Restriction and modification enzymes and their recognition sequences

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Introduction

Since the last compilation of restriction endonucleases (160), 97 new entries have been added, including 17 new specificities. Most notable among the new specificities is AhaIII (TTTAAA), which is the first restriction enzyme to recognize only A/T base pairs. Other valuable new specificities are AdaI (GGGCCC), AflIII (CTTAAG), CfrI (PyGGCCPu), EcoRV (GATATC), FokI (GGATG), HgiIII (GPuGCPyC), MluI (ACGCGT), NdeI (CATATG), NaeI (GCCGGC), NarI (GGCGCC), NcoI (CCATGG), NruI (TCGCGA), NspBII (GC^CGC), NspCI (PuCATGPy), SerFI (CCNGG) and XmnI (GAA[N]₄TTC). Two entries have been removed, RruI and RruII, because the strain producing them has been lost. Fortunately an isoschizomer of RruI has been found. This is ScaI (AGTACT).

Among the 355 enzymes listed, there are a minimum of 85 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 (190). 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 shown 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case, refers to the purification procedure for the restriction enzyme, or from the individuals who have provided their unpublished results.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 contains the purification procedure for the methylase, and the fourth describes the recognition sequence for 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	Number of cleavage sites ^c λ Ad2 SV40 φX PBR	References
<i>Acetobacter aceti</i> sub. liquefaciens	IFO 12388	AacI (BamHI)	GGATCC	5 3 1 0 1	177
<i>Acetobacter aceti</i> sub. liquefaciens	M. Van Montagu	AacI (BamHI)	GGATCC	5 3 1 0 1	177
<i>Acetobacter aceti</i> sub. orleansensis	NCIB 8622	AorI (EcoRII)	CC-($\frac{A}{P}$)GG	>35 >35 16 2 6	177
<i>Acetobacter pasteurianus</i> sub. pasteurianus	NCIB 7215	AapI	GGGCC ^c C	1 >10 1 0 0	177
<i>Achromobacter immobilis</i>	ATCC 15934	AimI	?	? ? ? ? ?	47
<i>Acinetobacter calcoaceticus</i> ^h	R.J. Roberts	AacI	GT-($\frac{P}{P}$)($\frac{P}{P}$)AC	7 8 1 2 2	233
		AacII (EcoRII)	CGCG	>50 >50 0 14 23	233
		AacIII	?	>10 >6 ? ? ?	147
<i>Agmenellum quadruplicatum</i>	W.F. Doolittle	AquI (AvaI)	CPYCGPuG	8 15 0 1 1	112
<i>Agrobacterium tumefaciens</i>	ATCC 15955	AtuAI	?	>30 >30 ? ? ?	176
<i>Agrobacterium tumefaciens</i> B6806	E. Nester	AtuBI (EcoRII)	CC($\frac{A}{P}$)GG	>35d >35 16 2 6	167
<i>Agrobacterium tumefaciens</i> IIBV7	G. Roizes	AtuBVI	?	>14 ? 1 0 ?	166
<i>Agrobacterium tumefaciens</i> ID 135	C. Kado	AtuII (EcoRII)	CC($\frac{A}{P}$)GG	>35d >35 16 2 6	117
<i>Agrobacterium tumefaciens</i> C58	E. Nester	AtuCI (BclI)	TGATCA	7d 5 1 0 0	176
<i>Alcaligenes</i> species	N. Brown	AsdAI (BstEII)	G ^c GTNACC	11 8 0 0 0	19
<i>Anabaena catanula</i>	CCAP 1403/1	AcaI	?	? ? ? ? ?	88
<i>Anabaena cylindrica</i>	CCAP 1403/2a	AcyI	GPu ^c CGPyC	>14 >14 0 7 6	38
<i>Anabaena flos-aquae</i>	A.E. Walsby	AcliI (AvaII)	G ^c G($\frac{A}{P}$)CC	>17 >30 6 1 8	24
&		AcliII	C ^c TTAAG	3 ? 0 2 0	24
&		AcliIII	?	? ? ? ? ?	24

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 DX DBR	References
Anabaena oscillarioides	CCAP 1403/11	AosI (HstI)	TGC ⁺ GCA	>10 >15 0 1 4	39
		AosII (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	39
Anabaena strain Waterbury	ATCC 29208	AstWI (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	37
Anabaena subcylindrica	CCAP 1403/4b	AsuI	G ⁺ GNC	>30 >30 11 2 15	89
		AsuII	TT ⁺ CGAA	7 1 0 0 0	147, 37; 37
		AsuIII (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	37
Anabaena variabilis	ATCC 27892	AvaI	C ⁺ PyCGPUG	8 15 0 1 1	144; 90
		AvaII	G ⁺ G(⁺)CC	>17 >30 6 1 8	144; 202, 90, 53
		AvaIII	ATGCAT	? ? 3 0 0	165; 165, 183
Anabaena variabilis UW	E.C. Rosenfold	AvrI (AvaI)	CPyCGPUG	8 15 0 1 1	168
		AvrII	CCTAGG	2 2 2 0 0	168
& Aphanothece halophytica	ATCC 29534	AhaI (CauII)	CC(⁺)GG	>30 >30 0 1 10	24
&		AhaII	?	? ? ? ? ?	24
&		AhaIII	TTT ⁺ AAA	13 >16 12 2 3	24
Arthrobacter luteus	ATCC 21606	AluI	AG ⁺ CT	>50 >50 35 24 16	162
Arthrobacter pyridinolis	R. DiLauro	AdyI (EcoRII)	CC ⁺ (⁺)GG	>35 ^d >35 16 2 6	40
Bacillus acidocaldarius	ATCC 27009	BaqI (SaqII)	CCGCGG	4 >25 0 1 0	134, 147
Bacillus amyloliquefaciens F	ATCC 23350	BamFI (BamHI)	GGATCC	5 3 1 0 1	182
Bacillus amyloliquefaciens H	F.E. Young	BamHI	G ⁺ GATCC	5 3 1 0 1	226; 164; 79; 79
Bacillus amyloliquefaciens K	T. Kaneko	BamKI (BamHI)	GGATCC	5 3 1 0 1	182
Bacillus amyloliquefaciens N	T. Ando	BamNI (BamHI)	GGATCC	5 3 1 0 1	181
		BamV _x (AvaII)	G ⁺ G(⁺)CC	>17 >30 6 1 8	180, 181; 93

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 ØX PBR	References
<i>Bacillus brevis</i> S	A.P. Zarubina	BbvSI	GC(↓)GC	specific methylase	218
<i>Bacillus brevis</i>	ATCC 9999	BbvI	GCAGC (8/12)	>30	62; 61, 174; 79; 79
<i>Bacillus caldolyticus</i>	A. Atkinson	BclI	T ⁺ GATCA	7 ^d	10
& <i>Bacillus centroporus</i>	A.A. Janulaitis	BcnI (NciI)	CC ⁺ CGG	>15	94
<i>Bacillus cereus</i>	ATCC 14579	BceI ¹⁴⁵⁷⁹	?	>10	182
<i>Bacillus cereus</i>	IAM 1229	Bcg1229	?	>10	182
<i>Bacillus cereus</i>	T. Ando	Bca170 (PstI)	CTGCAG	18	182
<i>Bacillus cereus</i> Rf sm st	T. Ando	BceR (EcoRII)	CGCG	>50	182
<i>Bacillus globigii</i>	G.A. Wilson	BglI	GCCNNNN ⁺ NGGC	22	42, 227; 6, 214
		BglII	A ⁺ GATCT	6	42, 227; 155
<i>Bacillus megaterium</i> 899	B899	Bme899	?	>5	182
<i>Bacillus megaterium</i> B205-3	T. Kaneko	Bme205	?	>10	182
<i>Bacillus megaterium</i>	J. Upcroft	BmeI	?	>10	58
<i>Bacillus pumilus</i> AHU1387A	T. Ando	BpuI	?	6	92
<i>Bacillus sphaericus</i>	IAM 1286	Bsp1286	?	?	182
<i>Bacillus sphaericus</i> R	P. Venetianer	BspRI (HaeIII)	GC ⁺ CC	>50	102; 220; 105
& <i>Bacillus stearothermophilus</i> C1	N. Welker	BstCI (HaeIII)	GGCC	>50	111
& <i>Bacillus stearothermophilus</i> C11	N. Welker	BsaCI (HaeIII)	GGCC	>50	111
& <i>Bacillus stearothermophilus</i> G3	N. Welker	BstGI (BclI)	TGATCA	7 ^d	111
&		BstGII (EcoRII)	CC(↓)GG	>35 ^d	111
& <i>Bacillus stearothermophilus</i> G6	N. Welker	BsaCI (BstXI)	?	10	111
&		BsaGII (HboI)	GATC	>50 ^d	111

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c Δ AG2 SV40 ΔX DBR	References
<i>Bacillus stearothermophilus</i> H1	N. Welker	BstHI (XhoI)	CTCGAG	1 6 0 1 0	111
<i>Bacillus stearothermophilus</i> H3	N. Welker	BstHI (XhoI)	CTCGAG	1 6 0 1 0	111
<i>Bacillus stearothermophilus</i> H4	N. Welker	BstHII (BspPI)	?	6 >18 0 2 0	111
<i>Bacillus stearothermophilus</i> P1	N. Welker	BstHI (BspPI)	?	6 >18 0 2 0	111
<i>Bacillus stearothermophilus</i> P5	N. Welker	BspPI	?	>8 ? ? ?	111
<i>Bacillus stearothermophilus</i> P6	N. Welker	BstPI	?	11 >20 ? 0 0	111
<i>Bacillus stearothermophilus</i> P8	N. Welker	BstPII	?	>50 ? ? ?	111
<i>Bacillus stearothermophilus</i> P9	N. Welker	BspPI (MboI)	GATC	>50 >50 8 0 22	111
<i>Bacillus stearothermophilus</i> T12	N. Welker	BstPI (BspPI)	?	11 >20 ? 0 0	111
<i>Bacillus stearothermophilus</i> X1	N. Welker	BstPI (BstXI)	?	10 9 0 3 0	111
<i>Bacillus stearothermophilus</i> 1503-4R	N. Welker	BstXI	?	10 9 0 3 0	111
<i>Bacillus stearothermophilus</i> 240	A. Atkinson	BstXII (MboI)	GATC	>50 ^d >50 8 0 22	111
<i>Bacillus stearothermophilus</i> ET	N. Welker	BstI (BamHI)	G ⁺ GATCC	5 3 1 0 1	26; 29
<i>Bacillus stearothermophilus</i> ATCC 12980	D. Comb	BstAI	?	? ? ? ? ?	12
<i>Bacillus stearothermophilus</i>	D. Comb	BstEI	?	? ? ? ? ?	136
<i>Bacillus stearothermophilus</i>	D. Comb	BstEII	G ⁺ GTNACC	11 8 0 0 0	136; 113
<i>Bacillus stearothermophilus</i>	D. Comb	BstEIII (MboI)	GATC	>50 ^d >50 >8 0 22	136; 67; 147
<i>Bacillus stearothermophilus</i>	D. Comb	BstPI (BstEII)	G ⁺ GTNACC	11 8 0 0 0	157
<i>Bacillus stearothermophilus</i>	D. Comb	BstNI (EcoRII)	CC ⁺ (⁺)GG	>35 ^d >35 16 2 6	175

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				λ	Ad2	SV40	OX	PBR
<i>Bacillus stearothermophilus</i> 822	T. Oshima	BaeI (HaeIII)	GGCC	>50	>50	19	11	22
		BaeII (HpaI)	GTTAAC	13	6	4	3	0
<i>Bacillus subtilis</i> strain R	T. Trautner	BauRI (HaeIII)	GG ⁺ CC	>50	>50	19	11	22
<i>Bacillus subtilis</i> Marburg 168	T. Ando	BsuM	?	>10	?	?	?	?
<i>Bacillus subtilis</i>	ATCC 6633	Bsu6663	?	>20	?	?	?	?
<i>Bacillus subtilis</i>	IAM 1076	Bsu1076 (HaeIII)	GGCC	>50	>50	19	11	22
<i>Bacillus subtilis</i>	IAM 1114	Bsu1114 (HaeIII)	GGCC	>50	>50	19	11	22
<i>Bacillus subtilis</i>	IAM 1247	Bsu1247 (PstI)	CTGCAG	18	25	2	1	1
<i>Bacillus subtilis</i>	ATCC 14593	Bsu1145	?	>20	?	?	?	?
<i>Bacillus subtilis</i>	IAM 1192	Bsu1192	?	>10	?	?	?	?
<i>Bacillus subtilis</i>	IAM 1193	Bsu1193	?	>30	?	?	?	?
<i>Bacillus subtilis</i>	IAM 1231	Bsu1231	?	>20	?	?	?	?
<i>Bacillus subtilis</i>	IAM 1259	Bsu1259	?	>8	?	?	?	?
<i>Bifidobacterium breve</i>	H. Takahashi	BdeI (NarI)	GGGCG ⁺ C	>2	18	0	2	4
<i>Bordetella bronchiseptica</i>	ATCC 19395	BbrI (HindIII)	AAGCTT	6	11	6	0	1
<i>Bordetella pertussis</i>	P. Novotny	BdeI (HindIII)	AAGCTT	6	11	6	0	1
<i>Brevibacterium albidum</i>	ATCC 15831	BalI	TGG ⁺ CCA	15	17	0	0	1
<i>Brevibacterium luteum</i>	ATCC 15830	BluI (XhoI)	C ⁺ TCGAG	1	6	0	1	0
		BluII (HaeIII)	GGCC	>50	>50	19	11	22
<i>Calothrix scopulorum</i>	CCAP 1410/5	CacI (SacII)	CCGC ⁺ GG	4	>25	0	1	0
<i>Caryophanon latum</i> L	H. Mayer	ClaI	AT ⁺ CGAT	15	2	0	0	1

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				λ	Ad2	SV40	ϕ X	
Caryophanon latum	ATCC 15219	ClaI (HaeII)	GGCC	>50	>50	19	11	22
		ClaII (AvaII)	GG($\frac{A}{C}$)CC	>17	>30	6	1	8
Caryophanon latum	DSM #84	ClaI (HaeII)	GG ⁺ CC	>50	>50	19	11	22
& Caryophanon latum RII	H. Mayer	ClaI	?	>20	?	?	?	?
& Caryophanon latum H7	W.C. Trentini	ClaI	?	14	?	?	?	?
& Caulobacter crescentus CB-13	R.J. Syddall	CorI	?	1	>10	0	1	1
&	A. Bingham	CorII (XhoI)	CTCGAG	1	6	0	1	0
		CauI (AvaII)	GG($\frac{A}{C}$)CC	>30	>30	6	1	8
Chloroflexus aurantiacus		CauII	CC ⁺ ($\frac{G}{C}$)GG	>30	>30	0	1	10
& Chromatium vinosum	G.C. Grosveld	CunI (SauI)	CC ⁺ TNAGG	>10	>15	0	1	0
		CuiI	?	?	?	?	?	?
Chromobacterium violaceum	ATCC 12472	CfrI	Py ⁺ GGCCPu	>25	>35	0	2	6
& Citrobacter freundii	A.A. Janulaitis	CfoI (HhaI)	GGCC	>50	>50	2	18	31
Clostridium formicoaceticum	ATCC 23439	CfoI (HhaI)	GGCC	>50	>50	2	18	31
& Clostridium pasteurianum	NRCC 33011	CbaI (MboI)	GATC	>50 ^d	>50	8	0	22
Corynebacterium humiferum	ATCC 21108	CnuI (HindIII)	AAGCTT	6	11	6	0	1
Corynebacterium petrophilum	ATCC 19080	CnuII (HindII)	GTTPuAC	34	>20	7	13	2
		CbaI (BclI)	TGATCA	7 ^d	5	1	0	0
& Cystobacter velatus Plv9	H. Reichenbach	CuaI	?	?	?	?	?	?
Desulfovibrio desulfuricans Norway strain	H. Peck	DdeI	C ⁺ TNAG	>50	>50	19	14	8
Desulfovibrio desulfuricans	ATCC 27774	DdeII (XhoI)	CTCGAG	1	6	0	1	0
		DdsI (BamHI)	GGATCC	5	3	1	0	1
Diplococcus pneumoniae	S. Lacks	DpnI	G ⁺ A ⁺ TC	only cleaves methylated DNA				

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Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 φX PBR	References
Diplococcus pneumoniae	S. Lacks	DpnII (MboI)	GATC	>50 ^d 8 0 22	108; 109
Enterobacter aerogenes	P. R. Whitehead	EaeI (CfrI)	Py ⁺ GGCCPu	>25 >35 0 2 6	24
Enterobacter cloacae	H. Hartmann	EclI	?	14 ? ? ? ?	77
		EclII (EcoRII)	CC($\frac{A}{P}$)GG	>35 ^d >35 16 2 6	77
Enterobacter cloacae	DSM 30056	EaeI (BstEII)	G ⁺ GTNACC	11 8 0 0 0	84
		EaeII (EcoRII)	CC($\frac{A}{P}$)GG	>35 ^d >35 16 2 6	147
Enterobacter cloacae	DSM 30060	EaeI (SaeII)	CCGCCG	4 >25 0 1 0	133; 147
Escherichia coli J62 pLG74	L. I. Glatman	EcoRV	GATAT ⁺ C	14 8 1 0 1	100
Escherichia coli RY13	R. N. Yoshimori	EcoRI	G ⁺ AATTC	5 5 1 0 1	70; 80; 70; 41
		EcoRI ⁺	PuPuA ⁺ TPyPy	>10 >10 24 16 15	143
Escherichia coli R245	R. N. Yoshimori	EcoRII	⁺ CC($\frac{A}{P}$)GG	>35 ^d >35 16 2 6	232; 8, 14; 232; 14
Escherichia coli B	W. Arber	EcoB	TGA(N)GTGCT	Type I 1 0 0	49; 114, 158; 115; 216
Escherichia coli K	M. Meselson	EcoK	AAC(N)GTGC	Type I 0 0 2	137; 7, 97; 74
Escherichia coli (PI)	K. Murray	EcoPI	AGACC	Type IIIe 4 7 4	73; 4; 15, 16; 4, 78
Escherichia coli P15	W. Arber	EcoP15	CAGCAG	Type IIIe 12 5 7	159; 75
Flavobacterium okeanokoites	IFO 12536	FokI	GGATG (9/13)	>50 >50 11 8 6	199
Fremyella diplophron	PCC 7601	EdII (AvaII)	G ⁺ G($\frac{A}{P}$)CC	>17 >30 6 1 8	213, 197
		EdII (MstI)	TGC ⁺ GCA	>10 >15 0 1 4	213, 197
Fusobacterium nucleatum A	M. Smith	FnuAI (HinfI)	G ⁺ ATC	>50 >50 10 21 10	123
		FnuAII (MboI)	GATC	>50 ^d >50 8 0 22	123; 147
Fusobacterium nucleatum C	M. Smith	FnuCI (MboI)	⁺ GATC	>50 ^d >50 8 0 22	123

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	φX	PBR	
Fusobacterium nucleatum D	M. Smith	FnuDI (HaeIII)	GG ⁺ CC	>50	>50	19	11	22	123
		FnuDII	CG ⁺ CG	>50	>50	0	14	23	123
		FnuDIII (HhaI)	CGC ⁺ C	>50	>50	2	18	31	123
Fusobacterium nucleatum E	M. Smith	FnuEI (MboI)	⁺ GATC	>50 ^d	>50	8	0	22	123
Fusobacterium nucleatum 48	M. Smith	Fnu48I	?	>50	?	?	>10	?	122
Fusobacterium nucleatum 4H	M. Smith	Fnu4HI	GC ⁺ NGC	>50	>50	25	31	42	119
Gluconobacter dioxyacetonius	IAM 1814	GdiI (StuI)	AGG ⁺ CCT	5	12	7	1	0	215
		GdiII	Py ⁺ GGCGG	>10	>20	0	2	5	215
Gluconobacter dioxyacetonius	IAM 1840	GdiI (BamHI)	GGATCC	5	3	1	0	1	177
Gluconobacter oxydans sub. melonigenes	IAM 1836	GoxI (BamHI)	GGATCC	5	3	1	0	1	177
Haemophilus aegyptius	ATCC 11116	HaeI	(λ)GG ⁺ CC(λ)	?	?	11	6	7	146
		HaeII	PuGGCC ⁺ Py	>30	>30	1	8	11	161; 212
		HaeIII	GG ⁺ CC	>50	>50	19	11	22	138; 18; 130; 130
Haemophilus aphrophilus	ATCC 19415	HapI	?	>30	?	?	?	?	147
		HapII (HpaII)	C ⁺ CGG	>50	>50	1	5	26	207; 200
Haemophilus gallinarum	ATCC 14385	HgaI	GACGC (5/10)	>50	>50	0	14	11	207; 22, 198
Haemophilus haemoglobinophilus	ATCC 19416	HhgI (HaeIII)	GGCC	>50	>50	19	11	22	147
Haemophilus haemolyticus	ATCC 10014	HhaI	GCG ⁺ C	>50	>50	2	18	31	163; 163; 131
		HhaII (HinfI)	GATC	>50	>50	10	21	10	129
Haemophilus influenzae GU	J. Chirikjian	HingUI (HhaI)	GGCC	>50	>50	2	18	31	194 and 28
		HingUII (FokI)	GGATG	>50	>50	11	8	6	194; 148

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	DX	DBR	
Haemophilus influenzae 173	J. Chirikjian	Hin173 (HindIII)	AAGCTT	6	11	6	0	1	194
Haemophilus influenzae 1056	J. Stuy	Hin1056I (EcoDII)	CGCG	>50	>50	0	14	22	151
		Hin1056II	?	>30	>30	0	5	?	151
Haemophilus influenzae b (1076)	J. Stuy	HinbIII (HindIII)	AAGCTT	6	11	6	0	1	151
Haemophilus influenzae c (1160)	J. Stuy	HincII (HindII)	GTPyPuAC	34	>20	7	13	2	151
Haemophilus influenzae c (1161)	J. Stuy	HincII (HindII)	GTPyPuAC	34	>20	7	13	2	151
& Haemophilus influenzae e	A. Piekarowicz	HineI (HinfIII)	CGAATf	Type IIIe	0	5	1	152	
Haemophilus influenzae R _b	C.A. Hutchison	HinbIII (HindIII)	AAGCTT	6	11	6	0	1	139, 147
Haemophilus influenzae R _c	A. Landy	HincII (HindII)	GTPyPuAC	34	>20	7	13	2	110
Haemophilus influenzae R _d	S.H. Goodgal (exo-mutant)	HindI	CAC	specific methylase					169; 170
		HindII	GTPy ⁺ PuAC	34	>20	7	13	2	191; 99; 169; 170
		HindIII	A ⁺ AGCTT	6	11	6	0	1	150; 150; 169; 170
		HindIV	CAC	specific methylase					169; 170
Haemophilus influenzae R _f	C.A. Hutchison	HinfI	G ⁺ ANTC	>50	>50	10	21	10	139; 91, 145
		HinfII (HindIII)	AAGCTT	6	11	6	0	1	131
		HinfIII	CGAATf	Type IIIe	0	5	1	1	98, 153
Haemophilus influenzae H-1	M. Takanami	HinHI (HaeII)	PuGGGCPy	>30	>30	1	8	11	207
& Haemophilus influenzae P ₁	S. Shen	HinP ₁ I (HhaI)	G ⁺ CGC	>50	>50	2	18	31	179
& Haemophilus influenzae S ₁	S. Shen	HinS ₁ (HhaI)	GCGC	>50	>50	2	18	31	179
Haemophilus influenzae S ₂	S. Shen	HinS ₂ (HhaI)	GCGC	>50	>50	2	18	31	179

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 φX PBR	References
Haemophilus influenzae JC9	A. Piekarowicz	HinfI (HindII)	GTPy ⁺ PuAC	34 >20 7 13 2	154
Haemophilus parahaemolyticus	C.A. Hutchison	HinfII (HindIII)	AAGCTT	6 11 6 0 1	154
Haemophilus parainfluenzae	J. Setlow	HobI	GGTGA (8/7) ^b	>50 4 9 12	139; 103
		HobI	GTT ⁺ AAC	13 6 4 3 0	178; 55, 2
		HobII	C ⁺ CGG	>50 >50 1 5 26	178; 55, 130; 130
Haemophilus suis	ATCC 19417	HsuI (HindIII)	A ⁺ AGCTT	6 11 6 0 1	147
Herpetosiphon giganteus HP1023	J.H. Parish	HgiAI	G ^(A) CC(^A) ⁺ C	24 >20 0 3 8	21
Herpetosiphon giganteus Hpg 5	H. Reichenbach	HgiBI (AvaII)	G ⁺ G(^A)CC	>17 >30 6 1 8	83
Herpetosiphon giganteus Hpg 9	H. Reichenbach	HgiCI	G ⁺ GPpPuCC	13 >25 1 3 9	83, 106
		HgiCII (AvaII)	G ⁺ G(^A)CC	>17 >30 6 1 8	83
		HgiCIII (SalI)	G ⁺ TCGAC	2 3 0 0 1	83
Herpetosiphon giganteus Hpa 2	H. Reichenbach	HgiDI (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	83, 106
		HgiDII (SalI)	G ⁺ TCGAC	2 3 0 0 1	83
Herpetosiphon giganteus Hpg 24	H. Reichenbach	HgiEI (AvaII)	G ⁺ G(^A)CC	>17 >30 6 1 8	83
		HgiEII	ACC(N) ₆ GGT	? ? 1 1 2	83
Herpetosiphon giganteus Hpg 14	H. Reichenbach	HgiFI	?	? 15 ? ? ?	134
Herpetosiphon giganteus Hpa 1	H. Reichenbach	HgiGI (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	106
Herpetosiphon giganteus HP 1049	J.H. Parish	HgiHI (HgiCI)	G ⁺ GPpPuCC	>13 >25 1 3 9	24
		HgiHII (AcyI)	GPu ⁺ CGPyC	>14 >14 0 7 6	24
		HgiHIII (AvaII)	G ⁺ G(^A)CC	>17 >30 6 1 8	24
Herpetosiphon giganteus HFS 101	H. Foster	HgiJI	?	? ? ? ? ?	24
		HgiJII	GPuGCPy ⁺ C	7 >35 2 0 2	24

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 φX DBR	References
& Herpesotiphon giganteus Hpg 32	H. Reichenbach	HpaKI	?	>18 ? ? ?	134
Klebsiella pneumoniae OK8	J. Davies	KpnI	GGTAC ^c C	2 8 1 0 0	189; 209
Nastigololadus lammosus	CCAP 1447/1	MlaI (AseII)	TT ^c CGAA	7 1 0 0 0	43
& Microbacterium thermosphactum	ATCC 11509	MthI (MboI)	GATC	>50 ^d >50 8 0 22	111
& Micrococcus luteus	IFO 12992	MluI	A ^c CGGT	? 5 0 2 0	199
& Micrococcus radiodurans	ATCC 13939	MraI (SaeII)	CCGCGG	4 >25 0 1 0	224
Microcoleus species	D. Comb	HsiI	TGC ^c GCA	>10 >15 0 1 4	32; 61
		MstII (SauI)	CC ^c TNAGG	2 7 0 0 0	174
Moraxella bovis	ATCC 10900	MboI	^c GATC	>50 ^d >50 8 0 22	57
		MboII	GAAGA (8/7)	>50 >50 16 11 11	57; 20, 46
Moraxella bovis	ATCC 17947	MbvI	?	? ? ? ? ?	96
Moraxella glueidi LG1	J. Davies	MzII	?	? ? ? ? ?	189
Moraxella glueidi LG2	J. Davies	MzII	?	? ? ? ? ?	189
Moraxella kingae	ATCC 23331	MklI (HindIII)	AAGCTT	6 11 6 0 1	96
Moraxella nonliquefaciens	ATCC 19975	MnoI (HpaII)	C ^c CGG	>50 >50 1 5 26	147; 5
		MnoII (MnnIII)	?	>10 >6 3 ? ?	147
		MnoIII (MboI)	GATC	>50 ^d >50 8 0 22	147
Moraxella nonliquefaciens	ATCC 17953	MnlI	CCTC (7/7)	>50 >50 51 34 26	234; 174
Moraxella nonliquefaciens	ATCC 17954	MnnI (HindII)	GTPyPuAC	34 >20 7 13 2	76
		MnnII (HaeIII)	GGCC	>50 >50 19 11 22	76
		MnnIII	?	>10 >6 3 ? ?	76
		MnnIV (HhaI)	GGCC	>50 >50 2 18 31	76

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				λ	Ad2	SV40	ϕ X	
<i>Moraxella nonliquefaciens</i>	ATCC 19996	MnlI (HaeIII)	GGCC	>50	>50	19	11	22
		MnlII (HpaII)	CCGG	>50	>50	1	5	26
<i>Moraxella osloensis</i>	ATCC 19976	MsaI (MboI)	GATC	>50 ^d	>50	8	0	22
<i>Moraxella phenylpyruvica</i>	ATCC 17955	MbhI (EcoRII)	CC(A)GG	>35 ^d	>35	16	2	6
<i>Moraxella speciesh</i>	R.J. Roberts	MsaI (HpaII)	C*CGG	>50	>50	1	5	26
<i>Myxococcus stipitatus</i> Mxs2H	H. Reichenbach	MslI (XhoI)	CTCGAG	1	6	0	1	0
&		MslII	?	?	?	?	?	134
<i>Myxococcus virescens</i> V-2	H. Reichenbach	MvlI	?	1	?	?	?	141
		MvII	?	?	?	?	?	141
& <i>Neisseria caviae</i>	NRCC 31003	NsaI (HinfI)	GATC	>50	>50	10	21	10
<i>Neisseria cinerea</i>	NRCC 31006	NciI (CauII)	CC*(G)GG	>15	>15	0	1	10
& <i>Neisseria denitrificans</i>	NRCC 31009	NdaI	CATATG	?	?	2	0	1
&		NdeII (MboI)	GATC	>50 ^d	>50	8	0	22
& <i>Neisseria flavescens</i>	NRCC 31011	NfiI (MboI)	GATC	>50 ^d	>50	8	0	22
&		NfII	?	?	?	?	?	221
&		NfIII	?	?	?	?	?	221
<i>Neisseria gonorrhoea</i>	G. Wilson	NgaI (HaeII)	PuGGCGPy	>30	>30	1	8	11
<i>Neisseria gonorrhoea</i>	CDC 66	NgaII (HaeIII)	GGCC	>50	>50	19	11	22
& <i>Neisseria gonorrhoea</i> KH 7764-45	L. Mayer	NsiIII (SaqII)	CCCGGG	4	>25	0	1	0
& <i>Neisseria mucosa</i>	NRCC 31013	NnuI (NaeI)	GCCGGC	2	>13	1	0	4
& <i>Neisseria ovis</i>	NRCC 31020	NovI	?	?	?	?	?	?
&		NovII (HinfI)	GATC	>50	>50	10	21	10

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References	
				λ	Ad2	SV40	ØX	DBR	
& <i>Nocardia aerocolonigenes</i>	ATCC 23870	NaeI	GCC ⁺ GGC	2	>13	1	0	4	34
	& <i>Nocardia argentinensis</i>	NarI	GG ⁺ CGCC	2	10	0	2	4	33
& <i>Nocardia blackwellii</i>	ATCC 6846	NblI (PvuI)	CGAT ⁺ CG	3	7	0	0	1	174
& <i>Nocardia corallina</i>	ATCC 19070	NcoI	CCATGG	6	14	3	0	0	111
& <i>Nocardia opaca</i>	ATCC 21507	NorI (SalI)	G ⁺ TCGAC	2	3	0	0	1	174
&		NorII (SalII)	?	?	?	?	?	?	111
& <i>Nocardia otitidis-caviarum</i>	ATCC 14630	NotI	?	0	6	0	0	0	13
& <i>Nocardia rubra</i>	ATCC 15906	NruI	TCG ⁺ CGA	7	6	0	2	1	31
& <i>Nocardia uniformis</i>	ATCC 21806	NunI	?	?	?	?	?	?	111
&		NunII (NarI)	GG ⁺ CGCC	2	14	0	2	4	111
& <i>Nostoc species</i>	PCC 6705	NapBI	?	?	?	?	?	?	45
&		NapBII	GC(G ₆)G ⁺ C	?	?	1	17	21	45
& <i>Nostoc species</i>	PCC 7524	NspCI	PuCATG ⁺ Py	>15	>15	2	0	4	45
& <i>Nostoc species</i>	PCC 7413	NspHI (NspCI)	PuCATG ⁺ Py	>15	>15	2	0	4	45
<i>Oerskovia xanthineolytica</i>	R. Shekman	OxaI (AluI)	AGCT	>50	>50	35	24	16	196
		OxaII	?	?	?	?	?	?	196
<i>Proteus vulgaris</i>	ATCC 13315	PvuI	CGAT ⁺ CG	3	7	0	0	1	64
		PvuII	CAG ⁺ CTG	15	22	3	0	1	64
<i>Providencia alcalifaciens</i>	ATCC 9886	Pali (HaeIII)	GGCC	>50	>50	19	11	22	58
<i>Providencia stuartii</i> 164	J. Davies	PakI	CTGCA ⁺ G	18	25	2	1	1	189; 22
& <i>Pseudoanabaena species</i>	ATCC 27263	PspI (AsuI)	GGNCC	>30	>30	11	2	15	142
<i>Pseudomonas aeruginosa</i>	G.A. Jacoby	Paer7	?	1	5	0	0	0	82

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 OX DBR	References
<i>Pseudomonas facilis</i>	M. VanMontagu	PfaI (HhoI)	GATC	>50 ^d 8 0 22	216
<i>Pseudomonas maltophilia</i>	D. Comb	PmaI (PstI)	CTGCAG	18 25 2 1 1	174
<i>Rhizobium leguminosarum</i> 300	J. Beringer	RleI	?	6 >10 ? ? ?	230
<i>Rhizobium lupini</i> #1	W. Heumann	RluI	?	1 8 ? ? ?	229, 81
<i>Rhizobium meliloti</i>	J.L. Denarie	RmeI	?	8 >10 ? ? ?	81
<i>Rhodospirillum rubrum</i>	J. Chirikjian	RrbI	?	? 4 5 1 ?	118
<i>Rhodopseudomonas sphaeroides</i>	R. Lascelles	RsdI (PvuI)	CGATCG	3 7 0 0 1	9
<i>Rhodopseudomonas sphaeroides</i>	S. Kaplan	RshI (PvuI)	CGATCG	3 7 0 0 1	125
<i>Rhodopseudomonas sphaeroides</i>	S. Kaplan	RsaI	GTAC	>50 >50 11 11 3	126
<i>Rhodopseudomonas sphaeroides</i>	S. Kaplan	RsrI (EcoRI)	GAATTC	5 5 1 0 1	54
<i>Rhodopseudomonas sphaeroides</i>	A. deWaard	SinI (AvaII)	GG(A)CC	>17 >30 6 1 8	124
<i>Serratia marcescens</i> S _b	C. Mulder	SmaI	CCC*GGG	3 12 0 0 0	69; 48
<i>Serratia species</i> SAI	B. Torheim	SsdI	?	? ? ? ? ?	210
<i>Sphaerotilus natans</i> C	A. Pope	SnaI	GTATAC	2 ? 0 0 1	156
<i>Spiroplasma citri</i> ASP2	M.A. Stephens	SclNI (HhaI)	G*CGC	>50 >50 2 18 31	192
<i>Staphylococcus aureus</i> 3A	E.E. Stobberingh	Sau3A (HhoI)	*GATC	>50 ^d >50 8 0 22	201
<i>Staphylococcus aureus</i> PS96	E.E. Stobberingh	Sau96I (AsuI)	G*GNCC	>30 >30 11 2 15	202
<i>Staphylococcus saprophyticus</i>	ATCC 13518	SsaI	?	>10 ? ? ?	111
<i>Streptococcus cremoris</i> F	C. Daly	SerFI	CCNGG	>50 >50 16 3 16	51
<i>Streptococcus faecalis</i> var. <i>zymogenes</i>	R. Wu	SfaI (HaeIII)	GG*CC	>50 >50 19 11 22	231
<i>Streptococcus faecalis</i> GU	J. Chirikjian	SfaGU I (HpaII)	CCGG	>50 >50 1 5 26	30

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavages sites ^c λ Ad2 SV40 2X DBR	References
<i>Streptococcus faecalis</i> ND 547	D. Ciewell	<u>Sfa</u> NI	GCATC (5/9)	>50 30 6 12 22	176
<i>Streptomyces achromogenes</i>	ATCC 12767	<u>Sac</u> I	GAGCT ^c C	2 7 0 0 0	1
		<u>Sac</u> II	CCGC ^c GG	4 >25 0 1 0	1
		<u>Sac</u> III	?	>100 >100 ? ? ?	1
<i>Streptomyces albus</i>	CM1 52766	<u>Sal</u> PI (<u>Pat</u> I)	CTGCA ^c G	18 25 2 1 1	27; 25
<i>Streptomyces albus</i> subspecies <i>pathocidicus</i>	KCC 50166	<u>Sna</u> I (<u>Xho</u> I)	CTCGAG	1 6 0 1 0	185
<i>Streptomyces albus</i> G	J.M. Ghuyssen	<u>Sal</u> I	G ^c TCGAC	2 3 0 0 1	3
		<u>Sal</u> II	?	>20 ? ? ?	3
<i>Streptomyces aureofaciens</i> IKA 18/4	J. Timko	<u>Sau</u> I	CC ^c TNAGG	2 7 0 0 0	208
<i>Streptomyces bobillii</i>	ATCC 3310	<u>Sbo</u> I (<u>Sac</u> II)	CCGGGG	4 >25 0 1 0	185; 206
<i>Streptomyces caespitosus</i>	H. Takahashi	<u>Sac</u> I	AGTACT	6 5 0 0 1	104
<i>Streptomyces cupidosporus</i>	KCC 50316	<u>Sou</u> I (<u>Xho</u> I)	CTCGAG	1 6 0 1 0	185
<i>Streptomyces exfoliatus</i>	KCC 50030	<u>Sax</u> I (<u>Xho</u> I)	CTCGAG	1 6 0 1 0	185
		<u>Sax</u> II	?	2 ? ? ?	185
<i>Streptomyces fradiae</i>	ATCC 3355	<u>Sfr</u> I (<u>Sac</u> II)	CCGGGG	4 >25 0 1 0	185; 206
<i>Streptomyces ganmycicus</i>	KCC 50759	<u>Ssa</u> I (<u>Xho</u> I)	CTCGAG	1 6 0 1 0	185
<i>Streptomyces goshikiensis</i>	KCC 50294	<u>Sko</u> I (<u>Xho</u> I)	CTCGAG	1 6 0 1 0	185
<i>Streptomyces griseus</i>	ATCC 23345	<u>Sgr</u> I	?	0 7 0 ? ?	1
<i>Streptomyces hygroscopicus</i>	T. Yamaguchi	<u>Shy</u> TI	?	2 ? ? ? ?	185
<i>Streptomyces hygroscopicus</i>	F. Walter	<u>Shy</u> I (<u>Sac</u> II)	CCGGGG	4 >25 0 1 0	222
<i>Streptomyces lavendulae</i>	ATCC 8664	<u>Sla</u> I (<u>Xho</u> I)	C ^c TCGAG	1 6 0 1 0	205

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c λ Ad2 SV40 DX DBR	References
Streptomyces luteoreticuli	KCC S0788	SluI (XhoI)	CTCGAG	1 6 0 1 0	206
& Streptomyces oderifer	ATCC 6246	SodI	?	? ? ? ? ?	111
&		SodII	?	? ? ? ? ?	111
Streptomyces phaeochromogenes	F. Bolivar	SphI	GCATG ⁺ C	4 9 2 0 1	52
Streptomyces stanford	S. Goff, A. Rambach	SatI (SagI)	GAGCT ⁺ C	2 7 0 0 0	65; 140
		SstII (SacII)	CCGC ⁺ GG	4 >25 0 1 0	65
		SstIII (SagIII)	?	>100 >100 ? ? ?	65
		SstIV (BclI)	TGATCA	7 5 1 0 0	86
Streptomyces tubercidicus	H. Takahashi	StuI	AGG ⁺ CCT	5 12 7 1 0	184
& Streptovorticillium flavopersicum	Upjohn UC 5066	SfiI (PstI)	CTGCA ⁺ G	18 25 2 1 1	96
Thermoplasma acidophilum	D. Searcy	ThaI (EcoDII)	CG ⁺ CG	>50 >50 0 14 23	135
Thermopolyspora glauca	ATCC 15345	TelI (SagII)	CCGCGG	4 >25 0 1 0	62
Thermus aquaticus YTI	J.I. Harris	TaqI	T ⁺ CGA ⁺	>50 >50 1 10 7	171; 171; -; 172
		TaqII	?	>30 >30 4 6 ?	147
& Thermus aquaticus	S.A. Grachev	TaqXI (EcoRII)	CC ⁺ (A ⁺)GG	>35 ^d >35 16 2 6	66
Thermus flavus AT62	T. Oshima	TclI (TaqI)	TCCA	>50 >50 1 10 7	172
Thermus thermophilus HB8	T. Oshima	TthHB8 I (TaqI)	TCCA ⁺	>50 >50 1 10 7	173; 219; 173, 219; 172; 172
Thermus thermophilus strain 23	T. Oshima	IttI (Tth111 I)	GACNNNGTC	2 >12 0 0 1	188
Thermus thermophilus strain 110	T. Oshima	IttI (Tth111 I)	GACNNNGTC	2 >12 0 0 1	188

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				Δ Ad2	SV40	PA	PCR	
<i>Thermus thermophilus</i> strain 111	T. Oshima	Ith111 I	GACN ⁺ NGTC	2	>12	0	0	188, 188
		Ith111 II	CAAPuCA	>30	>30	12	11	187, 187
		Ith111 III	?	?	?	?	?	186
<i>Tolypothrix tenuis</i>	W. Siegelman	IthI (HaeIII)	GGCC	>50	>50	19	11	22
<i>Xanthomonas amaranthicola</i>	ATCC 11645	XamI (SmaI)	GTGCAC	2	3	0	0	1
<i>Xanthomonas badrii</i>	ATCC 11672	XbaI	T ⁺ CTAGA	1 ^d	4	0	0	0
<i>Xanthomonas holcicola</i>	ATCC 13461	XhoI	C ⁺ TCGAG	1	6	0	1	0
		XhoII	Pu ⁺ GATCPy	>20	>20	3	0	8
<i>Xanthomonas malvacearum</i>	ATCC 9924	XmaI (SmaI)	C ⁺ CCGGG	3	12	0	0	0
		XmaII (PstI)	CTGCAG	18	25	2	1	1
		XmaIII	C ⁺ GGCCG	2	10	0	0	1
& <i>Xanthomonas manihotis</i> 7AS1	B-C. Lin	XmuI	GAANNNTTC	>11	?	0	3	2
		XnuI (PvuI)	CGATCG	3	7	0	0	1
		XorI (PstI)	CTGCAG	18	25	2	1	1
		XorII (PvuI)	CGAT ⁺ CG	3	7	0	0	1
<i>Xanthomonas nigromaculans</i>	ATCC 23390	XbaI (XhoI)	C ⁺ TCGAG	1	6	0	1	0
<i>Xanthomonas oryzae</i>	M. Ehrlich							
<i>Xanthomonas papavericola</i>	ATCC 14180							

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