
Restriction and modification enzymes and their recognition sequences

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Introduction

Since the last compilation of restriction endonucleases (214) forty-nine new entries have been added, including nine new specificities, these are *DraII* (PuGGNCCPy), *DraIII* (CACNNGTG), *EcoD* (TTA(N)₂GTCPy), *EspI* (GCTNAGC), *NheI* (GCTAGC), *RsrII* (CGG(A/T)CCG), *SryI* (CC(A/T)(A/T)GG), *SspI* (AATATT) and *SpeI* (ACTAGT). In addition, the enzyme *Asp718* is an interesting isoschizomer of *KpnI*. It cleaves the recognition sequence to leave a 5' terminal extension instead of the 3' terminal extension left by *KpnI*.

Among the 515 enzymes listed, there are a minimum of 116 different specificities. New entries, together with new information about recognition sequences are indicated (#).

In forming this list, 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. These endonucleases are named in accordance with the proposal of Smith and Nathans (256). Within the table, the source of each microorganism is given either as an individual or a National Culture Collection. If further information is required, it can be found either in the first reference which, in each case, refers to the purification procedure for the restriction enzyme, or from the individuals who have provided their unpublished results. Where more than one reference appears, the second concerns the recognition sequence for the restriction enzyme, the third describes the purification procedure for the methylase and the fourth describes the recognition sequence of the methylase. In some cases, several references appear in one of these categories when independent groups have reached similar conclusions.

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Ad2	SV40	ΦX	pBR	References
<i>Acetobacter aceti</i>	IFO 3281	<i>AacI</i> (<i>SmaI</i>)	AGGCCT	6	11	7	1	0	267
<i>Acetobacter aceti</i> sub. <i>liquefaciens</i>	IFO 12388	<i>AacII</i>	GACGTTC	10	3	0	1	1	267
<i>Acetobacter aceti</i> sub. <i>orleanensis</i>	M. Van Montagu	<i>AacI</i> (<i>BamHI</i>)	GGATCC	5	3	1	0	1	242
<i>Acetobacter liquefaciens</i>	NCIB 8622	<i>AaeI</i> (<i>BamHI</i>)	GGATCC	5	3	1	0	1	242
<i>Acetobacter aceti</i> sub. <i>pasteurianus</i>	NCIB 7215	<i>AorI</i> (<i>BsrNI</i>)	CC↓T↓GG	71	136	17	2	6	242
<i>Acetobacter liquefaciens</i>	IAM 1834	<i>AJI</i> (<i>BamHI</i>)	G↓GATCC	5	3	1	0	1	310
<i>Acetobacter pasteurianus</i> sub. <i>pasteurianus</i>	NCIB 7215	<i>Apal</i>	GGGCC↓C	1	12	1	0	0	241
<i>Acetobacter xylinus</i>	IFO 3288	<i>AxyI</i> (<i>SmaI</i>)	CC↓T↓NAGG	2	7	0	0	0	312
<i>Achromobacter immobilis</i>	ATCC 15934	<i>AImI</i>	?	7	7	7	7	7	62
<i>Achromobacter species 697</i>	C. Kessler	<i>Asp697</i> (<i>AvaII</i>)	GG↓T↓CC	35	73	6	1	8	132
<i>Achromobacter species 700</i>	C. Kessler	<i>Asp700</i> (<i>XmaI</i>)	GAANN↓NNTTC	24	5	0	3	2	132
<i>Achromobacter species 703</i>	C. Kessler	<i>Asp703</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	132
<i>Achromobacter species 707</i>	C. Kessler	<i>Asp707</i> (<i>ClaI</i>)	ATCGAT	15	2	0	0	1	132
<i>Achromobacter species 708</i>	C. Kessler	<i>Asp708</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	132
<i>Achromobacter species 718</i>	C. Kessler	<i>Asp718</i> (<i>KpnI</i>)	G↓GTACC	2	8	1	0	0	17
<i>Acinetobacter calcoaceticus</i>	R.J. Roberts	<i>AccI</i>	GTT↓(↓)↓G↓AC	9	17	1	2	2	315
		<i>AccII</i> (<i>PvuDII</i>)	CGCG	157	303	0	14	23	315
		<i>AccIII</i>	?	>10	>6	?	?	?	192
<i>Actinomadura madurae</i>	ATCC 15904	<i>AmaI</i> (<i>NruI</i>)	TGGGA	5	5	0	2	1	109

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c			References
					Ad2	SV40 ΦX	pBR	
<i>Agmenellum quadruplicatum</i>	W.F. Doolittle	<i>Ava</i> I (AvaI)	CPYCGPUG	8	40	0	1	150
<i>Agrobacterium tumefaciens</i>	ATCC 15955	<i>Ara</i> VI	?	>30	>30	?	?	240
<i>Agrobacterium tumefaciens</i> B6806	E. Neeter	<i>Ara</i> BI (<i>Eco</i> RII)	CC(↓)GG	71	136	17	2	222
<i>Agrobacterium tumefaciens</i> IIBV7	G. Roizes	<i>Ara</i> BVI	?	>14	?	1	0	?
<i>Agrobacterium tumefaciens</i> ID 135	C. Kado	<i>Ara</i> II (<i>Eco</i> RII)	CC(↓)GG	71	136	17	2	6
<i>Agrobacterium tumefaciens</i> C58	E. Neeter	<i>Ara</i> CI (<i>Bcl</i> I)	TGATCA	8	5	1	0	0
<i>Agrobacterium tumefaciens</i>	IAM B-26-1	<i>Ara</i> IAMI	?	?	?	?	?	?
<i>Alcaligenes species</i>	N. Brown	<i>Asp</i> AI (<i>Bst</i> EII)	G↓GTNACC	13	10	0	0	0
<i>Anabaena catenula</i>	CCAP 1403/1	<i>Aca</i> I	?	?	?	?	?	?
<i>Anabaena cylindrica</i>	CCAP 1403/2a	<i>Acy</i> I	GPU↓CGPYC	40	44	0	7	6
<i>Anabaena flos-aquae</i>	A.E. Walaby	<i>Ara</i> I (<i>Ava</i> I)	G↓G(↓)CC	35	73	6	1	8
		<i>Ara</i> II	C↓TTAAG	3	4	1	2	0
		<i>Ara</i> III	A↓CPuPYGT	20	25	0	2	1
<i>Anabaena oscillarioides</i>	CCAP 1403/11	<i>Aos</i> I (<i>Mst</i> I)	TGC↓GCA	15	17	0	1	4
		<i>Aos</i> II (<i>Acy</i> I)	GPU↓CGPYC	40	44	0	7	6
* <i>Anabaena species</i>	CCAP 1403/9	<i>Aoc</i> I (<i>Sau</i> I)	CC↓TNAGG	2	7	0	0	0
*		<i>Aoc</i> II	?	?	?	?	?	?
<i>Anabaena strain Waterbury</i>	ATCC 29208	<i>Ara</i> WI (<i>Acy</i> I)	GPU↓CGPYC	40	44	0	7	6

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Ad2	SV40	Φ X	pBR	References
<i>Anabaena subcylindrica</i>	CCAP 1403/4b	AsuI	GfGNCC	74	164	11	2	15	106
		AsuII	TTfCGAA	7	1	0	0	0	192,50;50
		AsuIII (AcyI)	GPuTcGPyC	40	44	0	7	6	50
<i>Anabaena variabilis</i>	ATCC 27892	AvaI	CfPyCGPuG	8	40	0	1	1	189;108
		AvaII	GfGfTCC	35	73	6	1	8	189;273,108,67
		AvaIII	ATGCAT	14	9	3	0	0	220;220,248
<i>Anabaena variabilis</i> UW	E.C. Rosenvoid	AvrI (AvaI)	CPyCGPuG	8	40	0	1	1	224
		AvrII	CfCTAGG	2	2	2	0	0	224;223
<i>Aphanothece halophytica</i>	ATCC 29534	AhaI (CauII)	CCfGGG	114	97	0	1	10	303
		AhaII (AcyI)	GPuTcGPyC	40	44	0	7	6	303;25,234
		AhaIII	TTTfAAA	13	12	12	2	3	302
<i>Arthrobaacter luteus</i>	ATCC 21606	AfuI	AGfCT	143	158	34	24	16	217
<i>Arthrobaacter pyridinolis</i>	R. DiLauro	ApyI (BsrNI)	CCfAGG	71	136	17	2	6	54
* <i>Azospirillum brasilense</i>	ATCC 29711	AbrI (XhoI)	CTCGAG	1	6	0	1	0	239
<i>Bacillus acidocaldarius</i>	ATCC 27009	BacI (SacII)	CCGGGG	4	33	0	1	0	175,192
<i>Bacillus amyloliquefaciens</i> F	ATCC 23350	BamFI (BamHI)	GGATCC	5	3	1	0	1	247
<i>Bacillus amyloliquefaciens</i> H	F.E. Young	BamHI	GfGATcC	5	3	1	0	1	304;219;98;98
<i>Bacillus amyloliquefaciens</i> K	T. Kaneko	BamKI (BamHI)	GGATCC	5	3	1	0	1	247
<i>Bacillus amyloliquefaciens</i> N	T. Ando	BamNI (BamHI)	GGATCC	5	3	1	0	1	246
		BamN ^x (AvaII)	GfGfTCC	35	73	6	1	8	245,246;112

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 ΦX pBR	References
<i>Bacillus aneurinolyticus</i>	IAM 1077	<i>BanI</i> (<i>HgtCI</i>)	G↑GPyPuCC	25	57 1 3 9	267;267,230
		<i>BanII</i> (<i>HgtJII</i>)	GPuGCPy↑C	7	57 2 0 2	267
		<i>BanIII</i> (<i>ClaI</i>)	ATCGAT	15	2 0 0 1	267
<i>Bacillus brevis</i> S	A.P. Zarubina	<i>BbvSI</i>	GC(↓)AGC		specific methylase	291
<i>Bacillus brevis</i>	ATCC 9999	<i>BbvI</i>	GCAGC (8/12)	199	179 22 14 21	81;79;230;98;98
<i>Bacillus caldolyticus</i>	A. Atkinson	<i>BcII</i>	T↑GATCA	8	5 1 0 0	14
<i>Bacillus centrosporus</i>	A.A. Janulaitis	<i>BcnI</i> (<i>CauII</i>)	CC(↓)TGG	114	97 0 1 10	120,121
<i>Bacillus cereus</i>	ATCC 14579	<i>BceI</i> 4579	?	>10	7 7 7 7	247
<i>Bacillus cereus</i>	ATCC 31293	<i>BceFI</i> (<i>FnuDII</i>)	CGCG	157	303 0 14 23	200
* <i>Bacillus cereus</i>	IOC 243	<i>Bce243</i> (<i>Sau3A</i>)	↑GATC	116	87 8 0 22	48
<i>Bacillus cereus</i>	IAM 1229	<i>BceI</i> 229	?	>10	7 7 7 7	247
<i>Bacillus cereus</i>	T. Ando	<i>BceI</i> 70 (<i>PstI</i>)	CTGCAG	28	30 2 1 1	247
<i>Bacillus cereus</i> Rf sm st	T. Ando	<i>BceR</i> (<i>FnuDII</i>)	CGCG	157	303 0 14 23	247
<i>Bacillus globigii</i>	G.A. Wilson	<i>BglI</i>	GCCNNNN↑NGGC	29	20 1 0 3	56;305;10,287
		<i>BglII</i>	A↑GATCT	6	11 0 0 0	56;305;205
* <i>Bacillus megaterium</i> 216	V.M. Kramarov	<i>Bme216</i> (<i>AvaI</i>)	GG(↓)CC	35	73 6 1 8	142
<i>Bacillus megaterium</i> 899	B899	<i>Bme899</i>	?	>5	7 7 7 7	247
<i>Bacillus megaterium</i> B205-3	T. Kaneko	<i>Bme205</i>	?	>10	7 7 7 7	247
<i>Bacillus megaterium</i>	J. Uperoft	<i>BmeI</i>	?	>10	>20 4 7 7	74
<i>Bacillus pumilus</i> AHU1387A	T. Ando	<i>Bpml</i>	?	6	>30 2 7 7	111
<i>Bacillus sphaericus</i>	IAM 1286	<i>BspI</i> 286 (<i>SdaI</i>)	G(A)GC(A)↑TC	38	105 4 3 10	247;192,232

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c			References	
					Ad2	SV40 ΦX	pBR		
<i>Bacillus sphaericus</i> R	P. Venetianer	<i>BspRI</i> (<i>HaeIII</i>)	GGTCC	149	216	18	11	22	137;293;140
<i>Bacillus stearothermophilus</i> NUB 36	N. Welker	<i>BsmI</i>	GAATGC (1/-1)	46	10	4	3	1	192
<i>Bacillus stearothermophilus</i> C1	N. Welker	<i>BstCI</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	149
<i>Bacillus stearothermophilus</i> C11	N. Welker	<i>BstCI</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	149
<i>Bacillus stearothermophilus</i> G3	N. Welker	<i>BstGI</i> (<i>BclI</i>)	TGATCA	8	5	1	0	0	149
<i>Bacillus stearothermophilus</i> G6	N. Welker	<i>BstGII</i> (<i>EcoRII</i>)	CCG ⁺ GG	71	136	17	2	6	149
<i>Bacillus stearothermophilus</i> H1	N. Welker	<i>BstGI</i> (<i>BstXI</i>)	CCANN ⁺ NTGG	13	10	1	3	0	149
<i>Bacillus stearothermophilus</i> H3	N. Welker	<i>BstGII</i> (<i>MboI</i>)	GATC	116	87	8	0	22	149
<i>Bacillus stearothermophilus</i> H4	N. Welker	<i>BstHI</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	149
<i>Bacillus stearothermophilus</i> P1	N. Welker	<i>BstHI</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	149
<i>Bacillus stearothermophilus</i> P5	N. Welker	<i>BstIII</i> (<i>BsePI</i>)	GTCGCGC	6	52	0	1	0	149;235
<i>Bacillus stearothermophilus</i> P6	N. Welker	<i>BstPI</i>	GCGCGC	6	52	0	1	0	149
<i>Bacillus stearothermophilus</i> P8	N. Welker	<i>BstPI</i>	?	>80	7	7	7	7	149
<i>Bacillus stearothermophilus</i> P9	N. Welker	<i>BstPI</i>	?	11	>20	7	0	0	149
<i>Bacillus stearothermophilus</i> T12	N. Welker	<i>BstPII</i> (<i>Sau3A</i>)	GATC	116	87	8	0	22	149
<i>Bacillus stearothermophilus</i> X1	N. Welker	<i>BsePI</i>	GCGCGC	6	52	0	1	0	149
		<i>BsePI</i> (<i>MboI</i>)	GATC	116	87	8	0	22	149
		<i>BsoPI</i> (<i>BsePI</i>)	GCGCGC	6	52	0	1	0	149
		<i>BstII</i> (<i>BstXI</i>)	CCANN ⁺ NTGG	13	10	1	3	0	149
		<i>BstXI</i>	CCANN ⁺ NTGG	13	10	1	3	0	149;236
		<i>BstXII</i> (<i>MboI</i>)	GATC	116	87	8	0	22	149

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	ΦX pBR		
<i>Bacillus stearothermophilus</i> 1503-4R	N. Welker	<i>Bst</i> I (<i>Bam</i> HI)	G↓GATCC	5	3	1	0	1	34;37
<i>Bacillus stearothermophilus</i> 240	A. Atkinson	<i>Bst</i> AI	?	7	7	7	7	7	16
<i>Bacillus stearothermophilus</i> ET	N. Welker	<i>Bst</i> EI	?	7	7	7	7	7	178
		<i>Bst</i> EII	G↓GTNACC	13	10	0	0	0	178;151
		<i>Bst</i> EIII (<i>Mbol</i>)	GATC	116	87	8	0	22	178;84;192
<i>Bacillus stearothermophilus</i>	ATCC 12980	<i>Bst</i> PI (<i>Bst</i> EII)	G↓GTNACC	13	10	0	0	0	207
<i>Bacillus stearothermophilus</i>	D. Comb	<i>Bst</i> NI (<i>Bco</i> RII)	CC↓T(↓)GG	71	136	17	2	6	233
<i>Bacillus stearothermophilus</i> strain 822	T. Oshima	<i>Bse</i> I (<i>Hae</i> III)	GGCC	149	216	18	11	22	251
		<i>Bse</i> II (<i>Hpa</i> I)	GTTAAC	14	6	4	3	0	251
<i>Bacillus subtilis</i> strain R	T. Trautner	<i>Bsu</i> RI (<i>Hae</i> III)	GG↓CC	149	216	18	11	22	24;23;90
<i>Bacillus subtilis</i> Marburg 168	T. Ando	<i>Bsu</i> M (<i>Xho</i> I)	CT↓GAG	1	6	0	1	0	247;125;-125
† <i>Bacillus subtilis</i>	ATCC 6633	<i>Bsu</i> 6633 (<i>Fnu</i> DII)	CGCG	157	303	0	14	23	247;113
<i>Bacillus subtilis</i>	IAM 1076	<i>Bsu</i> 1076 (<i>Hae</i> III)	GGCC	149	216	18	11	22	247
<i>Bacillus subtilis</i>	IAM 1114	<i>Bsu</i> 1114 (<i>Hae</i> III)	GGCC	149	216	18	11	22	247
<i>Bacillus subtilis</i>	IAM 1247	<i>Bsu</i> 1247 (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	247;103
<i>Bacillus subtilis</i>	ATCC 14593	<i>Bsu</i> 1145	?	>20	7	7	7	7	247
<i>Bacillus subtilis</i>	IAM 1192	<i>Bsu</i> 1192I (<i>Hpa</i> II)	CCGG	338	171	1	5	26	247;209
		<i>Bsu</i> 1192II (<i>Fnu</i> DII)	CGCG	157	303	0	14	23	209
<i>Bacillus subtilis</i>	IAM 1193	<i>Bsu</i> 1193 (<i>Fnu</i> DII)	CGCG	157	303	0	14	23	247;209
<i>Bacillus subtilis</i>	IAM 1231	<i>Bsu</i> FI (<i>Hpa</i> I)	CCGG	338	171	1	5	26	247;209;125
		<i>Bsu</i> EII (<i>Fnu</i> DII)	CGCG	157	303	0	14	23	209;209;-125

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c			References	
					Ad2	SV40 ΦX	pBR		
<i>Bacillus subtilis</i>	IAM 1259	<i>Bsu</i> 1259	?	>8	?	?	?	247	
• <i>Bacillus thuringiensis</i>	R.R. Azizbekyan	<i>BthI</i> (<i>Ava</i> II)	GGC ₁ CC	35	73	6	1	8	4
<i>Bacillus vulgatus</i>	OSB816	<i>BvuI</i> (<i>Eg</i> IIII)	GPuGCPyC	7	57	2	0	2	8
<i>Bifidobacterium bifidum</i> YIT4007	T. Khosaka	<i>BbfI</i> (<i>Pst</i> I)	CTGCAG	28	30	2	1	1	134
		<i>BbII</i> (<i>Acy</i> I)	GPuCGPyC	40	44	0	7	6	134
		<i>BbIII</i> (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	134
		<i>BbIV</i>	?	?	?	0	0	0	134
<i>Bifidobacterium breve</i> YIT4006	H. Takahashi	<i>BbeI</i> (<i>Nar</i> I)	GGGGC ₁ C	1	20	0	2	4	136
		<i>BbeII</i>	?	?	?	?	?	?	134
<i>Bifidobacterium breve</i> S1	ATCC 15700	<i>BbeSI</i>	?	?	?	?	?	?	134
<i>Bifidobacterium breve</i> S50	ATCC 15698	<i>BbeAI</i> (<i>Nar</i> I)	GGCGCC	1	20	0	2	4	134
		<i>BbeAII</i>	?	?	?	?	?	?	134
<i>Bifidobacterium infantis</i> 659	ATCC 25962	<i>BbAI</i>	GGATC (<i>A/S</i>)	58	35	6	0	12	135
<i>Bifidobacterium infantis</i> S76c	ATCC 15702	<i>BbAS1</i> (<i>Eco</i> RII)	CC ₁ GG	71	136	17	2	6	134
		<i>BbASII</i> (<i>Nar</i> I)	GGCGCC	1	20	0	2	4	134
<i>Bifidobacterium longum</i> E194b	ATCC 15707	<i>BbOI</i>	?	?	?	?	?	?	134
<i>Bifidobacterium thermophilum</i> RU326	ATCC 25866	<i>BbthI</i> (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	134
		<i>BbthII</i> (<i>Bst</i> AI)	GGATC	58	35	6	0	12	134
<i>Bordetella bronchiseptica</i>	ATCC 19395	<i>BbrI</i> (<i>Hind</i> III)	AAGCTT	6	12	6	0	1	192
<i>Bordetella pertussis</i>	P. Novotny	<i>BpeI</i> (<i>Hind</i> III)	AAGCTT	6	12	6	0	1	86,130
<i>Brevibacterium albidum</i>	ATCC 15831	<i>BaBI</i>	TGG ₁ CCA	18	17	0	0	1	75;75;283

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 Φ X pBR	References	
<i>Brevibacterium luteum</i>	ATCC 15830	<i>BlnI</i> (<i>XhoI</i>)	CTCGAG	1	6	0 1 0	80
		<i>BlnII</i> (<i>HaeIII</i>)	GGCC	149	216	18 11 22	288
<i>Brevibacterium protophormiae</i>	IFO 12128	<i>BprI</i>	?	?	?	?	268
<i>Calothrix scopulorum</i>	CCAP 1410/5	<i>CscI</i> (<i>SacII</i>)	CCGC $\overline{\text{GG}}$	4	33	0 1 0	58
<i>Caryophanon latum</i> L	H. Mayer	<i>ClaI</i>	ATTCGAT	15	2	0 0 1	173
<i>Caryophanon latum</i>	ATCC 15219	<i>CimI</i> (<i>HaeIII</i>)	GGCC	149	216	18 11 22	258
		<i>CimII</i> (<i>AvaII</i>)	GG $\overline{\text{ACC}}$	35	73	6 1 8	258
<i>Caryophanon latum</i>	DSM 484	<i>CitI</i> (<i>HaeIII</i>)	GGTCC	149	216	18 11 22	175
<i>Caryophanon latum</i> RII	H. Mayer	<i>ClaI</i>	?	>20	?	?	?
<i>Caryophanon latum</i> H7	W.C. Trentini	<i>CadI</i>	?	14	?	?	?
<i>Caulobacter crescentus</i> CB-13	R.J. Syddall	<i>CcrI</i>	?	1	>10	0 1 1	274
		<i>CcrII</i> (<i>XhoI</i>)	CTCGAG	1	6	0 1 0	274
<i>Caulobacter fusiformis</i>	A.A. Janulaitis	<i>CfmI</i> (<i>DpnI</i>)	GATC	only cleaves methylated DNA			109
<i>Chloroflexus aurantiacus</i>	A. Bingham	<i>CauI</i> (<i>AvaII</i>)	G $\overline{\text{G}}\overline{\text{ACC}}$	35	73	6 1 8	15;184
		<i>CauII</i>	CC $\overline{\text{T}}\overline{\text{GG}}$	114	97	0 1 10	15;159,184
		<i>CauIII</i> (<i>PstI</i>)	CTGCAG	28	30	2 1 1	9
<i>Chromatium vinosum</i>	G.C. Grosveld	<i>CvnI</i> (<i>SauI</i>)	CC $\overline{\text{T}}\overline{\text{NAGG}}$	2	7	0 0 0	89
<i>Chromobacterium violaceum</i>	ATCC 12472	<i>CvII</i>	?	?	?	?	?
<i>Citrobacter freundii</i> RFL2	A.A. Janulaitis	<i>CfPI</i>	Py $\overline{\text{T}}\overline{\text{GGCC}}\overline{\text{Pu}}$	39	70	0 2 6	123
<i>Citrobacter freundii</i> RFL4	A.A. Janulaitis	<i>CfF4I</i> (<i>AraI</i>)	GGNCC	74	164	11 2 15	122
<i>Citrobacter freundii</i> RFL5	A.A. Janulaitis	<i>CfF5I</i> (<i>EcoRII</i>)	CC $\overline{\text{A}}\overline{\text{GG}}$	71	136	17 2 6	122

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c			References	
					Ad2	SV40 ΦX	pBR		
<i>Citrobacter freundii</i> RFL6	A.A. Janulaitis	<i>Cfr6I</i> (<i>PvuII</i>)	CAGCTG	15	24	3	0	1	122
<i>Citrobacter freundii</i> RFL7	A.A. Janulaitis	<i>Cfr7I</i> (<i>BsrEII</i>)	GGTNACC	13	10	0	0	0	114
<i>Citrobacter freundii</i> RFL8	A.A. Janulaitis	<i>Cfr8I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	122
<i>Citrobacter freundii</i> RFL9	A.A. Janulaitis	<i>Cfr9I</i> (<i>SmaI</i>)	C↑CCGGG	3	12	0	0	0	122
<i>Citrobacter freundii</i> RFL10	A.A. Janulaitis	<i>Cfr10I</i>	PuCGGGPy	61	40	1	0	7	122
<i>Citrobacter freundii</i> RFL11	A.A. Janulaitis	<i>Cfr11I</i> (<i>BcoRII</i>)	CC(A)GG	71	136	17	2	6	122
<i>Citrobacter freundii</i> RFL13	A.A. Janulaitis	<i>Cfr13I</i> (<i>AsuI</i>)	GGNCC	74	164	11	2	15	122
<i>Citrobacter freundii</i> RFL14	A.A. Janulaitis	<i>Cfr14I</i> (<i>CfrI</i>)	Py↑GGCCPu	39	70	0	2	6	122
<i>Clostridium formicoaceticum</i>	ATCC 23439	<i>CfoI</i> (<i>HhaI</i>)	GCGC	215	375	2	18	31	168
<i>Clostridium histolyticum</i>	R. Hansen	<i>CHI</i>	?	?	?	?	?	?	95
<i>Clostridium pasteurianum</i>	NRCC 33011	<i>CpeI</i> (<i>MboI</i>)	GATC	116	87	8	0	22	293
<i>Clostridium perfringens</i>	R. Hansen	<i>CpfI</i> (<i>Sau3A</i>)	↑GATC	116	87	8	0	22	95
<i>Corynebacterium humiferum</i>	ATCC 21108	<i>ChuI</i> (<i>HindIII</i>)	AAGCTT	6	12	6	0	1	62
<i>Corynebacterium petrophilum</i>	ATCC 19080	<i>ChuII</i> (<i>HindIII</i>)	GTPyPuAC	35	25	7	13	2	62
<i>Cystobacter velatus</i> Plv9	H. Reichenbach	<i>CveI</i> (<i>BclI</i>)	TGATCA	8	5	1	0	0	64
<i>Deinococcus radiophilus</i>	ATCC 27603	<i>DraI</i> (<i>AbaII</i>)	TTTAAA	?	?	?	?	?	175
†		<i>DraII</i>	Pu↑GNCCPy	13	12	12	2	3	208
†		<i>DraIII</i>	CACNN↑GTG	3	44	3	0	4	95:53
† <i>Desulfococcus mobilis</i>	W. Zillig	<i>DmoI</i>	?	10	10	0	1	0	95:53
				?	?	?	?	?	177

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c				References
					Ad2	SV40	ΦX	pBR	
Desulfovibrio desulfuricans Norway strain	H. Peck	<i>DdeI</i>	C↓T↓NAG	104	97	20	14	8	168;76
		<i>DdeII</i> (<i>XhoI</i>)	CTCGAG	1	6	0	1	0	192
Desulfovibrio desulfuricans	ATCC 27774	<i>DdsI</i> (<i>BamHI</i>)	GGATCC	5	3	1	0	1	167
Diplococcus pneumoniae	S. Lacks	<i>DpmI</i>	G↓A↓TC	only cleaves methylated DNA					146;72,147
Diplococcus pneumoniae	S. Lacks	<i>DpmII</i> (<i>MboI</i>)	GATC	116	87	8	0	22	146;147
Enterobacter aerogenes	P.R. Whitehead	<i>EaeI</i> (<i>CfrI</i>)	Py↓GGCCPu	39	70	0	2	6	303
Enterobacter aerogenes	ATCC 15038	<i>EaePI</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	200
Enterobacter cloacae	H. Hartmann	<i>EchI</i>	?	14	7	7	7	7	96
		<i>EcoIII</i> (<i>EcoRII</i>)	CC↓A↓GG	71	136	17	2	6	96
Enterobacter cloacae	DSM 30056	<i>EcoI</i> (<i>BstEII</i>)	G↓GTNACC	13	10	0	0	0	102
		<i>EcoII</i> (<i>EcoRII</i>)	CC↓A↓GG	71	136	17	2	6	192
Enterobacter cloacae	DSM 30060	<i>EcoI</i> (<i>SacII</i>)	CCGCGG	4	33	0	1	0	174;192
* <i>Escherichia coli</i> E1585-68	M. Yoshikawa	<i>EcoVII</i> (<i>HindIII</i>)	A↓AGCTT	6	12	6	0	1	182
* <i>Escherichia coli</i> TB14	Terakado	<i>EcoT14</i> (<i>SryI</i>)	CC↓A↓GG	10	44	8	0	1	311
* <i>Escherichia coli</i> TB104	Terakado	<i>EcoT104</i> (<i>SryI</i>)	CC↓A↓GG	10	44	8	0	1	311
<i>Escherichia coli</i> RFL 24	A.A. Janulaitis	<i>Eco24I</i> (<i>HgfJIII</i>)	GPUGP↓YC	7	57	2	0	2	114
<i>Escherichia coli</i> RFL 25	A.A. Janulaitis	<i>Eco25I</i> (<i>HgfJIII</i>)	GPUGP↓YC	7	57	2	0	2	114
<i>Escherichia coli</i> RFL 26	A.A. Janulaitis	<i>Eco26I</i> (<i>HgfJIII</i>)	GPUGP↓YC	7	57	2	0	2	114
<i>Escherichia coli</i> RFL 27	A.A. Janulaitis	<i>Eco27I</i> (<i>EcoRII</i>)	CC↓A↓GG	71	136	17	2	6	114
<i>Escherichia coli</i> RFL 32	A.A. Janulaitis	<i>Eco32I</i> (<i>EcoRV</i>)	GATATC	21	9	1	0	1	114
<i>Escherichia coli</i> RFL 35	A.A. Janulaitis	<i>Eco35I</i> (<i>HgfJIII</i>)	GPUGP↓YC	7	57	2	0	2	114

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c Ad2 SV40 Φ X pBR	References
<i>Escherichia coli</i> RFL 36	A.A. Janulaitis	<i>Eco</i> 361 (<i>Pst</i> I)	CTGCAG	28	2 1 1	114
<i>Escherichia coli</i> RFL 38	A.A. Janulaitis	<i>Eco</i> 381 (<i>Eco</i> RII)	CC(A)GG	71	136 17 2 6	114
<i>Escherichia coli</i> RFL 39	A.A. Janulaitis	<i>Eco</i> 391 (<i>Asu</i> I)	GGNCC	74	164 11 2 15	114
<i>Escherichia coli</i> RFL 40	A.A. Janulaitis	<i>Eco</i> 401 (<i>Hgt</i> JI)	GPUGCPYC	7	57 2 0 2	114
<i>Escherichia coli</i> RFL 41	A.A. Janulaitis	<i>Eco</i> 411 (<i>Hgt</i> JII)	GPUGCPYC	7	57 2 0 2	114
<i>Escherichia coli</i> RFL 47	A.A. Janulaitis	<i>Eco</i> 471 (<i>Ava</i> II)	GG(A)CC	35	73 6 1 8	119
		<i>Eco</i> 47II (<i>Asu</i> I)	GGNCC	74	164 11 2 15	119
		<i>Eco</i> 47III	AGCGCT	2	13 1 0 4	119
<i>Escherichia coli</i> RFL 48	A.A. Janulaitis	<i>Eco</i> 481 (<i>Pst</i> I)	CTGCAG	28	30 2 1 1	119
<i>Escherichia coli</i> RFL 49	A.A. Janulaitis	<i>Eco</i> 491 (<i>Pst</i> I)	CTGCAG	28	30 2 1 1	119
<i>Escherichia coli</i> RFL 50	A.A. Janulaitis	<i>Eco</i> 501 (<i>Hgt</i> CI)	GGPYuCC	25	57 1 3 9	119
* <i>Escherichia coli</i> CK	S.S. Debov	<i>Eco</i> CK	?	4	7 7 7 7	285
<i>Escherichia coli</i> 2bT	ICR 0020	<i>Eco</i> ICRI (<i>Sac</i> I)	GAGCTC	2	16 0 0 0	268
<i>Escherichia coli</i> pDX1	A. Piekarowicz	<i>Eco</i> DX1	ATCAN(N) ₂ ATTC	Type I	1 2 0 0	202
<i>Escherichia coli</i> J62 pLG74	L.I. Glatman	<i>Eco</i> RV	GATATC	21	9 1 0 1	133;133,231
<i>Escherichia coli</i> RY13	R.N. Yoshimori	<i>Eco</i> RI	G(A)ATTC	5	5 1 0 1	87;99;87;55
<i>Escherichia coli</i> R245	R.N. Yoshimori	<i>Eco</i> RI'	PuPuA(T)PY	190	100 24 16 15	188
		<i>Eco</i> RII	TCC(A)GG	71	136 17 2 6	313;12,20; 313;20
<i>Escherichia coli</i> 15T ⁻	T. Bickle	<i>Eco</i> A	GAG(N) ₂ GTCA ^h	Type I	0 0 0 0	270,143
<i>Escherichia coli</i> B	W. Arber	<i>Eco</i> B	TG(A(N) ₂ TGCT	Type I	1 0 0 0	63;152,212; 153;290

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c			References	
					AG2	SV40 ΦX	pBR		
* <i>Escherichia coli</i> E166	N.E. Murray	<i>EcoD</i>	TTA(N) ₇ GTCPY	Type I	1	0	0	193	
<i>Escherichia coli</i> K	M. Meselson	<i>EcoK</i>	AAC(N) ₆ GTGC	Type I	0	0	2	179;11,128;92	
<i>Escherichia coli</i> (P1)	K. Murray	<i>EcoPI</i>	AGACC	Type III ^d	4	7	4	91;5;21, 22;5;97	
<i>Escherichia coli</i> P15	W. Arber	<i>EcoP15</i>	CAGCAG	Type III ^d	12	5	7	214;93	
* <i>Eucapsia</i> species	PCC 6906	<i>EspI</i>	GC↑TNAGC	7	8	1	0	0	30
* <i>Fischerella</i> species	ATCC 29114	<i>FspI (MsrI)</i>	TGCGCA	15	17	0	1	4	275
*		<i>FspII (AraII)</i>	TT↑CGAA	7	1	0	0	0	275
<i>Flavobacterium okeanoicoles</i>	IFO 12536	<i>FokI</i>	GGATG (9/13)	150	78	11	8	12	266
<i>Fremyella diplosiphon</i>	PCC 7601	<i>FdHI (AvaII)</i>	G↑G↑CC	35	73	6	1	8	286,264
		<i>FdHII (MsrI)</i>	TGC↑GCA	15	17	0	1	4	286,264
<i>Fusobacterium nucleatum</i> A	M. Smith	<i>FnuAI (HhaI)</i>	G↑ANTC	148	72	10	21	10	163
		<i>FnuAII (MboI)</i>	GATC	116	87	8	0	22	163;192
<i>Fusobacterium nucleatum</i> C	M. Smith	<i>FnuCI (MboI)</i>	↑GATC	116	87	8	0	22	163
<i>Fusobacterium nucleatum</i> D	M. Smith	<i>FnuDI (HaeIII)</i>	GG↑CC	149	216	18	11	22	163
		<i>FnuDII</i>	CG↑CG	157	303	0	14	23	163
		<i>FnuDIII (HhaI)</i>	GCG↑C	215	375	2	18	31	163
<i>Fusobacterium nucleatum</i> E	M. Smith	<i>FnuEI (SmaI)</i>	↑GATC	116	87	8	0	22	163
<i>Fusobacterium nucleatum</i> 48	M. Smith	<i>Fnu48I</i>	?	>50	?	?	>10	?	162
<i>Fusobacterium nucleatum</i> 4H	M. Smith	<i>Fnu4HI</i>	GC↑NGC	379	411	24	31	42	158
<i>Gluconobacter dioxyacetonicus</i>	IAM 1814	<i>GdHI (SmaI)</i>	AGG↑CCT	6	11	7	1	0	288
		<i>GdHII</i>	Py↑GGCCG	21	53	0	2	5	288

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c Ad2 SV40 Φ X pBR	References
<i>Glucobacter dioxyacetonicus</i>	IAM 1840	<i>GdoI</i> (<i>Bam</i> HI)	GGATCC	5	3 1 0 1	242
<i>Glucobacter gluconicus</i>	IFO 3285	<i>GgII</i>	?	7	7 7 7 7	268
<i>Glucobacter industriicus</i>	IFO 3260	<i>GmiI</i> (<i>Bam</i> HI)	GGATCC	5	3 1 0 1	268
<i>Glucobacter oxydans</i> sub. melonigenes	IAM 1836	<i>GoxI</i> (<i>Bam</i> HI)	GGATCC	5	3 1 0 1	242
<i>Glucobacter suboxydans</i> H-15T	M.S. Loytsianskaya	<i>GsmI</i>	CTCCAG	25	32 6 3 4	115
<i>Glucobacter suboxydans</i>	M.S. Loytsianskaya	<i>GsbI</i> (<i>GsmI</i>)	CTCCAG	25	32 6 3 4	108
<i>Haemophilus segypticus</i>	ATCC 11116	<i>HaeI</i>	(<u>AGG</u> TCC(A))	64	56 11 6 7	194
		<i>HaeII</i>	PuGGCGTPy	48	76 1 8 11	216;284
		<i>HaeIII</i>	GGTCC	149	216 18 11 22	180;23;170;170
<i>Haemophilus sphaerophilus</i>	ATCC 19415	<i>HepI</i>	?	>30	7 7 7 7	192
		<i>HepII</i> (<i>Hpa</i> II)	CTCGG	328	171 1 5 26	278;269
<i>Haemophilus gallinarum</i>	ATCC 14385	<i>HgeI</i>	GACGC (s/10)	102	87 0 14 11	278;28;265
<i>Haemophilus haemoglobinophilus</i>	ATCC 19416	<i>HhgI</i> (<i>Hae</i> III)	GGCC	149	216 18 11 22	192
<i>Haemophilus haemolyticus</i>	ATCC 10014	<i>HhaI</i>	GCGTC	215	375 2 18 31	218;218;171
		<i>HhaII</i> (<i>Hha</i> I)	GANTC	148	72 10 21 10	169
<i>Haemophilus influenzae</i> GU	J. Chirikjan	<i>Hha</i> III (<i>Hha</i> I)	GGGC	215	375 2 18 31	259;36
		<i>Hha</i> IV (<i>Fok</i> I)	GGATG	150	78 11 8 12	259;194;280
<i>Haemophilus influenzae</i> 173	J. Chirikjan	<i>Hha</i> 173 (<i>Hha</i> III)	AAGCTT	6	12 6 0 1	259
<i>Haemophilus influenzae</i> 1056	J. Stuy	<i>Hha</i> 10561 (<i>Fnu</i> DI)	CGCG	157	303 0 14 23	198
		<i>Hha</i> 10561I	?	>30	>30 0 5 7	198

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References
				λ	Ad2	SV40 ΦX PBR	
Haemophilus influenzae serotype b, 1076	J. Stuy	<i>HincIII</i> (<i>HindIII</i>)	AAGCTT	6	12	6 0 1	198
Haemophilus influenzae serotype c, 1160	J. Stuy	<i>HincII</i> (<i>HindII</i>)	GTPyPuAC	35	25	7 13 2	198
Haemophilus influenzae serotype c, 1161	J. Stuy	<i>HincII</i> (<i>HindII</i>)	GTPyPuAC	35	25	7 13 2	198
Haemophilus influenzae R _b	C.A. Hutchison	<i>HincIII</i> (<i>HindIII</i>)	AAGCTT	6	12	6 0 1	181,192
Haemophilus influenzae R _c	A. Landy, G. Leidy	<i>HincII</i> (<i>HindII</i>)	GTPyPuAC	35	25	7 13 2	148
Haemophilus influenzae R _d (exo mutant)	S. H. Goodgal	<i>HindI</i>	CAC			specific methylase	225;226
		<i>HindII</i>	GTPyPuAC	35	25	7 13 2	257;131;225;226
		<i>HindIII</i>	ATAGCTT	6	12	6 0 1	197;197;225;226
		<i>HindIV</i>	GAC			specific methylase	225;226
Haemophilus influenzae serotype e	A. Piekarowicz	<i>HincI</i> (<i>HincIII</i>)	CGAAT ^o	Type III ^d	0	5 1	201
Haemophilus influenzae R _γ	C.A. Hutchison	<i>HincI</i>	GATANTC	148	72	10 21 10	181;110,190
		<i>HincII</i> (<i>HindIII</i>)	AAGCTT	6	12	6 0 1	171
		<i>HincIII</i>	CGAAT ^o	Type III ^d	0	5 1	129;203
Haemophilus influenzae H-1	M. Takanami	<i>HincHI</i> (<i>HincII</i>)	PuGCGCPy	48	76	1 8 11	278
Haemophilus influenzae P ₁	S. Shen	<i>HincP₁</i> (<i>HincI</i>)	GTCGC	215	375	2 18 31	244
Haemophilus influenzae S ₁	S. Shen	<i>HincS₁</i> (<i>HincI</i>)	GCGC	215	375	2 18 31	244
Haemophilus influenzae S ₂	S. Shen	<i>HincS₂</i> (<i>HincI</i>)	GCGC	215	375	2 18 31	244
Haemophilus influenzae JC9	A. Piekarowicz	<i>HincJCI</i> (<i>HindII</i>)	GTPyPuAC	35	25	7 13 2	204
		<i>HincJCI</i> (<i>HindIII</i>)	AAGCTT	6	12	6 0 1	204
Haemophilus parahaemolyticus	C.A. Hutchison	<i>HphI</i>	GGTGA (8/7)	168	99	4 9 12	181;138

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 Φ X pBR	References
<i>Haemophilus parainfluenzae</i>	J. Setlow	<i>HpaI</i>	GTTTAAAC	14	6 4 3 0	243;70;1
		<i>HpaII</i>	C ¹ CGG	328	171 1 5 26	243;70;170;170
<i>Haemophilus suis</i>	ATCC 19417	<i>HsuI</i> (<i>HindIII</i>)	A ¹ AGCTT	6	12 6 0 1	192
<i>Halococcus agglomeratus</i>	ATCC 25862	<i>HagI</i>	?	7	7 7 7 7	209
<i>Herpetosiphon giganteus</i> HP1023	J.H. Parish	<i>HgIAI</i>	G ¹ AGC(A) ¹ TC	28	38 0 3 8	27
<i>Herpetosiphon giganteus</i> Hpg5	H. Reichenbach	<i>HgIBI</i> (<i>AvaII</i>)	G ¹ G(A) ¹ CC	35	73 6 1 8	144
<i>Herpetosiphon giganteus</i> Hpg9	H. Reichenbach	<i>HgIC1</i>	TGGPyPuCC	25	57 1 3 9	144
		<i>HgICII</i> (<i>AvaII</i>)	G ¹ G(A) ¹ CC	35	73 6 1 8	144
		<i>HgICIII</i> (<i>SmaI</i>)	G ¹ TCGAC	2	3 0 0 1	144
<i>Herpetosiphon giganteus</i> Hpa2	H. Reichenbach	<i>HgIDI</i> (<i>Acyl</i>)	GPu ¹ CGPyC	40	44 0 7 6	144
		<i>HgIDII</i> (<i>SmaI</i>)	G ¹ TCGAC	2	3 0 0 1	144
<i>Herpetosiphon giganteus</i> Hpg24	H. Reichenbach	<i>HgIEI</i> (<i>AvaII</i>)	G ¹ G(A) ¹ CC	35	73 6 1 8	144
		<i>HgIEII</i>	ACC(N) ₆ GGT	14	10 1 1 2	144
<i>Herpetosiphon giganteus</i> Hpg 14	H. Reichenbach	<i>HgIFI</i>	?	7	15 7 7 7	175
<i>Herpetosiphon giganteus</i> Hpa1	H. Reichenbach	<i>HgIGI</i> (<i>Acyl</i>)	GPu ¹ CGPyC	40	44 0 7 6	144
<i>Herpetosiphon giganteus</i> HP1049	J.H. Parish	<i>HgIHI</i> (<i>HgiCI</i>)	G ¹ GPYPuCC	25	57 1 3 9	303
		<i>HgIHII</i> (<i>Acyl</i>)	GPu ¹ CGPyC	40	44 0 7 6	303
		<i>HgIHIII</i> (<i>AvaII</i>)	G ¹ G(A) ¹ CC	35	73 6 1 8	303
<i>Herpetosiphon giganteus</i> HFS101	H. Foster	<i>HgJII</i>	?	7	7 7 7 7	303
		<i>HgJIII</i>	GPu ¹ CGPy ¹ C	7	57 2 0 2	303

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				λ	SV40	Φ X	pBR	
Herpetosiphon giganteus Hpg 32	H. Reichenbach	HgtKI	?	>18	>20	?	?	175
Klebsiella pneumoniae OK8	J. Davies	KpnI	GGTAC \uparrow C	2	8	1	0	255;281
Mastigocladus laminosus	CCAP 1447/1	Mzal (AmsII)	TT \uparrow CGAA	7	1	0	0	57
Methanococcus aeolicus PL-15/H	K.O. Stetter	MaeI	C \uparrow TAG	13	54	12	3	238
		MaeII	A \uparrow CGT	143	83	0	19	10 238
		MaeIII	\uparrow GTNAC	156	118	14	17	17 238
* Methanococcus jannaschii	H. Escalante	Mjai (MaeI)	CTAG	13	54	12	3	5 317
*		MjaiI (AmsI)	GGNCC	74	164	11	2	15 317
Microbacterium thermosphactum	ATCC 11509	Mthi (Sau3A)	GATC	116	87	8	0	22 149
Micrococcus aurantiacus	IFO 12422	MauI (PstI)	CTGCAG	28	30	2	1	1 268
Micrococcus luteus	IFO 12992	MluI	A \uparrow CGCGT	7	5	0	2	0 266
Micrococcus radiodurans	ATCC 13939	Mrai (SacII)	CCGGGG	4	33	0	1	0 299
* Micrococcus species	R. Meagher	MrsI (NaeI)	GCCGGC	1	13	1	0	4 178
Micrococcus varians	RFL 19	Mval (BstNI)	CC \uparrow GG	71	136	17	2	6 124
Microcoleus species	D. Comb	MziI	TGC \uparrow GCA	15	17	0	1	4 45;79
* Micromonospora carbonacea	C. Kessler	MrsII (SmaI)	CC \uparrow TNAGG	2	7	0	0	0 230
Moraxella bovis	ATCC 10900	Mcal (XhoI)	CTCGAG	1	6	0	1	0 132
		MboI	\uparrow GATC	116	87	8	0	22 73
		MboII	GAAGA (8/7)	130	113	16	11	11 73;36,60
Moraxella bovis	ATCC 17947	MbyI	?	?	?	?	?	? 127
Moraxella glucidi LG1	J. Davies	MgiI	?	?	?	?	?	? 255

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c Ad2	SV40	Φ X	pBR	References
<i>Moraxella glucidi</i> LG2	J. Davies	<i>Mgl</i> II	?	?	?	?	?	?	255
<i>Moraxella kingae</i>	ATCC 23331	<i>Mkl</i> I (<i>Hind</i> III)	AAGCTT	6	12	6	0	1	127
<i>Moraxella nonliquefaciens</i>	ATCC 19975	<i>Mnl</i> I (<i>Hpa</i> II)	C \uparrow CGG	328	171	1	5	26	192;7
		<i>Mnl</i> II (<i>Mra</i> III)	?	>10	>6	3	?	?	192
		<i>Mnl</i> III (<i>Mbo</i> I)	GATC	116	87	8	0	22	192
<i>Moraxella nonliquefaciens</i>	ATCC 17953	<i>Mnl</i> I	CCTC (7/7)	262	397	51	34	26	314;230
<i>Moraxella nonliquefaciens</i>	ATCC 17954	<i>Mnl</i> I (<i>Hind</i> II)	GTPyPuAC	35	25	7	13	2	94
		<i>Mnl</i> II (<i>Hae</i> III)	GGCC	149	216	18	11	22	94
		<i>Mnl</i> III	?	>10	>6	3	?	?	94
		<i>Mnl</i> IV (<i>Hha</i> I)	GCGC	215	375	2	18	31	94
<i>Moraxella nonliquefaciens</i>	ATCC 19996	<i>Mnl</i> I (<i>Hae</i> III)	GGCC	149	216	18	11	22	127
		<i>Mnl</i> II (<i>Hpa</i> II)	CCGG	328	171	1	5	26	127
<i>Moraxella osloensis</i>	ATCC 19976	<i>Mnl</i> I (<i>Mbo</i> I)	GATC	116	87	8	0	22	73
<i>Moraxella phenylpyruvica</i>	ATCC 17955	<i>Mpl</i> I (<i>Eco</i> RII)	CC \uparrow GGG	71	136	17	2	6	127
<i>Moraxella</i> species	R.J. Roberts	<i>Mpl</i> I (<i>Hpa</i> II)	C \uparrow CGG	328	171	1	5	26	289;289,230;126
<i>Myxococcus stipitatus</i> Mx2	H. Reichenbach	<i>Msl</i> I (<i>Xho</i> I)	CTCGAG	1	6	0	1	0	181,192
		<i>Msl</i> II	?	?	?	?	?	?	175
<i>Myxococcus virescens</i> V-2	H. Reichenbach	<i>Mvl</i> I	?	1	?	?	?	?	185
		<i>Mvl</i> II	?	?	?	?	?	?	185
<i>Neisseria caviae</i>	NRCC 31003	<i>Nca</i> I (<i>Hinf</i> I)	GANTC	148	72	10	21	10	295

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	Φ X174		PBR
<i>Neisseria cinerea</i>	NRCC 31006	<i>NciI</i> (CaulI)	CCT(C)GG ^f	114	97	0	1	10	300:105
<i>Neisseria cuniculi</i>	ATCC 14688	<i>NcuI</i> (MbolII)	GAAGA	130	113	16	11	11	28
<i>Neisseria demitricans</i>	NRCC 31009	<i>NdeI</i>	CAATTAG	7	2	2	0	1	301
<i>Neisseria flavescens</i>	NRCC 31011	<i>NdeII</i> (Mbol)	GATC	116	87	8	0	22	295
		<i>NfiI</i> (Mbol)	GATC	116	87	8	0	22	295
* <i>Neisseria flavescens</i>	ATCC 13120	<i>NfIII</i>	?	?	?	?	?	?	295
		<i>NfIII</i>	?	?	?	?	?	?	295
		<i>NfAI</i> (EcoRV)	GATATC	21	9	1	0	1	172
* <i>Neisseria gonorrhoea</i>	G. Wilson	<i>NfAII</i> (Mbol)	GATC	116	87	8	0	22	172
		<i>NgoI</i> (HaeIII)	PuGGGCPy	48	76	1	8	11	306
<i>Neisseria gonorrhoea</i>	CDC 66	<i>NgoII</i> (HaeIII)	GGCC	149	216	18	11	22	38
<i>Neisseria gonorrhoea</i> KH 7764-45	L. Mayer	<i>NgoIII</i> (SccII)	CCGGCG	4	33	0	1	0	195
<i>Neisseria lactamica</i>	NRCC 2118	<i>NlaI</i> (HaeIII)	GGCC	149	216	18	11	22	211
		<i>NlaII</i> (Mbol)	GATC	116	87	8	0	22	211
<i>Neisseria lactamica</i>	NRCC 31016	<i>NlaIII</i>	CATG [†]	181	183	17	22	26	211
		<i>NlaIV</i>	GGN [†] NC	82	178	16	6	24	211
* <i>Neisseria meningitidis</i> DRES-W34	R. Sparling	<i>NlaSI</i> (SccII)	CCGGCG	4	33	0	1	0	32
		<i>NlaSII</i> (Acyl)	GPuGGPYC	40	44	0	7	6	32
* <i>Neisseria meningitidis</i> M1011	R. Sparling	<i>NmeI</i>	?	18	?	?	?	?	260
* <i>Neisseria meningitidis</i> M1011	R. Sparling	<i>NmeII</i>	?	28	?	0	0	?	260
		<i>NmeIII</i>	?	?	?	?	?	?	260

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40 ΦX	pBR		
# <i>Neisseria meningitidis</i> DRES-30	R. Sparling	<i>NmeIV</i>	?	7	7	7	7	260	
<i>Neisseria mucosa</i>	ATCC 19693	<i>NmuSI (AseI)</i>	GGNCC	74	164	11	2	15	43
<i>Neisseria mucosa</i>	ATCC 19697	<i>NmuFI (NaeI)</i>	GCCGGC	1	13	1	0	4	31
<i>Neisseria mucosa</i>	ATCC 25996	<i>NmuEI (DpmI)</i>	GATC	only cleaves methylated DNA				28	
		<i>NmuEII (AseI)</i>	GGNCC	74	164	11	2	15	31
<i>Neisseria mucosa</i>	ATCC 25997	<i>NmuDI (DpmI)</i>	GATC	only cleaves methylated DNA				31	
<i>Neisseria mucosa</i>	NRCC 31013	<i>NmusI (NaeI)</i>	GCCGGC	1	13	1	0	4	295
# <i>Neisseria mucosa</i>	ATCC 25999	<i>NhesI</i>	GfCTAGC	1	4	0	0	1	44
<i>Neisseria ovis</i>	NRCC 31020	<i>NovI</i>	?	7	7	7	7	7	295
		<i>NovII (HinfI)</i>	GANTC	148	72	10	21	10	295
<i>Neisseria sicca</i>	ATCC 9913	<i>NsIAI (Sma3A)</i>	GATC	116	87	8	0	22	40
<i>Neisseria sicca</i>	ATCC 29256	<i>NsII (AvaII)</i>	ATGCAfT	14	9	3	0	0	42
<i>Neisseria sicca</i>	NRCC 31004	<i>NsIII (HinfI)</i>	GANTC	148	72	10	21	10	294
<i>Neisseria subflava</i>	ATCC 19243	<i>NsuDI (DpmI)</i>	GATC	only cleaves methylated DNA				31	
<i>Neisseria subflava</i>	ATCC 14221	<i>NsuI (MboI)</i>	GATC	116	87	8	0	22	31
<i>Nocardia asteroides</i>	ATCC 23870	<i>NaeI</i>	GCCfGGC	1	13	1	0	4	47
<i>Nocardia amarae</i>	ATCC 27809	<i>Nami (NarI)</i>	GGGCC	1	20	0	2	4	161
<i>Nocardia argentinensis</i>	ATCC 31306	<i>NarI</i>	GGfCGCC	1	20	0	2	4	46
<i>Nocardia blackwellii</i>	ATCC 6846	<i>NbII (PvuI)</i>	CGATfCG	3	7	0	0	1	230
<i>Nocardia brasiliensis</i>	ATCC 27936	<i>NbrI (NaeI)</i>	GCCGGC	1	13	1	0	4	209
<i>Nocardia brasiliensis</i>	ATCC 19296	<i>NbaI (NaeI)</i>	GCCGGC	1	13	1	0	4	209

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 Φ X pBR	References
<i>Nocardia corallina</i>	ATCC 19070	<i>Nco</i> I	C ¹ CATGG	4	20 3 0 0	149
<i>Nocardia dassonvillei</i>	ATCC 21944	<i>Nda</i> I (<i>Nar</i> I)	GG ¹ CGCC	1	20 0 2 4	41
<i>Nocardia minima</i>	ATCC 19150	<i>Nmi</i> I (<i>Kpm</i> I)	GGTACC	2	8 1 0 0	44
<i>Nocardia opaca</i>	ATCC 21507	<i>Nop</i> I (<i>Sad</i> I)	G ¹ TCGAC	2	3 0 0 1	230
		<i>Nop</i> II	?	?	7 7 7 7	149
<i>Nocardia otitidis-caviarum</i>	ATCC 14630	<i>Nor</i> I	GC ¹ GGCCGC	0	7 0 0 0	19:237
<i>Nocardia otitidis-caviarum</i>	ATCC 14629	<i>Noc</i> I (<i>Pzt</i> I)	CTGCAG	28	30 2 1 1	44
<i>Nocardia rubra</i>	ATCC 15906	<i>Nra</i> I	TCG ¹ CGA	5	5 0 2 1	44
<i>Nocardia uniformis</i>	ATCC 21806	<i>Nua</i> I	?	?	7 7 7 7	149
		<i>Nua</i> II (<i>Nvar</i> I)	GG ¹ CGCC	1	20 0 2 4	149
<i>Noctoc species</i>	PCC 6705	<i>Nsp</i> BI (<i>Ass</i> II)	TTCGAA	7	1 0 0 0	59
		<i>Nsp</i> BII	C ¹ ₂ G ¹ C ¹ ₂ G ¹ ₂	75	95 4 5 6	59
		<i>Nsp</i> (7524)I	PuCATG ¹ Py _G	32	41 2 0 4	213
	PCC 7524	<i>Nsp</i> (7524)II (<i>Sda</i> I)	G ¹ (A)G ¹ C ¹ (A) ¹ T _C	38	105 4 3 10	213
		<i>Nsp</i> (7524)III (<i>Ava</i> I)	C ¹ PyCGP _G UG	8	40 0 1 1	213
		<i>Nsp</i> (7524)IV (<i>Ass</i> I)	G ¹ GNCC	74	164 11 2 15	213
		<i>Nsp</i> (7524)V (<i>Ass</i> II)	TTCGAA	7	1 0 0 0	213
	PCC 7413	<i>Nsp</i> HI (<i>Nsp</i> (7524)I)	PuCATG ¹ Py	32	41 2 0 4	59
		<i>Nsp</i> III (<i>Ava</i> I)	GG ¹ (₁)CC	35	73 6 1 8	59
<i>Oerthovia xanthineolytica</i>	R. Shetman	<i>Oxa</i> I (<i>Adu</i> I)	AGCT	143	158 34 24 16	263
		<i>Oxa</i> II	?	?	7 7 7 7	263

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References
				λ	Ad2	SV40 ΦX pBR	
<i>Proteus vulgaris</i>	ATCC 13315	<i>PvuI</i>	CGATTCG	3	7	0 0 1	78
		<i>PvuII</i>	CAGTCG	15	24	3 0 1	78
<i>Providencia alcalifaciens</i>	ATCC 9886	<i>PaiI (HaeIII)</i>	GGCC	149	216	18 11 22	74
<i>Providencia stuartii</i> 164	J. Davies	<i>PstI</i>	CTGCAIG	28	30	2 1 1	255;29
<i>Pseudonabaena</i> species	ATCC 27263	<i>PspI (AraI)</i>	GGNCC	74	164	11 2 15	187
<i>Pseudomonas aeruginosa</i>	G.A. Jacoby	<i>PaeR7 (XhoI)</i>	CCTCGAG	1	5 ^g	0 0 0	101;77
<i>Pseudomonas alkaligenes</i>	ATCC 12815	<i>PaiI (HaeIII)</i>	GGCC	149	216	18 11 22	268
<i>Pseudomonas alkanolytica</i>	IFO 12319	<i>PanI (XhoI)</i>	CCTCGAG	1	6	0 1 0	268
<i>Pseudomonas facilis</i>	M. VanMontagu	<i>Pfal (Sma3A)</i>	GATC	116	87	8 0 22	289
<i>Pseudomonas fluorescens</i>	IFO 3507	<i>PfII</i>	?	?	?	?	268
* <i>Pseudomonas fluorescens</i>	T.S. Wang	<i>PfWI (XhoI)</i>	CTCGAG	1	6	0 1 0	297
<i>Pseudomonas glycinae</i>	J.V. Leary	<i>PglI (NaeI)</i>	GCCGGC	1	13	1 0 4	155
		<i>PgII</i>	?	0	>25	0 ? 1	155
<i>Pseudomonas maltophilia</i>	D. Comb	<i>PmaI (PstI)</i>	CTGCAG	28	30	2 1 1	230
<i>Pseudomonas putida</i> C-83	Toyoboseki Co.	<i>PpaI (HaeIII)</i>	GGCC	149	216	18 11 22	268
<i>Rhizobium leguminosarum</i> 300	J. Beringer	<i>RleI</i>	?	6	>10	?	308
<i>Rhizobium lupini</i> 1	W. Heumann	<i>RlsI (NaeI)</i>	GCCGGC	1	13	1 0 4	307,100;254
<i>Rhizobium meliloti</i>	J.L. Denarie	<i>RmeI</i>	?	8	>10	?	100
<i>Rhodococcus rhodochrous</i>	ATCC 14349	<i>RrAI (SaiI)</i>	GTCGAC	2	3	0 0 1	209
		<i>RrMI</i>	?	?	?	?	209
<i>Rhodococcus rhodochrous</i>	ATCC 4276	<i>RrOI (SaiI)</i>	GTCGAC	2	3	0 0 1	209

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	ΦX ₁₇₄ pBR		
Rhodococcus species	ATCC 13259	RhsI (BamHI)	GGATCC	5	3	1	0	1	109
Rhodococcus species	ATCC 19148	RhpI (SafI)	GTCGAC	2	3	0	0	1	109
		RhpII	?	?	?	?	?	?	109
Rhodococcus species	ATCC 21664	RheI (SafI)	GTCGAC	2	3	0	0	1	109
Rhodopseudomonas sphaeroides	R. Lascelles	RspI (PvuI)	CGATCG	3	7	0	0	1	13
Rhodopseudomonas sphaeroides	S. Kaplan	RshI (PvuI)	CGATTCG	3	7	0	0	1	165
Rhodopseudomonas sphaeroides	S. Kaplan	Rzal	GTATAC	113	83	12	11	3	166
Rhodopseudomonas sphaeroides	S. Kaplan	RsrI (EcoRI)	GAATTC	5	5	1	0	1	69
*		RsrII	CGTGAJCCG	5	2	0	0	0	196
* Rhodopseudomonas sphaeroides	V.M. Kramarov	RshII (CauII)	CCGJGG	114	97	0	1	10	142
Rhodospirillum rubrum	J. Chirikjian	RrbI	?	?	4	5	1	?	157
Salmonella infantis	A. deWaard	ShiI (AvaII)	GGJCC	35	73	6	1	8	164
* Salmonella typhi 27	E.S. Anderson	StyI	CTCJAJGG	10	44	8	0	1	166b
Serratia marcescens S _b	C. Mulder	Smal	CCCJGGG	3	12	0	0	0	88;61
Serratia species SAI	B. Torheim	SspI	?	?	?	?	?	?	282
* Shigella boydii 13	NCTC 9361	Sbo13 (NruI)	TCGCGA	5	5	0	2	1	311
Sphaerotilus natans C	A. Pope	SnaI	GTATAC	3	3	0	0	1	206
Sphaerotilus natans	ATCC 15291	SnaBI	TACJGTA	1	0	0	0	0	18
* Sphaerotilus natans	ATCC 13925	SspI	AATJATT	20	5	1	6	1	85
* Sphaerotilus natans	ATCC 13923	SspI	AJCTAGT	0	3	0	0	0	44
Spiroplasma citri ASP2	M.A. Stephens	ScfNI (HhaI)	GJCGC	215	375	2	18	31	261

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 ΦX pBR	References
<i>Staphylococcus aureus</i> 3A	E.E. Stobberingh	<i>Sau</i> 3A (<i>M</i> boI)	↑GATC	116	87 8 0 22	271
<i>Staphylococcus aureus</i> PS96	E.E. Stobberingh	<i>Sau</i> 96I (<i>A</i> suI)	G↑GNCC	74	164 11 2 15	272
<i>Staphylococcus intermedius</i>	ATCC 29663	<i>St</i> aMI (<i>M</i> boI)	GATC	116	87 8 0 22	31
		<i>St</i> aMII	?	?	?	?
<i>Staphylococcus saprophyticus</i>	ATCC 13518	<i>S</i> saI	?	>10	?	?
<i>Streptococcus cremoris</i> F	C. Daly	<i>Ser</i> FI	CC↑NGG	185	233 17 3 16	65
<i>Streptococcus durans</i>	A. Janulaitis	<i>S</i> duI	G(A)GC(A)C T	38	105 4 3 10	118
<i>Streptococcus dysgalactiae</i>	ATCC 9926	<i>S</i> dyI (<i>A</i> suI)	GGNCC	74	164 11 2 15	209
<i>Streptococcus faecalis</i> var. <i>zymogenes</i>	R. Wu	<i>S</i> faI (<i>H</i> aeIII)	GG↑CC	149	216 18 11 22	309
<i>Streptococcus faecalis</i> GU	J. Chirikjian	<i>S</i> faGU I (<i>H</i> paII)	CCGG	328	171 1 5 26	39
<i>Streptococcus faecalis</i> ND547	D. Clewell	<i>S</i> faNI	GCATC (s/9)	169	84 6 12 22	240
<i>Streptomyces achromogenes</i>	ATCC 12767	<i>S</i> acI	GAGCT↑C	2	16 0 0 0	2
		<i>S</i> acII	CCGC↑GG	4	33 0 1 0	2
		<i>S</i> acIII	?	>100	>100 7 7 7	2
<i>Streptomyces albus</i>	CMI 52766	<i>S</i> alPI (<i>P</i> stI)	CTGCA↑G	28	30 2 1 1	35;33
<i>Streptomyces albus</i> subspecies <i>pathocidicus</i>	KCC S-0166	<i>S</i> paI (<i>X</i> hoI)	CTCGAG	1	6 0 1 0	250
<i>Streptomyces albus</i> G	J.M. Ghuyssen	<i>S</i> alI	G↑TCGAC	2	3 0 0 1	3
		<i>S</i> alII	?	>20	?	?
<i>Streptomyces aureofaciens</i> IKA 18/4	J. Timko	<i>S</i> auI	CC↑TNAGG	2	7 0 0 0	279
<i>Streptomyces aureofaciens</i>	CCM 3239	<i>S</i> au3239 I	?	1	?	?
<i>Streptomyces boblii</i>	ATCC 3310	<i>S</i> boI (<i>S</i> acII)	CCGCGG	4	33 0 1 0	250;276

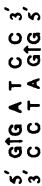
Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c SV40 Φ X pBR	References
<i>Streptomyces caespitosus</i>	H. Takahashi	ScaI	AGTACT	5	5 0 0 1	139;85
<i>Streptomyces cupidosporus</i>	KCC S0316	ScaI (XhoI)	CTCGAG	1	6 0 1 0	250
<i>Streptomyces exfoliatus</i>	KCC S0030	SaxI (XhoI)	CTCGAG	1	6 0 1 0	250
		SaxII	?	2	7 7 7 7	250
<i>Streptomyces fimbriatus</i>	ATCC 15051	SfiI	GGCCNNNTGGCC	0	3 1 0 0	210
<i>Streptomyces fradiae</i>	ATCC 3355	SfrI (SacII)	CCGCGG	4	33 0 1 0	250;276
<i>Streptomyces ganmycicus</i>	KCC S0759	SgeI (XhoI)	CTCGAG	1	6 0 1 0	250
<i>Streptomyces goshikiensis</i>	KCC S0294	SgoI (XhoI)	CTCGAG	1	6 0 1 0	250
<i>Streptomyces griseus</i>	ATCC 23345	SgrI	?	0	7 0 7 7	2
* <i>Streptomyces griseus</i> Kr. 20	A.V. Orekhov	SgrII (EcoRII)	CCCTGG	71	136 17 2 6	199
<i>Streptomyces hygroscopicus</i>	T. Yamaguchi	ShyTI	?	2	7 7 7 7	250
<i>Streptomyces hygroscopicus</i>	F. Walter	ShyI (SacII)	CCGCGG	4	33 0 1 0	296
<i>Streptomyces karnatakensis</i>	ATCC 25463	Skal (NaeI)	GCCGGC	1	13 1 0 4	31
		SkalI (PstI)	CTGCAG	28	30 2 1 1	31
<i>Streptomyces lavendulae</i>	ATCC 8664	SlaI (XhoI)	CCTCGAG	1	6 0 1 0	277
<i>Streptomyces lateoreticuli</i>	KCC S0788	SlaI (XhoI)	CTCGAG	1	6 0 1 0	276
<i>Streptomyces odorifer</i>	ATCC 6246	SodI	?	7	7 7 7 7	149
		SodII	?	7	7 7 7 7	149
<i>Streptomyces phaeochromogenes</i>	F. Bolivar	SpmI	GCATGTC	6	8 2 0 1	68
<i>Streptomyces phaeochromogenes</i>	IFO 3108	SpeI (SpmI)	GCATGC	6	8 2 0 1	268

Microorganism	Source	Enzyme ^a	Sequence ^b	λ	Number of cleavage sites ^c Ad2 SV40 Φ X pBR	References			
Streptomyces stanford	S. Goff, A. Rambach	<i>Sst</i> I (<i>Sac</i> I)	GAGCT \uparrow C	2	16	0	0	0	82;186
		<i>Sst</i> II (<i>Sac</i> II)	CCGC \uparrow GG	4	33	0	1	0	82
		<i>Sst</i> III (<i>Sac</i> III)	?	>100	>100	?	?	?	82
		<i>Sst</i> IV (<i>Bcl</i> I)	TGATCA	8	5	1	0	0	104
Streptomyces tubercidicus	H. Takahashi	<i>Stal</i>	AGG \uparrow CCCT	6	11	7	1	0	249
Streptovorticillium flavoperanicum	Uppjohn UC 5066	<i>Sy</i> II (<i>Pst</i> I)	CTGCA \uparrow TG	28	30	2	1	1	127
* Sulfolobus acidocaldarius	W. Zillig	<i>Sul</i> I (<i>Hae</i> III)	GGCC	149	216	18	11	22	177
* Thermococcus celer	W. Zillig	<i>Tce</i> I (<i>Mbo</i> II)	GAAGA	130	113	16	11	11	177
Thermoplasma acidophilum	D. Seary	<i>Tha</i> I (<i>Pvu</i> DII)	CG \uparrow CG	157	303	0	14	23	176
Thermoplyspora glauca	ATCC 15345	<i>Tgh</i> I (<i>Sac</i> II)	CCGCGG	4	33	0	1	0	81
Thermus aquaticus YTI	J.I. Harris	<i>Taq</i> I	T \uparrow CGA	121	50	1	10	7	227;227-;228
		<i>Taq</i> II	GACCGA (11/9) CACCCA (11/9)	28	36	1	2	6	192,6
Thermus aquaticus	S.A. Grachev	<i>Taq</i> XI (<i>Bst</i> NI)	CC \uparrow (A)GG	71	136	17	2	6	83
Thermus flavus AT62	T. Oshima	<i>Tf</i> II (<i>Taq</i> I)	TCGA	121	50	1	10	7	228
Thermus thermophilus HB8	T. Oshima	<i>Th</i> HB8 I (<i>Taq</i> I)	TCGA	121	50	1	10	7	229,293;229, 292;228;228
Thermus thermophilus strain 23	T. Oshima	<i>Th</i> rI (<i>Tth</i> III I)	GACNNNGTC	2	12	0	0	1	253
Thermus thermophilus strain 110	T. Oshima	<i>Tte</i> I (<i>Tth</i> III I)	GACNNNGTC	2	12	0	0	1	253
Thermus thermophilus strain 111	T. Oshima	<i>Tth</i> III I	GACNTNGTC	2	12	0	0	1	253
		<i>Tth</i> III II	CAAPUCA (11/9)	49	53	11	11	5	252
		<i>Tth</i> III III	?	?	?	?	?	?	251

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40 ΦX	pBR		
<i>Tolypothrix tenuis</i>	W. Siegelman	<i>TniI</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	264
<i>Vibrio harveyi</i>	ATCC 14126	<i>VhaI</i> (<i>HaeIII</i>)	GGCC	149	216	18	11	22	109
<i>Xanthomonas amaranthicola</i>	ATCC 11645	<i>XamI</i> (<i>SalI</i>)	GTCGAC	2	3	0	0	1	3
<i>Xanthomonas badrii</i>	ATCC 11672	<i>XbaI</i>	TTC TAGA	1	5	0	0	0	316
* <i>Xanthomonas cyanopoidis</i> 13D5	C.I. Kado	<i>XcyI</i> (<i>SmaI</i>)	C ⁺ CCGGG	3	12	0	0	0	66
<i>Xanthomonas holcicola</i>	ATCC 13461	<i>XhoI</i>	C ⁺ TCGAG	1	6	0	1	0	80
<i>Xanthomonas malvacearum</i>	ATCC 9924	<i>XhoII</i>	Pu ⁺ GATCPY	21	22	3	0	8	198;81,141
		<i>XmaI</i> (<i>SmaI</i>)	C ⁺ CCGGG	3	12	0	0	0	61
		<i>XmaII</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	61
		<i>XmaIII</i>	C ⁺ GGCCG	2	19	0	0	1	145
<i>Xanthomonas manihotis</i> 7AS1	B-C. Lin	<i>XmaI</i>	GAANN ⁺ NNTTC	24	5	0	3	2	160,209
<i>Xanthomonas nigromaculans</i>	ATCC 23390	<i>XmiI</i> (<i>PvuI</i>)	CGATCG	3	7	0	0	1	94
<i>Xanthomonas oryzae</i>	M. Ehrlich	<i>XorI</i> (<i>PstI</i>)	CTGCAG	28	30	2	1	1	298
		<i>XorII</i> (<i>PvuI</i>)	CGAT ⁺ CG	3	7	0	0	1	298;78
<i>Xanthomonas papavericola</i>	ATCC 14180	<i>XpaI</i> (<i>XhoI</i>)	C ⁺ TCGAG	1	6	0	1	0	80

Footnotes to Table

- a. When two enzymes recognize the same sequence, i.e., are isochizomers, the prototype (i.e., the first example isolated) is indicated in parentheses. Note that *Mbo*I is sensitive to *dam* methylation, whereas its isochizomer *Sau*3A is not and *Eco*RII is sensitive to *dcm* methylation whereas its isochizomer *Bst*NI is not. For other isochizomers of these two enzymes the corresponding prototype is indicated according to its methylation sensitivity.
- b. 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, G↑GATCC is an abbreviation for



For enzymes such as *Hga*I, *Mbo*II etc, which cleave away from their recognition sequence the sites of cleavage are indicated in parentheses. For example *Hga*I GACGCGS/10 indicates cleavage as shown below



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

- Bases appearing in parentheses signify that either base may occupy that position in the recognition sequence. Thus, *Acl*I cleaves the sequences GTAGAC, GTATAC, GTCGAC, and GTCTAC. Where known, the base modified by the corresponding specific methylase is indicated by an asterisk. Å is N⁶-methyladenosine. C̄ is 5-methylcytosine.
- c. 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.

- d. *Eco*PI, *Eco*PI5, *Hma*I and *Hma*III have characteristics intermediate between those of the Type I and Type II restriction endonucleases. They are designated Type III in accordance with the suggestion of Kauc and Piękarowicz (129).
- e. Both *Hma*III and *Hma*I cleave about 25 bases 3' of the recognition sequence.
- f. *Nci*I leaves termini carrying a 3'-phosphate group (105).
- g. *Pae*RI fails to cleave the *Xho*I site at 26.5% on the Ad2 genome (77).
- h. The * placed under the T residue signifies that the A residue, on the complementary strand at that position, is modified by the *Eco*A methylase.

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