO128I (BstEII)	GtGTNACC	13	10	0	0	0	43		
Escherichia coli RFL112	A.A. Janulaitis	Eco112I (Eco57I)	CTGAAG	40	23	3	0	2	27		
Escherichia coli RFL151	A.A. Janulaitis	Eco151I (SacII)	CCGCCG	4	33	0	1	0	27		
Escherichia coli RFL152	A.A. Janulaitis	Eco152I (BsePI)	GCGCGC	6	52	0	1	0	27		
Escherichia coli RFL249	A.A. Janulaitis	Eco249I (HgiII)	GRGCYC	7	57	2	0	2	27		
Escherichia coli RFL254	A.A. Janulaitis	Eco254I (EcoRII)	CCWGG	71	136	17	2	6	27		
Escherichia coli RFL255	A.A. Janulaitis	Eco255I (ScaI)	AGTACT	5	5	0	0	1	29		
Escherichia coli RFL256	A.A. Janulaitis	Eco256I (EcoRII)	CCWGG	71	136	17	2	6	27		
Frankia species	NEB 685	FsII	RtAATTY	58	29	7	7	2	45		
Geodermatophilus obscurus	Glaxo 2323C	GobAI (SmaI)	AGGCCT	6	11	7	1	0	13		
Klebsiella planticola RFL79	A.A. Janulaitis	KpI79I (PvuII)	CGATCG	3	7	0	0	1	27		
Klebsiella pneumoniae 378	Y.P. Zernov	Kpn378I (SacII)	CCGCtGG	4	33	0	1	0	84		
Klebsiella pneumoniae RFL19	A.A. Janulaitis	Kpn19I (SacII)	CCGCCG	4	33	0	1	0	27		
Kluyvera ascorbata	NEB 593	KasI (NarI)	GtGGCC	1	20	0	2	4	52		
Lactobacillus casei	N.N. Sokolov	Lcal	?	>12	?	?	?	1	67		

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	Φ X	pBR			
Micromonospora aurantiaca	NRRL B16091	<i>MauAI</i> (<i>NaeI</i>)	GCCGGC	1	13	1	0	4	4	39	
Micromonospora carbonacea	NRRL 2997	<i>McaAI</i> (<i>NarI</i>)	GGCGCC	1	20	0	2	4	4	13	
Micromonospora chalybea sp. izumensis		ATCC 21561	<i>MizI</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	139	
Micromonospora halophytica	NRRL 3097	<i>MhaI</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	0	39	
Micromonospora saitanica	NRRL B16084	<i>MsaI</i> (<i>NarI</i>)	GGCGCC	1	20	0	2	4	4	39	
Micromonospora scalbiana sp. sporogenes	NRRL B16086	<i>MscAI</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	0	39	
Nocardia carnea C-212	Y. Li	<i>NcrI</i> (<i>BglII</i>)	A↑GATCT	6	11	0	0	0	0	42	
Nostoc species	ATCC 29132	<i>Nsp29132I</i> (<i>AsuII</i>)	TTTCGAA	7	1	0	0	0	0	47	
		<i>Nsp29132II</i> (<i>BamHI</i>)	GGATCC	5	3	1	0	1	1	47,79	
Phormidium lapideum	H. Ochiai	<i>PlaI</i> (<i>HaeIII</i>)	GG↑CC	149	216	18	11	22	22	50	
		<i>PlaII</i> (<i>AsuII</i>)	TT↑CGAA	7	1	0	0	0	0	50	
		<i>Pvu84I</i> (<i>PvuII</i>)	CGATCG	3	7	0	0	1	1	12	
		<i>Pvu84II</i> (<i>PvuII</i>)	CAG↑CTG	15	24	3	0	1	1	12	
Proteus vulgaris 84	S.K. Degtyarev	<i>PaeCI</i> (<i>SphI</i>)	GCATGC	6	8	2	0	1	1	13	
Pseudomonas aeruginosa	NRC 5003	<i>Pae7I</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	0	27	
Pseudomonas aeruginosa RFL7	A.A. Janulaitis	<i>Pae8I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL8	A.A. Janulaitis	<i>Pae9I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL9	A.A. Janulaitis	<i>Pae14I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL14	A.A. Janulaitis	<i>Pae15I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL15	A.A. Janulaitis	<i>Pae17I</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	0	27	
Pseudomonas aeruginosa RFL17	A.A. Janulaitis	<i>Pae22I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL22	A.A. Janulaitis	<i>Pae24I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL24	A.A. Janulaitis	<i>Pae25I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL25	A.A. Janulaitis	<i>Pae26I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	1	27	
Pseudomonas aeruginosa RFL26	A.A. Janulaitis	<i>Pae36I</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	0	27	

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³						References
				λ	Ad2	SV40	ΦX	pBR		
<i>Pseudomonas aeruginosa</i> RFL39	A.A. Janulaitis	<i>Pae39I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas aeruginosa</i> RFL40	A.A. Janulaitis	<i>Pae40I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas aeruginosa</i> RFL41	A.A. Janulaitis	<i>Pae41I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas aeruginosa</i> RFL42	A.A. Janulaitis	<i>Pae42I</i> (<i>SacII</i>)	CCGCCG	4	33	0	1	0	27	
<i>Pseudomonas aeruginosa</i> RFL43	A.A. Janulaitis	<i>Pae43I</i> (<i>SacII</i>)	CCGCCG	4	33	0	1	0	27	
<i>Pseudomonas aeruginosa</i> RFL44	A.A. Janulaitis	<i>Pae44I</i> (<i>SacII</i>)	CCGCCG	4	33	0	1	0	27	
<i>Pseudomonas alcaligenes</i>	NEB 585	<i>PacI</i>	TTAATTTAA	0	1	0	0	0	51	
<i>Pseudomonas fluorescens</i>	CAMB 2619	<i>PTK1</i> (<i>HaeIII</i>)	GG↑CC	149	216	18	11	22	48	
<i>Pseudomonas fluorescens</i> RFL18	A.A. Janulaitis	<i>PT118I</i> (<i>SacI</i>)	GAGCTC	2	16	0	0	0	27	
<i>Pseudomonas fluorescens</i> RFL19	A.A. Janulaitis	<i>PT119I</i> (<i>AvaII</i>)	GGWCC	35	73	6	1	8	27	
<i>Pseudomonas fluorescens</i> RFL23	A.A. Janulaitis	<i>PT123I</i> (<i>ApaI</i>)	GTGCAC	4	7	0	1	3	27	
		<i>PT123II</i> (<i>SplI</i>)	CGTACG	1	4	0	2	0	30	
<i>Pseudomonas fluorescens</i> RFL37	A.A. Janulaitis	<i>PT137I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas fluorescens</i> RFL67	A.A. Janulaitis	<i>PT167I</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	27	
<i>Pseudomonas fluoroviolaceus</i> RFL16	A.A. Janulaitis	<i>PT116I</i> (<i>EcoRV</i>)	GATATC	21	9	1	0	1	27	
<i>Pseudomonas fragi</i> RFL12	A.A. Janulaitis	<i>PT112I</i> (<i>ApaI</i>)	GTGCAC	4	7	0	1	3	27	
<i>Pseudomonas glathei</i> RFL34	A.A. Janulaitis	<i>Pgl34I</i> (<i>PmaCI</i>)	CACGTG	3	10	0	0	0	27	
<i>Pseudomonas indigofera</i>	ATCC 14036	<i>Pini</i> (<i>ScaI</i>)	AGTACT	5	5	0	0	1	39	
<i>Pseudomonas lindbergii</i>	ATCC 31099	<i>PilI</i> (<i>ApaI</i>)	GTGCAC	4	7	0	1	3	39	
<i>Pseudomonas medicaginis</i> RFL35	A.A. Janulaitis	<i>Pme35I</i> (<i>HpaII</i>)	CCGG	328	171	1	5	26	27	
<i>Pseudomonas putida</i> A1	P. Adams	<i>PpuA1</i> (<i>SplI</i>)	C↑GTACG	1	4	0	2	0	49	
<i>Pseudomonas putida</i> RFL6	A.A. Janulaitis	<i>Ppu6I</i> (<i>BsaAI</i>)	YACGTR	14	22	0	2	1	27	
<i>Pseudomonas putida</i> RFL10	A.A. Janulaitis	<i>Ppu10I</i> (<i>AvaII</i>)	ATGCAT	14	9	3	0	0	27	
<i>Pseudomonas putida</i> RFL11	A.A. Janulaitis	<i>Ppu11I</i> (<i>BsaAI</i>)	YACGTR	14	22	0	2	1	27	
<i>Pseudomonas putida</i> RFL13	A.A. Janulaitis	<i>Ppu13I</i> (<i>SnaI</i>)	AGGCT	6	11	7	1	0	27	

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³						References
				λ	Ad2	SV40	ϕ X	pBR		
<i>Pseudomonas putida</i> RFL20	A.A. Janulaitis	<i>Ppu20I</i> (<i>HgiIII</i>)	GRGCYC	7	57	2	0	2	27	
<i>Pseudomonas putida</i> RFL21	A.A. Janulaitis	<i>Ppu21I</i> (<i>BsaAI</i>)	YACGTR	14	22	0	2	1	35	
<i>Pseudomonas</i> species	D. White	<i>PspAI</i> (<i>SmaI</i>)	CTCCGGG	3	12	0	0	0	80	
<i>Pseudomonas</i> species	D. Clark	<i>PspBI</i> (<i>PmaCI</i>)	CACGTG	3	10	0	0	0	9	
<i>Pseudomonas</i> species RFL3	A.A. Janulaitis	<i>Psp3I</i> (<i>PvuII</i>)	CAGCTG	15	24	3	0	1	27	
<i>Pseudomonas</i> species RFL4	A.A. Janulaitis	<i>Psp4I</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	27	
<i>Pseudomonas</i> species RFL5	A.A. Janulaitis	<i>Psp5I</i> (<i>PvuII</i>)	CAGCTG	15	24	3	0	1	37	
		<i>Psp5II</i> (<i>PpuMI</i>)	RGGWCCY	3	23	1	0	2	37	
<i>Pseudomonas</i> species RFL28	A.A. Janulaitis	<i>Psp28I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas</i> species RFL29	A.A. Janulaitis	<i>Psp29I</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	27	
<i>Pseudomonas</i> species RFL30	A.A. Janulaitis	<i>Psp30I</i> (<i>ApaI</i>)	GGGCCC	1	12	1	0	0	27	
<i>Pseudomonas</i> species RFL31	A.A. Janulaitis	<i>Psp31I</i> (<i>HgiII</i>)	GRGCYC	7	57	2	0	2	27	
<i>Pseudomonas</i> species RFL32	A.A. Janulaitis	<i>Psp32I</i> (<i>SalI</i>)	GTCGAC	2	3	0	0	1	27	
<i>Pseudomonas</i> species RFL33	A.A. Janulaitis	<i>Psp33I</i> (<i>SalI</i>)	GTCGAC	2	3	0	0	1	27	
<i>Pseudomonas</i> species RFL38	A.A. Janulaitis	<i>Psp38I</i> (<i>PmaCI</i>)	CACGTG	3	10	0	0	0	27	
<i>Pseudomonas</i> species RFL46	A.A. Janulaitis	<i>Psp46I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27	
<i>Pseudomonas</i> species RFL56	A.A. Janulaitis	<i>Psp56I</i> (<i>BanHI</i>)	GGATCC	5	3	1	0	1	34	
<i>Pseudomonas</i> species RFL89	A.A. Janulaitis	<i>Psp89I</i> (<i>SalI</i>)	GTCGAC	2	3	0	0	1	27	
<i>Rhodococcus capsulatum</i>	M.M. Wijdenbosch	<i>RcaI</i> (<i>BspHI</i>)	TTCATGA	8	3	2	3	4	81	
<i>Rhodococcus rhodochrous</i>	ATCC 4273	<i>Rrh4273I</i> (<i>SalI</i>)	GTCGAC	2	3	0	0	1	5	
<i>Rhodothermus marinus</i>	T. Tenkari	<i>RmaI</i> (<i>MaeI</i>)	CTTAG	13	54	12	3	5	60	
<i>Saccharopolyspora</i> species	NEB 597	<i>SapI</i>	GCTCTTC (1/4)	10	7	0	1	1	45	
<i>Staphylococcus aureus</i> RFL2	A.A. Janulaitis	<i>Sau2I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	27	
<i>Staphylococcus aureus</i> RFL5	A.A. Janulaitis	<i>Sau5I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	27	
<i>Staphylococcus aureus</i> RFL13	A.A. Janulaitis	<i>Sau13I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	36	

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	ΦX	pBR			
Staphylococcus aureus RFL14	A.A. Janulaitis	Sau14I (AsuI)	GGNCC	74	164	11	2	15	36		
Staphylococcus aureus RFL15	A.A. Janulaitis	Sau15I (MboI)	GATC	116	87	8	0	22	27		
Staphylococcus aureus RFL16	A.A. Janulaitis	Sau16I (EcoRII)	CCWGG	71	136	17	2	6	27		
Staphylococcus aureus RFL17	A.A. Janulaitis	Sau17I (AsuI)	GGNCC	74	164	11	2	15	27		
Staphylococcus warneri	B. Frey	SwaI	ATT↑AAAT	0	1	1	0	0	16		
Streptococcus faecium	NEB 674	SfiI	CTYRAG	17	29	4	5	6	53		
Streptococcus thermophilus strain 134 D.K.Y. Solaiman		Sth134I (HpaII)	C↑CGG	328	171	1	5	26	75		
Streptomyces bikiniensis JAM68	S.K. Degyarev	Sbi68I (XhoI)	C↑TCGAG	1	6	0	1	0	12		
Streptomyces corchorusii	ATCC 25444	ScoAI (PstI)	CTGCAG	28	30	2	1	1	13		
Streptomyces moderatus	DSM 40529	Smo40529I (NaeI)	GCCGGC	1	13	1	0	4	12		
Streptomyces olivochromogenes	S.K. Degyarev	Sol10179I (XhoI)	C↑TCGAG	1	6	0	1	0	12		
Streptomyces species 8387	Takara #8387	Sse8387I	CCTGCA↑GG	5	3	0	0	0	40		
Streptomyces takaoensis	ATCC 27649	StaI (SacII)	CCGCGG	4	33	0	1	0	39		
Streptomyces tanashiensis	ATCC 33159	StaAI (XhoI)	CTCGAG	1	6	0	1	0	13		
Synechococcus uniformis	M.M. Wijdenbosch	SunI (SplII)	C↑GTACG	1	4	0	2	0	81		
Synechocystis species	PCC 6308	SynI (AvaII)	GGWCC	35	73	6	1	8	15		
		SynII (XmnI)	GAANNNTTC	24	5	0	3	2	15		
Thermococcus litoralis	NEB 521	TliI (XhoI)	CTCGAG	1	6	0	1	0	45		
Thermophilic species	Z. Chen	TspAI (EcoRII)	CCWGG	71	136	17	2	6	8		
Thermus species strain 1	V.E. Repin	TspII (BsrI)	ACTGG (1/-1)	110	86	11	9	19	38		
Thiobacillus ferrooxidans AP19-3	K. Inagaki	TfeI	?	2	?	?	?	0	25		
Thiobacillus novellus	IFO 12443	TnoI	?	2	?	?	?	0	25		
Thiobacillus thiooxidans ON106	K. Inagaki	TtoI (SacII)	CCGCGG	4	33	0	1	0	24		
Thiobacillus versutus	IFO 14567	TveI	?	1	?	?	?	0	25		
Unidentified bacterium RFL4	A.A. Janulaitis	Uba4I (MboI)	GATC	116	87	8	0	22	27		

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³										References
				λ	Ad2	SV40	ΦX	pBR						
Unidentified bacterium RFL9	A.A. Janulaitis	<i>Uba9I (HaeII)</i>	GGCC	149	216	18	11	22	36					
Unidentified bacterium RFL11	A.A. Janulaitis	<i>Uba11I (EcoRII)</i>	CCWGG	71	136	17	2	6	36					
Unidentified bacterium RFL13	A.A. Janulaitis	<i>Uba13I (EcoRII)</i>	CCWGG	71	136	17	2	6	31					
Unidentified bacterium RFL17	A.A. Janulaitis	<i>Uba17I (SrfI)</i>	CCNGG	185	233	17	3	16	31					
Unidentified bacterium RFL19	A.A. Janulaitis	<i>Uba19I (BamHI)</i>	GGATCC	5	3	1	0	1	31					
Unidentified bacterium RFL20	A.A. Janulaitis	<i>Uba20I (EcoRII)</i>	CCWGG	71	136	17	2	6	31					
Unidentified bacterium RFL22	A.A. Janulaitis	<i>Uba22I (ClaI)</i>	ATCGAT	15	2	0	0	1	31					
Unidentified bacterium RFL24	A.A. Janulaitis	<i>Uba24I (ClaI)</i>	ATCGAT	15	2	0	0	1	31					
Unidentified bacterium RFL30	A.A. Janulaitis	<i>Uba30I (ClaI)</i>	ATCGAT	15	2	0	0	1	36					
Unidentified bacterium RFL31	A.A. Janulaitis	<i>Uba31I (BamHI)</i>	GGATCC	5	3	1	0	1	77					
Unidentified bacterium RFL34	A.A. Janulaitis	<i>Uba34I (ClaI)</i>	ATCGAT	15	2	0	0	1	77					
Unidentified bacterium RFL36	A.A. Janulaitis	<i>Uba36I (CfrI)</i>	YGGCCR	39	70	0	2	6	77					
Unidentified bacterium RFL38	A.A. Janulaitis	<i>Uba38I (BamHI)</i>	GGATCC	5	3	1	0	1	36					
Unidentified bacterium RFL39	A.A. Janulaitis	<i>Uba39I (HgiII)</i>	GRGCTC	7	57	2	0	2	77					
Unidentified bacterium RFL40	A.A. Janulaitis	<i>Uba40I (SnaI)</i>	AGGCCT	6	11	7	1	0	34					
Unidentified bacterium RFL41	A.A. Janulaitis	<i>Uba41I (CauII)</i>	CCSGG	114	97	0	1	10	34					
Unidentified bacterium RFL42	A.A. Janulaitis	<i>Uba42I (CauII)</i>	CCSGG	114	97	0	1	10	34					
Unidentified bacterium RFL43	A.A. Janulaitis	<i>Uba43I (ClaI)</i>	ATCGAT	15	2	0	0	1	34					
Unidentified bacterium RFL46	A.A. Janulaitis	<i>Uba46I (PstI)</i>	CTGCAG	28	30	2	1	1	27					
Unidentified bacterium RFL48	A.A. Janulaitis	<i>Uba48I (AvaII)</i>	GGWCC	35	73	6	1	8	27					
Unidentified bacterium RFL51	A.A. Janulaitis	<i>Uba51I (BamHI)</i>	GGATCC	5	3	1	0	1	27					
Unidentified bacterium RFL54	A.A. Janulaitis	<i>Uba54I (HaeII)</i>	GGCC	149	216	18	11	22	27					
Unidentified bacterium RFL57	A.A. Janulaitis	<i>Uba57I (HgiII)</i>	GRGCTC	7	57	2	0	2	27					
Unidentified bacterium RFL58	A.A. Janulaitis	<i>Uba58I (EcoRI)</i>	GAATTC	5	5	1	0	1	27					
Unidentified bacterium RFL59	A.A. Janulaitis	<i>Uba59I (MboI)</i>	GATC	116	87	8	0	22	27					

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³							References
				λ	Ad2	SV40	Φ X	pBR			
Unidentified bacterium RFL61	A.A. Janulaitis	<i>Uba61I (HaeIII)</i>	GGCC	149	216	18	11	22	27		
Unidentified bacterium RFL62	A.A. Janulaitis	<i>Uba62I (AvaII)</i>	GGWCC	35	73	6	1	8	27		
Unidentified bacterium RFL65	A.A. Janulaitis	<i>Uba65I (Eco31I)</i>	GGTCTC	2	18	0	0	1	27		
Unidentified bacterium RFL66	A.A. Janulaitis	<i>Uba66I (SacII)</i>	CCGCCGG	4	33	0	1	0	27		
Unidentified bacterium RFL69	A.A. Janulaitis	<i>Uba69I (BspI)</i>	GCGCGC	6	52	0	1	0	27		
Unidentified bacterium RFL71	A.A. Janulaitis	<i>Uba71I (PstI)</i>	CTGCAG	28	30	2	1	1	27		
Unidentified bacterium RFL72	A.A. Janulaitis	<i>Uba72I (PstI)</i>	CTGCAG	28	30	2	1	1	27		
Unidentified bacterium RFL76	A.A. Janulaitis	<i>Uba76I (KpnI)</i>	GGTACC	2	8	1	0	0	27		
Unidentified bacterium RFL77	A.A. Janulaitis	<i>Uba77I (SacII)</i>	CCGCGG	4	33	0	1	0	27		
Unidentified bacterium RFL81	A.A. Janulaitis	<i>Uba81I (EcoRII)</i>	CCWGG	71	136	17	2	6	27		
Unidentified bacterium RFL82	A.A. Janulaitis	<i>Uba82I (EcoRII)</i>	CCWGG	71	136	17	2	6	27		
Unidentified bacterium RFL83	A.A. Janulaitis	<i>Uba83I (HindIII)</i>	AAGCTT	6	12	6	0	1	27		
Unidentified bacterium RFL84	A.A. Janulaitis	<i>Uba84I (Eco31I)</i>	GGTCTC	2	18	0	0	1	27		
Unidentified bacterium RFL85	A.A. Janulaitis	<i>Uba85I (KpnI)</i>	GGTACC	2	8	1	0	0	27		
Unidentified bacterium RFL86	A.A. Janulaitis	<i>Uba86I (KpnI)</i>	GGTACC	2	8	1	0	0	27		
Unidentified bacterium RFL87	A.A. Janulaitis	<i>Uba87I (KpnI)</i>	GGTACC	2	8	1	0	0	27		
Unidentified bacterium RFL88	A.A. Janulaitis	<i>Uba88I (BamHI)</i>	GGATCC	5	3	1	0	1	27		
Unidentified bacterium RFL89	A.A. Janulaitis	<i>Uba89I (SalI)</i>	GTCGAC	2	3	0	0	1	27		
Unidentified bacterium RFL90	A.A. Janulaitis	<i>Uba90I (SacII)</i>	CCGCGG	4	33	0	1	0	27		
Unidentified bacterium RFL1093	A.A. Janulaitis	<i>Uba1093I (SacII)</i>	CCGCGG	4	33	0	1	0	27		
Unidentified bacterium RFL1094	A.A. Janulaitis	<i>Uba1094I (ScaI)</i>	AGTACT	5	5	0	0	1	27		
Unidentified bacterium RFL1095	A.A. Janulaitis	<i>Uba1095I (SacII)</i>	CCGCGG	4	33	0	1	0	27		
Unidentified bacterium RFL1096	A.A. Janulaitis	<i>Uba1096I (ClaI)</i>	ATCGAT	15	2	0	0	1	27		
Unidentified bacterium RFL1097	A.A. Janulaitis	<i>Uba1097I (HaeIII)</i>	GGCC	149	216	18	11	22	27		
Unidentified bacterium RFL1098	A.A. Janulaitis	<i>Uba1098I (BamHI)</i>	GGATCC	5	3	1	0	1	27		

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³						References
				λ	Ad2	SV40	Φ X	pBR		
Unidentified bacterium RFL1099	A.A. Janulaitis	<i>Uba1099I (AsuI)</i>	GGNCC	74	164	11	2	15	27	
Unidentified bacterium RFL1100	A.A. Janulaitis	<i>Uba1100I (CldI)</i>	ATCGAT	15	2	0	0	1	27	
Unidentified bacterium RFL1101	A.A. Janulaitis	<i>Uba1101I (MboI)</i>	GATC	116	87	8	0	22	27	
Unidentified bacterium RFL1108	A.A. Janulaitis	<i>Uba1108II (SacII)</i>	CCGCGG	4	33	0	1	0	27	
Unidentified bacterium RFL1109	A.A. Janulaitis	<i>Uba1109II (MboI)</i>	GATC	116	87	8	0	22	33	
Unidentified bacterium RFL1110	A.A. Janulaitis	<i>Uba1110II (EcoRV)</i>	GGATCC	5	3	1	0	1	27	
Unidentified bacterium RFL1111	A.A. Janulaitis	<i>Uba1111I (SacII)</i>	CCGCGG	4	33	0	1	0	27	
Unidentified bacterium RFL1112	A.A. Janulaitis	<i>Uba1112I (PstI)</i>	CTGCAG	28	30	2	1	1	27	
Unidentified bacterium RFL1113	A.A. Janulaitis	<i>Uba1113I (SacII)</i>	CCGCGG	4	33	0	1	0	27	
Unidentified bacterium RFL1114	A.A. Janulaitis	<i>Uba1114I (EcoRII)</i>	CCWGG	71	136	17	2	6	27	
Unidentified bacterium RFL1115	A.A. Janulaitis	<i>Uba1115I (PstI)</i>	CTGCAG	28	30	2	1	1	27	
Unidentified bacterium RFL1116	A.A. Janulaitis	<i>Uba1116I (PstI)</i>	CTGCAG	28	30	2	1	1	27	
Unidentified bacterium RFL1117	A.A. Janulaitis	<i>Uba1117I (NruI)</i>	TCGCGA	5	5	0	2	1	27	
Unidentified bacterium RFL1118	A.A. Janulaitis	<i>Uba1118I (EcoRII)</i>	CCWGG	71	136	17	2	6	27	
Unidentified bacterium RFL1119	A.A. Janulaitis	<i>Uba1119I (PstI)</i>	CTGCAG	28	30	2	1	1	27	
Unidentified bacterium RFL1120	A.A. Janulaitis	<i>Uba1120I (EcoRII)</i>	CCWGG	71	136	17	2	6	27	
Unidentified bacterium RFL1121	A.A. Janulaitis	<i>Uba1121I (EcoRII)</i>	CCWGG	71	136	17	2	6	27	
Unidentified bacterium RFL1122	A.A. Janulaitis	<i>Uba1122I (NaeI)</i>	GCCGGC	1	13	1	0	4	27	
Unidentified bacterium RFL1123	A.A. Janulaitis	<i>Uba1123I (PstI)</i>	CTGCAG	28	30	2	1	1	27	
Unidentified bacterium RFL1124	A.A. Janulaitis	<i>Uba1124I (HgiII)</i>	GRGCYC	7	57	2	0	2	27	
Unidentified bacterium RFL1125	A.A. Janulaitis	<i>Uba1125I (EcoRII)</i>	CCWGG	71	136	17	2	6	27	
Unidentified bacterium RFL1126	A.A. Janulaitis	<i>Uba1126I (SacII)</i>	CCGCGG	4	33	0	1	0	27	
Unidentified bacterium RFL1127	A.A. Janulaitis	<i>Uba1127I (HgiCI)</i>	GGYRCC	25	57	1	3	9	27	
Unidentified bacterium RFL1128	A.A. Janulaitis	<i>Uba1128I (HpaII)</i>	CCGG	328	171	1	5	26	27	
Unidentified bacterium RFL1129	A.A. Janulaitis	<i>Uba1129I (PvuII)</i>	CGATCG	3	7	0	0	1	27	

Microorganism	Source	Enzyme ¹	Sequence ²	λ	Ad2	SV40	Φ X	pBR	References
Unidentified bacterium RFL1130	A.A. Janulaitis	<i>Uba1130I (XhoI)</i>	CTCGAG	1	6	0	1	0	27
Unidentified bacterium RFL1131	A.A. Janulaitis	<i>Uba1131I (AvaII)</i>	GGWCC	35	73	6	1	8	27
Unidentified bacterium RFL1133	A.A. Janulaitis	<i>Uba1133I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1134	A.A. Janulaitis	<i>Uba1134I (AsuI)</i>	GGNCC	74	164	11	2	15	27
Unidentified bacterium RFL1136	A.A. Janulaitis	<i>Uba1136I (BspMI)</i>	TCCCGA	24	8	0	0	1	27
Unidentified bacterium RFL1137	A.A. Janulaitis	<i>Uba1137I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1138	A.A. Janulaitis	<i>Uba1138I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1139	A.A. Janulaitis	<i>Uba1139I (PvuI)</i>	CGATCG	3	7	0	0	1	27
Unidentified bacterium RFL1140	A.A. Janulaitis	<i>Uba1140I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1141	A.A. Janulaitis	<i>Uba1141I (HpaII)</i>	CCCG	328	171	1	5	26	27
Unidentified bacterium RFL1142	A.A. Janulaitis	<i>Uba1142I (HgiII)</i>	GRGCTC	7	57	2	0	2	27
Unidentified bacterium RFL1144	A.A. Janulaitis	<i>Uba1144I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1145	A.A. Janulaitis	<i>Uba1145I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1146	A.A. Janulaitis	<i>Uba1146I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1147	A.A. Janulaitis	<i>Uba1147I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1148	A.A. Janulaitis	<i>Uba1148I (XhoI)</i>	CTCGAG	1	6	0	1	0	27
Unidentified bacterium RFL1149	A.A. Janulaitis	<i>Uba1149I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1150	A.A. Janulaitis	<i>Uba1150I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1152	A.A. Janulaitis	<i>Uba1152I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1153	A.A. Janulaitis	<i>Uba1153I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1154	A.A. Janulaitis	<i>Uba1154I (XhoI)</i>	CTCGAG	1	6	0	1	0	27
Unidentified bacterium RFL1155	A.A. Janulaitis	<i>Uba1155I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1156	A.A. Janulaitis	<i>Uba1156I (ApaI)</i>	GGGCCC	1	12	1	0	0	27
Unidentified bacterium RFL1157	A.A. Janulaitis	<i>Uba1157I (ApaI)</i>	GGGCCC	1	12	1	0	0	27
Unidentified bacterium RFL1158	A.A. Janulaitis	<i>Uba1158I (ScaI)</i>	AGTACT	5	5	0	0	1	27

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³					References
				λ	Ad2	SV40	Φ X	pBR	
Unidentified bacterium RFL1159	A.A. Janulaitis	<i>Uba1159I (HgiII)</i>	GRGCTC	7	57	2	0	2	27
Unidentified bacterium RFL1160	A.A. Janulaitis	<i>Uba1160I (AsuI)</i>	GGNCC	74	164	11	2	15	27
Unidentified bacterium RFL1161	A.A. Janulaitis	<i>Uba1161II (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1162	A.A. Janulaitis	<i>Uba1162I (SphI)</i>	GCATGC	6	8	2	0	1	27
Unidentified bacterium RFL1163	A.A. Janulaitis	<i>Uba1163I (BamHI)</i>	GGATCC	5	3	1	0	1	27
Unidentified bacterium RFL1164	A.A. Janulaitis	<i>Uba1164I (AsuI)</i>	GGNCC	74	164	11	2	15	27
		<i>Uba1164II (HindIII)</i>	AAGCTT	6	12	6	0	1	27
Unidentified bacterium RFL1165	A.A. Janulaitis	<i>Uba1165I (ApaI)</i>	GGGCCC	1	12	1	0	0	27
Unidentified bacterium RFL1166	A.A. Janulaitis	<i>Uba1166I (XhoI)</i>	CTCGAG	1	6	0	1	0	27
Unidentified bacterium RFL1167	A.A. Janulaitis	<i>Uba1167I (BamHI)</i>	GGATCC	5	3	1	0	1	27
Unidentified bacterium RFL1168	A.A. Janulaitis	<i>Uba1168I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1169	A.A. Janulaitis	<i>Uba1169I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1170	A.A. Janulaitis	<i>Uba1170I (SmaI)</i>	AGGCCT	6	11	7	1	0	27
Unidentified bacterium RFL1171	A.A. Janulaitis	<i>Uba1171II (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1172	A.A. Janulaitis	<i>Uba1172I (BamHI)</i>	GGATCC	5	3	1	0	1	27
Unidentified bacterium RFL1173	A.A. Janulaitis	<i>Uba1173I (BamHI)</i>	GGATCC	5	3	1	0	1	27
Unidentified bacterium RFL1174	A.A. Janulaitis	<i>Uba1174I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1175	A.A. Janulaitis	<i>Uba1175I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1176	A.A. Janulaitis	<i>Uba1176I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1177	A.A. Janulaitis	<i>Uba1177I (MboI)</i>	GATC	116	87	8	0	22	27
Unidentified bacterium RFL1178	A.A. Janulaitis	<i>Uba1178I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1179	A.A. Janulaitis	<i>Uba1179I (HaeIII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1180	A.A. Janulaitis	<i>Uba1180I (SmaI)</i>	AGGCCT	6	11	7	1	0	27
Unidentified bacterium RFL1181	A.A. Janulaitis	<i>Uba1181II (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1182	A.A. Janulaitis	<i>Uba1182I (MboI)</i>	GATC	116	87	8	0	22	27

Number of Cleavage Sites³

Microorganism	Source	Enzyme ¹	Sequence ²	λ	Ad2	SV40	Φ X	pBR	References
Unidentified bacterium RFL1183	A.A. Janulaitis	<i>Uba1183I (MboI)</i>	GATC	116	87	8	0	22	27
Unidentified bacterium RFL1184	A.A. Janulaitis	<i>Uba1184I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1185	A.A. Janulaitis	<i>Uba1184II (SmaI)</i>	CCTNAGG	2	7	0	0	0	27
Unidentified bacterium RFL1186	A.A. Janulaitis	<i>Uba1185I (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1187	A.A. Janulaitis	<i>Uba1186I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1188	A.A. Janulaitis	<i>Uba1187I (SacII)</i>	CCGCCG	4	33	0	1	0	27
Unidentified bacterium RFL1189	A.A. Janulaitis	<i>Uba1188I (CfrI)</i>	YGGCCR	39	70	0	2	6	27
Unidentified bacterium RFL1190	A.A. Janulaitis	<i>Uba1189I (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1191	A.A. Janulaitis	<i>Uba1190I (Eam1105I)</i>	GACNNNNNGTC	9	9	0	1	1	27
Unidentified bacterium RFL1192	A.A. Janulaitis	<i>Uba1191I (Eam1105I)</i>	GACNNNNNGTC	9	9	0	1	1	27
Unidentified bacterium RFL1193	A.A. Janulaitis	<i>Uba1192I (Ksp632I)</i>	CTCTTC	34	29	1	2	2	27
Unidentified bacterium RFL1195	A.A. Janulaitis	<i>Uba1193I (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1196	A.A. Janulaitis	<i>Uba1195I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1197	A.A. Janulaitis	<i>Uba1196I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1198	A.A. Janulaitis	<i>Uba1197I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1199	A.A. Janulaitis	<i>Uba1198I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1200	A.A. Janulaitis	<i>Uba1199I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1201	A.A. Janulaitis	<i>Uba1200I (ClaI)</i>	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1202	A.A. Janulaitis	<i>Uba1201I (KpnI)</i>	GGTACC	2	8	1	0	0	27
Unidentified bacterium RFL1203	A.A. Janulaitis	<i>Uba1202I (ApaI)</i>	GGGCCC	1	12	1	0	0	27
Unidentified bacterium RFL1204	A.A. Janulaitis	<i>Uba1203I (ApaI)</i>	GTGCAC	4	7	0	1	3	27
Unidentified bacterium RFL1205	A.A. Janulaitis	<i>Uba1204I (MboI)</i>	GATC	116	87	8	0	22	27
Unidentified bacterium RFL1206	A.A. Janulaitis	<i>Uba1205I (BamHI)</i>	GGATCC	5	3	1	0	1	27
		<i>Uba1205II (AvaI)</i>	CYCGRG	8	40	0	1	1	27
		<i>Uba1206I (HgiII)</i>	GRGCTC	7	57	2	0	2	27

Microorganism	Source	Enzyme ¹	Sequence ²	λ	Ad2	SV40	Φ X	pBR	References
Unidentified bacterium RFL1207	A.A. Janulaitis	<i>Uba1207I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1208	A.A. Janulaitis	<i>Uba1208I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1209	A.A. Janulaitis	<i>Uba1209I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1210	A.A. Janulaitis	<i>Uba1210I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1211	A.A. Janulaitis	<i>Uba1211I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1212	A.A. Janulaitis	<i>Uba1212I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1213	A.A. Janulaitis	<i>Uba1213I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1214	A.A. Janulaitis	<i>Uba1214I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1215	A.A. Janulaitis	<i>Uba1215I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1216	A.A. Janulaitis	<i>Uba1216I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1217	A.A. Janulaitis	<i>Uba1217I (SmaI)</i>	AGGCCT	6	11	7	1	0	27
Unidentified bacterium RFL1218	A.A. Janulaitis	<i>Uba1218I (EcoRII)</i>	CCWGG	71	136	17	2	6	27
Unidentified bacterium RFL1219	A.A. Janulaitis	<i>Uba1219I (HindIII)</i>	AAGCTT	6	12	6	0	1	27
Unidentified bacterium RFL1220	A.A. Janulaitis	<i>Uba1220I (SmaI)</i>	CCCGGG	3	12	0	0	0	27
Unidentified bacterium RFL1221	A.A. Janulaitis	<i>Uba1221I (EspI)</i>	GCTNAGC	6	8	1	0	0	27
Unidentified bacterium RFL1222	A.A. Janulaitis	<i>Uba1222I (EspI)</i>	GCTNAGC	6	8	1	0	0	27
Unidentified bacterium RFL1223	A.A. Janulaitis	<i>Uba1223I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1224	A.A. Janulaitis	<i>Uba1224I (BamHI)</i>	GGATCC	5	3	1	0	1	27
Unidentified bacterium RFL1225	A.A. Janulaitis	<i>Uba1225I (PstI)</i>	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1226	A.A. Janulaitis	<i>Uba1226I (SphI)</i>	GCATGC	6	8	2	0	1	27
Unidentified bacterium RFL1227	A.A. Janulaitis	<i>Uba1227I (PvuII)</i>	CAGCTG	15	24	3	0	1	27
Unidentified bacterium RFL1228	A.A. Janulaitis	<i>Uba1228I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1229	A.A. Janulaitis	<i>Uba1229I (SacII)</i>	CCGGGG	4	33	0	1	0	27
Unidentified bacterium RFL1230	A.A. Janulaitis	<i>Uba1230I (HaeII)</i>	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1231	A.A. Janulaitis	<i>Uba1231I (HaeII)</i>	GGCC	149	216	18	11	22	27

Microorganism	Source	Enzyme ¹	Sequence ²	Number of Cleavage Sites ³					References
				λ	Ad2 SV40	ΦX	pBR		
Unidentified bacterium RFL1232	A.A. Janulaitis	<i>Uba1232I</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	27
Unidentified bacterium RFL1233	A.A. Janulaitis	<i>Uba1233I</i> (<i>ClaI</i>)	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1234	A.A. Janulaitis	<i>Uba1234I</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	27
Unidentified bacterium RFL1235	A.A. Janulaitis	<i>Uba1235I</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	27
Unidentified bacterium RFL1236	A.A. Janulaitis	<i>Uba1236I</i> (<i>FnuDII</i>)	CGCG	157	303	0	14	23	27
Unidentified bacterium RFL1237	A.A. Janulaitis	<i>Uba1237I</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	27
Unidentified bacterium RFL1238	A.A. Janulaitis	<i>Uba1238I</i> (<i>ClaI</i>)	ATCGAT	15	2	0	0	1	27
Unidentified bacterium RFL1239	A.A. Janulaitis	<i>Uba1239I</i> (<i>SstI</i>)	AGGCCT	6	11	7	1	0	27
Unidentified bacterium RFL1240	A.A. Janulaitis	<i>Uba1240I</i> (<i>SnaBI</i>)	TACGTA	1	0	0	0	0	27
Unidentified bacterium RFL1241	A.A. Janulaitis	<i>Uba1241I</i> (<i>ApaI</i>)	GGGCCC	1	12	1	0	0	27
Unidentified bacterium RFL1242	A.A. Janulaitis	<i>Uba1242I</i> (<i>BamHI</i>)	GGATCC	5	3	1	0	1	27
<i>Vibrio anguillarum</i> RFL91	A.A. Janulaitis	<i>Var91I</i> (<i>EcoRI</i>)	GAATTC	5	5	1	0	1	27
		<i>Var91III</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	27
		<i>Var91IV</i>	?	?	?	?	?	?	27
<i>Vibrio parahaemolyticus</i> K25	T. Shimada	<i>VpaK25I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	44
<i>Vibrio parahaemolyticus</i> K57	T. Shimada	<i>VpaK57I</i>	?	?	?	?	?	?	44
<i>Vibrio parahaemolyticus</i> K65	T. Shimada	<i>VpaK65I</i> (<i>AvaI</i>)	GGWCC	35	73	6	1	8	44

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 *SapI* and *AclI*, 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

5' GCTCTTCN↑' 3'
3' CGAGAAGNNNN↑' 5'

AclI 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.

* A is N⁶-methyladenosine.

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 sequence²	Me site³
<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> DXXI	TCANNNNNNNNATTC	
<i>Eco</i> EI	GAGNNNNNNNNATGC	
<i>Eco</i> KI	AACNNNNNNNGTGC	2(6),-3(6)
<i>Eco</i> R124I	GAANNNNNNNRTCG	
<i>Eco</i> R124/3I	GAANNNNNNNRTCG	-3(6)
<i>Sty</i> SBI	GAGNNNNNNRRTAYG	2(6),-4(6)
<i>Sty</i> SJI	GAGNNNNNNNGTRC	
<i>Sty</i> SPI	AACNNNNNNNGTRC	2(6),-3(6)
<i>Sty</i> SQI	AACNNNNNNRRTAYG	

Type III enzymes

Enzyme	Recognition sequence²	Me site³
<i>Eco</i> PI	AGACC	3(6)
<i>Eco</i> P15I	CAGCAG	
<i>Hin</i> fIII	CGAAT	
<i>Sty</i> LTI	CAGAG	4(6)

Type II enzymes

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Aat</i> II		GACGT↑C		EGJLMNOPRSUVX
<i>Acc</i> I		GT↑MKAC		ABDEGIJKLMNOPQRSUVX
<i>Aci</i> I		CCGC(-2/-2)		N
<i>Acy</i> I		GR↑CGYC		EMRV
	<i>Aha</i> II	GR↑CGYC		GN
	<i>Bbi</i> II	GR↑CGYC		AK
	<i>Bsa</i> HI	GRCGYC		N
	<i>Hin</i> 1I	GR↑CGYC		FOU
<i>A</i> 7II		C↑TTAAG		ABGJKNU
	<i>Bfr</i> I	C↑TTAAG		M
<i>A</i> 7III		A↑CRYGT		BGJMNU
<i>Age</i> I		A↑CCGGT		N
<i>Aha</i> III		TTT↑AAA		
	<i>Dra</i> I	TTT↑AAA		ABDEFGHIJKLMNOPQRSUVX
<i>Alu</i> I		AG↑CT	3(5)	ABDEFGHIJKLMNOPQRSUVX
<i>Alw</i> NI		CAGNNN↑CTG		N
<i>Apa</i> I		GGGCC↑C	4(5)	BDEGIJKLMNOPRUVX
	<i>Bsp</i> 120I	G↑GGCCC		F
<i>Apa</i> BI		GCANNNNN↑TGC		
<i>Apa</i> LI		G↑TGCAC		EGJKNX
	<i>Alw</i> 44I	G↑TGCAC		FRU
	<i>Sno</i> I	G↑TGCAC		JLMV
	<i>Vne</i> I	G↑TGCAC		D
<i>Asc</i> I		GG↑CGCGCC		N
<i>Asu</i> I		G↑GNCC		R
	<i>Cfr</i> 13I	G↑GNCC	4(5)	FKOU
	<i>Nsp</i> IV	G↑GNCC		JP
	<i>Sau</i> 96I	G↑GNCC		BEGJLMNRVX
<i>Asu</i> II		TT↑CGAA		J
	<i>Bpu</i> 14I	TT↑CGAA		D
	<i>Bsp</i> 119I	TT↑CGAA		F
	<i>Bst</i> BI	TT↑CGAA		N
	<i>Csp</i> 45I	TT↑CGAA		RV
	<i>Lsp</i> I	TT↑CGAA		JL
	<i>Nsp</i> V	TTCGAA		ABGKPU

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Ava</i> I	<i>Sfu</i> I	TT↑CGAA		M
		C↑YCGRG		ABEGLJKLMNOPRSUVX
	<i>Eco</i> 88I	C↑YCGRG		F
<i>Ava</i> II	<i>Nsp</i> III	C↑YCGRG		JP
		G↑GWCC		ABEGLJKMNPRSX
	<i>Bme</i> 18I	G↑GWCC		D
	<i>Eco</i> 47I	G↑GWCC		FOU
	<i>Nsp</i> HII	GGWCC		J
<i>Ava</i> III	<i>Sin</i> I	G↑GWCC	4(5)	JLRSV
		ATGCAT		GJ
	<i>Eco</i> T22I	ATGCA↑T		KOU
<i>Avr</i> II	<i>Nsi</i> I	ATGCA↑T		BELMNRVX
		C↑CTAGG		N
	<i>Bln</i> I	C↑CTAGG		K
<i>Bae</i> I		ACNNNNGTAYC		
<i>Bal</i> I		TGG↑CCA	4(5)	ABEGLJKRSVX
	<i>Msc</i> I	TGG↑CCA		N
<i>Bam</i> HI		G↑GATCC	5(4)	ABDEFGHIJKLMNOPQRSUVX
	<i>Bst</i> I	G↑GATCC		GJP
<i>Bbv</i> I		GCAGC(8/12)	2(5),-2(5)	EGLJNX
<i>Bbv</i> II		GAAGAC(2/6)		
	<i>Bbs</i> I	GAAGAC		N
<i>Bcc</i> I		CCATC		
<i>Bce</i> II		ACGGC(12/13)		
<i>Bcg</i> I ⁵		GCANNNNNNTCG(12/10)		N
<i>Bcl</i> I		T↑GATCA		BEGJLMNOPRSUVX
	<i>Fba</i> I	TGATCA		K
<i>Bet</i> I		W↑CCGGW		
<i>Bgl</i> I		GCCNNNN↑NGGC		ABDEFGHIJLMNOPQRSUVX
<i>Bgl</i> II		A↑GATCT		ABDEFGHIJKLMNOPQRSUVX
<i>Bin</i> I		GGATC(4/5)		
	<i>Alw</i> I	GGATC(4/5)		N
<i>Bpu</i> 10I		CCTNAGC(-5/-2)		
<i>Bsa</i> AI		YAC↑GTR		N
<i>Bsa</i> BI		GATNN↑NNATC		N
	<i>Mam</i> I	GATNN↑NNATC		M

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>BsePI</i>		GCGCGC		
	<i>BssHII</i>	G↑CGCGC		DEGJLMNQRUVX
<i>BsgI</i>		GTGCAG(16/14)		
<i>BsiI</i>		CTCGTG(-5/-1)		
<i>BstYI</i>		CCNNNNN↑NNGG		
	<i>BsII</i>	CCNNNNN↑NNGG		N
<i>BsmI</i>		GAATGC(1/-1)		EGJLNUVX
<i>BsmAI</i>		GTCTC(1/5)		N
	<i>Alw26I</i>	GTCTC(1/5)		F
<i>BspGI</i>		CTGGAC		
<i>BspHI</i>		T↑CATGA		N
	<i>RspXI</i>	T↑CATGA		G
<i>BspMI</i>		ACCTGC(4/8)		N
<i>BspMII</i>		T↑CCGGA		
	<i>AccIII</i>	T↑CCGGA		DEGJKQRV
	<i>BspEI</i>	T↑CCGGA		N
	<i>Kpn2I</i>	T↑CCGGA		F
	<i>MroI</i>	T↑CCGGA		MOU
<i>BsrI</i>		ACTGG(1/-1)		N
<i>BstEII</i>		G↑GTNACC		BEGJLMNOPRSUVX
	<i>BstPI</i>	G↑GTNACC		K
	<i>Eco91I</i>	G↑GTNACC		F
	<i>EcoO65I</i>	G↑GTNACC		GK
<i>BstXI</i>		CCANNNNN↑NTGG		EGJKLMNOQRUVX
<i>CauII</i>		CC↑SGG		
	<i>BcnI</i>	CC↑SGG	2(4)	FK
	<i>NciI</i>	CC↑SGG		BEGJLMNOUVX
<i>CfrI</i>		Y↑GGCCR	4(5)	F
	<i>EaeI</i>	Y↑GGCCR	4(5)	EGJKLMNVX
<i>Cfr10I</i>		R↑CCGGY	2(5)	AFKMNOU
<i>ClaI</i>		AT↑CGAT	5(6)	ABDJKMNPQRSVX
	<i>BanIII</i>	ATCGAT		OU
	<i>BscI</i>	AT↑CGAT		JL
	<i>Bsp106I</i>	AT↑CGAT		E
	<i>BspDI</i>	AT↑CGAT		N
	<i>Bsu15I</i>	AT↑CGAT		DF

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Cvi</i> JI		RG↑CY	3(5)	
<i>Cvi</i> RI		TG↑CA	4(6)	
<i>Dde</i> I		C↑TNAG	1(5)	BEGIJLMNOPRUVX
<i>Dpn</i> I*		GA↑TC		ABEGIJLMNRSVX
<i>Dra</i> II		RG↑GNCCY		EGJM
	<i>Eco</i> O109I	RG↑GNCCY		FGJKLNOUVX
	<i>Pss</i> I	RGGNC↑CY		I
<i>Dra</i> III		CACNNN↑GTG		EMNX
<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		FN
<i>Eci</i> I		TCCGCC		
<i>Eco</i> 31I		GGTCTC(1/5)		F
	<i>Bsa</i> I	GGTCTC(1/5)		N
<i>Eco</i> 47III		AGC↑GCT		FKMNORU
<i>Eco</i> 57I		CTGAAG(16/14)	5(6),-5(6)	N
<i>Eco</i> NI		CCTNN↑NNNAGG		N
<i>Eco</i> RI		G↑AATTC	3(6)	ABDEFGHIJKLMNOPQRSUVX
<i>Eco</i> RII ⁶		↑CCWGG	2(5)	BDEGJUV
+	<i>Apy</i> I	CC↑WGG		M
+	<i>Bst</i> NI	CC↑WGG	2(4)	EJNX
+	<i>Mva</i> I	CC↑WGG	2(4)	AFKMOU
	<i>Tsp</i> AI	CCWGG		L
<i>Eco</i> RV		GAT↑ATC	2(6)	ABDEGIJKLMNOPQRSUVX
	<i>Eco</i> 32I	GAT↑ATC		F
<i>Esp</i> I		GC↑TNAGC		EGJU
	<i>Bpu</i> 1102I	GC↑TNAGC		FN
	<i>Cel</i> II	GC↑TNAGC		M
<i>Esp</i> 3I		CGTCTC(1/5)		FN
<i>Fau</i> I		CCCGC(4/6)		
<i>Fin</i> I		GTCCC		
<i>Fnu</i> 4HI		GC↑NGC		N
<i>Fnu</i> DII		CG↑CG		
	<i>Acc</i> II	CG↑CG		DEGJKQVX
	<i>Bsp</i> 50I	CG↑CG		F

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
	<i>Bst</i> UI	CG↑CG		N
	<i>Mun</i> I	CG↑CG		M
	<i>Tha</i> I	CG↑CG		BI
<i>Fok</i> I		GGATG(9/13)	3(6),-2(6)	DEGIKMNRUVX
<i>Fse</i> I		GGCCGG↑CC		
<i>Fsi</i> I		R↑AATTY		
<i>Gdi</i> II		YGGCCG(-5/-1)		
<i>Gsu</i> I		CTGGAG(16/14)		FN
<i>Hae</i> I		WGG↑CCW		
<i>Hae</i> II		RGCGC↑Y		BDEGLJKLMNOPRSUVX
<i>Hae</i> III		GG↑CC	3(5)	ABDGHILJKLMNOPQRSUVX
	<i>Bss</i> CI	GGCC		G
	<i>Bsu</i> RI	GG↑CC	3(5)	DFGJ
	<i>Pal</i> I	GG↑CC		EJPV
<i>Hga</i> I		GACGC(5/10)		DNX
<i>Hgi</i> AI		GWGCW↑C		NX
	<i>Alw</i> 21I	GWGCW↑C		F
	<i>Asp</i> HI	GWGCW↑C		M
<i>Hgi</i> CI		G↑GYRCC		
	<i>Ban</i> I	G↑GYRCC		EGIJMNOPUVX
	<i>Eco</i> 64I	G↑GYRCC		F
<i>Hgi</i> EII		ACNNNNNNNGGT		
<i>Hgi</i> JII		GRGCTY↑C		
	<i>Ban</i> II	GRGCTY↑C		EGIJKL MNOPRSUVX
	<i>Eco</i> 24I	GRGCTY↑C		F
<i>Hha</i> I		GCG↑C	2(5)	BDEGJKNOPRSUX
	<i>Cfo</i> I	GCG↑C		BIJLMRV
	<i>Hin</i> 6I	G↑CGC		F
	<i>Hin</i> P1I	G↑CGC		NX
<i>Hind</i> II		GTY↑RAC	5(6)	M
	<i>Hinc</i> II	GTY↑RAC		ABEFGIJKL MNOPRSUVX
<i>Hind</i> III		A↑AGCTT	1(6)	ABDEFGIJKL MNOPRSUVX
<i>Hin</i> fI		G↑ANTC		ABDEGLJKL MNOPRSUVX
<i>Hpa</i> I		GTT↑AAC	5(6)	ABDEGIJKL MNOPRSUVX
<i>Hpa</i> II		C↑CGG	2(5)	ABDEFGJL MNOPRSUVX
	<i>Hap</i> II	C↑CGG		GIK

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
	<i>MspI</i>	C↑CGG	1(5)	ABDEFGIJKLMNOPQRSUVX
<i>HphI</i>		GGTGA(8/7)	-2(5)	NVX
<i>KpnI</i>		GGTAC↑C		ABDEFGIJKLMNOPQRSUVX
	<i>Asp718I</i>	G↑GTACC		M
<i>Ksp632I</i>		CTCT↑TC(1/4)		M
	<i>Eam1104I</i>	CTCT↑TC(1/4)		F
	<i>EarI</i>	CTCT↑TC(1/4)		N
<i>MaeI</i>		C↑TAG		M
	<i>RmaI</i>	C↑TAG		N
<i>MaeII</i>		A↑CGT		M
<i>MaeIII</i>		↑GTNAC		M
<i>MboI</i> ⁷		↑GATC		BEGIJKNPQRSVX
+	<i>BspAI</i>	↑GATC		JL
	<i>DpnII</i>	GATC	2(6)	N
+	<i>Kzo9I</i>	↑GATC		D
	<i>NdeII</i>	↑GATC		BGM
	<i>Sau3AI</i>	↑GATC	4(5)	ABDEGLJKLMNOPQRSUVX
<i>MboII</i>		GAAGA(8/7)	5(6)	BGLJKNOPQRSUVX
<i>McrI</i>		CGRY↑CG		
<i>MfeI</i>		C↑AATTG		
<i>MluI</i>		A↑CGCGT		ABDEFGIJKLMNOPQRSUVX
<i>MlyI</i>		GACTC(5/5)		L
<i>MmeI</i>		TCCRAC(20/18)		
<i>MnlI</i>		CCTC(7/7)		EGJNX
<i>MseI</i>		T↑TAA		N
<i>MstI</i>		TGC↑GCA		X
	<i>AosI</i>	TGC↑GCA		GJ
	<i>AviII</i>	TGC↑GCA		M
	<i>FdiII</i>	TGC↑GCA		U
	<i>FspI</i>	TGC↑GCA		NS
<i>MwoI</i>		GCNNNNN↑NNGC		
<i>NaeI</i>		GCC↑GGC		EGKLMNOUVX
<i>NarI</i>		GG↑CGCC		BEGJMNPUVX
	<i>BbeI</i>	GGCGC↑C		K
	<i>EheI</i>	GGC↑GCC		FOU
	<i>KasI</i>	G↑GCGCC		N
	<i>NruII</i>	GG↑CGCC		GJ

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>Nco</i> I		C↑CATGG		ABDEFGHIJKLMNOPQRSUVX
<i>Nde</i> I		CA↑TATG	4(6)	BEFGKLMNP SVX
<i>Nhe</i> I		G↑CTAGC		BEGJKLMN OPRUVX
<i>Nla</i> III		CATG↑		N
<i>Nla</i> IV		GGN↑NCC		N
<i>Not</i> I		GC↑GGCCGC		ABDEFGHIJKLMNOPQRSUVX
<i>Nru</i> I		TCG↑CGA		BDEGLJKLMN OPUVX
	<i>Bsp</i> 68I	TCG↑CGA		F
	<i>Spo</i> I	TCG↑CGA		R
<i>Nsp</i> I		RCATG↑Y		AKMU
	<i>Nsp</i> HI	RCATG↑Y		GJ
<i>Nsp</i> BII		CMG↑CKG		J
<i>Pac</i> I		TTAAT↑TAA		N
<i>Pfl</i> 1108I		TCGTAG		
<i>Pfl</i> MI		CCANNNN↑NTGG		N
	<i>Van</i> 91I	CCANNNN↑NTGG		F
<i>Ple</i> I		GAGTC(4/5)		N
<i>Pma</i> CI		CAC↑GTG		AK
	<i>Bbr</i> PI	CAC↑GTG		M
	<i>Eco</i> 72I	CAC↑GTG		F
	<i>Pml</i> I	CAC↑GTG		N
<i>Ppu</i> MI		RG↑GWCCY		N
<i>Psh</i> AI		GACNN↑NNGTC		
<i>Pst</i> I		CTGCA↑G	5(6)	ABDEFGHIJKLMNOPQRSUVX
<i>Pvu</i> I		CGAT↑CG		ABDEFGJKLMN OPRSVX
	<i>Bsp</i> CI	CGAT↑CG		E
	<i>Xor</i> II	CGAT↑CG		B
<i>Pvu</i> II		CAG↑CTG	4(4)	ABDEFGHIJKLMNOPQRSUVX
<i>Rle</i> AI		CCCACA(12/9)		
<i>Rsa</i> I		GT↑AC		ABDEGLJLMN OPRSVX
	<i>Afa</i> I	GT↑AC		K
	<i>Csp</i> 6I	G↑TAC		F
<i>Rsr</i> II		CG↑GWCCG		BEGJNX
	<i>Cpo</i> I	CGGWCCG		K
	<i>Csp</i> I	CG↑GWCCG		RV
<i>Sac</i> I		GAGCT↑C		ADEGIJKLMNOPQRSUVX

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
SacII	<i>Ecl136II</i>	GAG↑CTC		F
	<i>SstI</i>	GAGCT↑C		B
		CCGC↑GG		EIJLNOPRUVX
	<i>Cfr42I</i>	CCGC↑GG		F
	<i>Kpn378I</i>	CCGC↑GG		D
	<i>KspI</i>	CCGC↑GG		M
	<i>MraI</i>	CCGCGG		GJ
	<i>Sfr303I</i>	CCGC↑GG		D
SalI	<i>SstII</i>	CCGC↑GG		B
		G↑TCGAC		ABDEFGHLJKLMNOPQRSUVX
	<i>SapI</i>	GCTCTTC(1/4)		
	<i>SauI</i>	CC↑TNAGG		M
	<i>AocI</i>	CC↑TNAGG		E
	<i>AxyI</i>	CC↑TNAGG		GJV
	<i>Bse21I</i>	CC↑TNAGG		D
	<i>Bsu36I</i>	CC↑TNAGG		NR
ScaI	<i>CunI</i>	CC↑TNAGG		B
	<i>Eco81I</i>	CC↑TNAGG		AFKOU
	<i>MstII</i>	CC↑TNAGG		EX
		AGT↑ACT		ABEFGIJKLMNOPRSUVX
	<i>ScrFI</i>	CC↑NGG		EGMNSUVX
	<i>DsaV</i>	↑CCNGG		M
	<i>SduI</i>	GDGCH↑C		FJ
	<i>BmyI</i>	GDGCH↑C		M
SecI	<i>Bsp1286I</i>	GDGCH↑C		EGKNRUX
	<i>NspII</i>	GDGCH↑C		J
		C↑CNNGG		
	<i>BsaJI</i>	C↑CNNGG		N
	<i>SfaNI</i>	GCATC(5/9)		DNX
	<i>SfcI</i>	CTYRAG		
	<i>SfeI</i>	C↑TRYAG		
	<i>SfiI</i>	GGCCNNNN↑NGGCC		ABDEGLJLMNOPQRSUVX
SmaI	<i>SgrAI</i>	CR↑CCGGYG		M
		CCC↑GGG	2(4)	ABDEFGIJKLMNOPQRSUVX
	<i>Cfr9I</i>	C↑CCGGG	2(4)	FU
	<i>XmaI</i>	C↑CCGGG		EINRVX

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
<i>SnaI</i>		GTATAC		
<i>SnaBI</i>		TAC↑GTA		EGJKMNVX
	<i>Eco105I</i>	TAC↑GTA		FOU
<i>SpeI</i>		A↑CTAGT		BEGKLMNORSUVX
<i>SphI</i>		GCATG↑C		ABDEGLJKLMNOPQRSUX
	<i>BbuI</i>	GCATG↑C		RV
	<i>PaeI</i>	GCATG↑C		F
<i>SplI</i>		C↑GTACG		AK
	<i>BsiWI</i>	C↑GTACG		N
<i>Sse8387I</i>		CCTGCA↑GG		AK
<i>SspI</i>		AAT↑ATT		BEGKLMNRUVX
<i>StuI</i>		AGG↑CCT		ABEGLJKLMNPRVX
	<i>AatI</i>	AGG↑CCT		OU
	<i>Eco147I</i>	AGG↑CCT		F
	<i>Pme55I</i>	AGG↑CCT		D
<i>StyI</i>		C↑CWWGG		BEGJMN RVX
	<i>BssT1I</i>	C↑CWWGG		D
	<i>Eco130I</i>	C↑CWWGG		FU
	<i>EcoT14I</i>	C↑CWWGG		AK
<i>SwaI</i>		ATTT↑AAAT		
<i>TaqI</i>		T↑CGA	4(6)	ABDEFGIJKLMNOPSUVX
	<i>TthHB8I</i>	T↑CGA	4(6)	K
<i>TaqII</i> ⁸		GACCGA(11/9) CACCCA(11/9)		
<i>TfiI</i>		GAWTC		N
<i>Tsp45I</i>		GTSAC		
<i>TspEI</i>		AATT		
<i>Tth111I</i>		GACN↑NNGTC		EGLJKNPVX
	<i>AspI</i>	GACN↑NNGTC		M
<i>Tth111II</i>		CAARCA(11/9)		
<i>VspI</i>		AT↑TAAT		DFK
	<i>AseI</i>	AT↑TAAT		N
	<i>AsnI</i>	AT↑TAAT		M
<i>XbaI</i>		T↑CTAGA	6(6)	ABDEFGHIJKLMNOPSUVX
<i>XcmI</i>		CCANNNNN↑NNNTGG		N
<i>XhoI</i>		C↑TCGAG		ABDEFGHIJKLMNOPSUVX
	<i>BstVI</i>	C↑TCGAG	5(6)	G

Enzyme ¹	Isoschizomers	Recognition ² Sequence	Me ³ site	Commercial ⁴ source
	<i>CcrI</i>	C↑TCGAG		X
	<i>PaeR7I</i>	C↑TCGAG	5(6)	NX
	<i>SlaI</i>	C↑TCGAG		D
<i>XhoII</i>		R↑GATCY		EGMVX
	<i>BstYI</i>	R↑GATCY		N
	<i>MflI</i>	R↑GATCY		AK
<i>XmaIII</i>		C↑GGCCG	4(5)	B
	<i>EagI</i>	C↑GGCCG		N
	<i>EclXI</i>	C↑GGCCG		M
	<i>Eco52I</i>	C↑GGCCG		EFKOU
<i>XmnI</i>		GAANN↑NNTTC		DEGJNX
	<i>Asp700I</i>	GAANN↑NNTTC		M

FOOTNOTES

- * signifies that *DpnI* and its isoschizomers require the presence of 6-methyladenosine within the recognition sequence GATC.
- 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
- 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.
- Commercial sources of restriction enzymes are abbreviated as follows:

A	Amersham (2/91)
B	BRL (2/91)
D	Palliard Chemical (11/90)
E	Stratagene (2/91)
F	ESP Fermentas (9/90)
G	BioExcellence (formerly Anglian) (11/90)
H	American Allied (12/90)
I	IBI (2/91)
J	Janssen Biochimica (2/91)

- K Takara (1/91)
- L Northumbria Biologicals Ltd. (9/90)
- M Boehringer Mannheim (2/91)
- N New England Biolabs (2/91)
- O Toyobo (2/91)
- P PL-Pharmacia-LKB (2/91)
- Q Molecular Biology Resources (1/91)
- R Promega Biotec (12/90)
- S Sigma (2/91)
- U USB (9/90)
- V Serva (2/91)
- X New York Biolabs (2/91)

5. *BcgI*⁵ cleaves on both sides of the recognition sequence: 10 bases 5' to the recognition sequence and 12 bases 3' to it on both strands. Thus the recognition site is excised in a fragment, 34 base pairs long, with 2-base 3'-extensions at each end.
6. *EcoRII* isoschizomers fall into two classes based upon their sensitivity to methylation. *EcoRII* will not cleave when the second cytosine in the recognition sequence is methylated to 5-methylcytosine whereas *MvaI* will cleave such a sequence. Isoschizomers of *EcoRII* that are like *MvaI* are indicated by +.
7. *MboI* isoschizomers fall into two classes based upon their sensitivity to methylation. *MboI* will not cleave when the recognition sequence contains 6-methyladenosine whereas *Sau3AI* will not cleave when its recognition sequence contains 5-methylcytosine. Isoschizomers of *MboI* that are like *Sau3AI* are indicated by +.
8. *TaqII* differs from other restriction enzymes in recognizing two distinct sequences: GACCG and CACCCA.