
Restriction and modification enzymes and their recognition sequences

Richard J. Roberts

Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA

Introduction

Since the last compilation of restriction endonucleases (110), more than 30 Type II restriction endonucleases have been discovered, including some valuable new specificities. These include AcyI (GPuCGPyC), DdeI (CTNAG), Fnu4HI (GCNGC), RsaI (GTAC), SphI (GCAGTC), and XmaIII (CGGCCG). In addition, a number of new isoschizomers have been discovered and further information about the recognition sequences of some old entries is now available. AvaX is renamed AvaIII.

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 (132). 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case, refers to the purification procedure for the restriction enzyme, or from the individuals who have provided their unpublished results.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.

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Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References	
				λ	$\frac{Ad2}{\lambda}$	$\frac{SV40}{\phi X174}$		
<i>Achromobacter immobilis</i>	ATCC 15934	<u>AimI</u>	?	?	?	?	33	
<i>Acinetobacter calcoaceticus</i>	R. J. Roberts	<u>AccI</u>	GT ₊ ($\overset{A}{C}$)($\overset{G}{T}$)AC	7	8	1	2	159
<i>Agrobacterium tumefaciens</i>	ATCC 15955	<u>AccII</u> (<u>FnuDII</u>)	CGCG	>50	>50	0	14	159
<i>Agrobacterium tumefaciens</i> B6806	E. Nester	<u>AtuAI</u>	?	>30	>30	?	?	125
<i>Agrobacterium tumefaciens</i> IIBV7	G. Roizes	<u>AtuBI</u> (<u>EcoRII</u>)	CC($\overset{A}{T}$)GG	>35 ^d	>35	16	2	118
<i>Agrobacterium tumefaciens</i> ID 135	C. Kado	<u>AtuII</u> (<u>EcoRII</u>)	CC($\overset{A}{T}$)GG	>35 ^d	>35	16	2	79
<i>Agrobacterium tumefaciens</i> C58	E. Nester	<u>AtuCI</u> (<u>BclI</u>)	TGATCA	7 ^d	5	1	0	125
<i>Anabaena catanula</i>	CCAP 1403/1	<u>AcaI</u>	?	?	?	?	?	62
<i>Anabaena cylindrica</i>	A. deWaard	<u>AcyI</u>	GPu+CGPyC	>14	>14	0	7	27
<i>Anabaena oscillarioidea</i>	CCAP 1403/11	<u>AosI</u> (<u>MstI</u>)	TGC+GCA	>10	>15	0	1	28
<i>Anabaena subcylindrica</i>	K. Murray	<u>AosII</u> (<u>AcyI</u>)	GPu+CGPyC	>14	>14	0	7	28
<i>Anabaena variabilis</i>	K. Murray	<u>AsuI</u>	G+GNCC	>30	>30	11	2	63
		<u>AsuII</u>	?	>5	1	0	0	112
		<u>AvzI</u>	C+PyCGPUG	8	15	0	1	100; 64
		<u>AvzII</u>	G+G($\overset{A}{T}$)CC	>17	>30	6	1	100; 140, 64, 37
<i>Anabaena variabilis</i> ^{uw}	E. C. Rosenvoid	<u>AvzIII</u>	ATGCAT	?	?	3	0	116; 116, 130
		<u>AvrI</u> (<u>AvzI</u>)	CPyCGPUG	8	15	0	1	119
		<u>AvrII</u>	CCTAGG	2	2	2	0	119
<i>Arthrobacter luteus</i>	ATCC 21606	<u>AluI</u>	AG+CT	>50	>50	35	24	113

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				$\frac{\lambda}{\lambda}$	Ad2	SV40	$\frac{\phi X174}{\phi X174}$	
<i>Arthrobacter pyridinolis</i>	R. DiLauro	<u>ApyI</u> (<u>EcoRII</u>)	CC+(A)GG	>35 ^d	>35	16	2	29
<i>Bacillus acidocaldarius</i>	ATCC 27009	<u>BacI</u> (<u>SacII</u>)	CCGGGG	3	>25	0	1	90, 112
<i>Bacillus amyloliquefaciens</i> F	ATCC 23350	<u>BamFI</u> (<u>BamHI</u>)	GGATCC	5	3	1	0	129
<i>Bacillus amyloliquefaciens</i> H	F.E. Young	<u>BamHI</u>	G+GATCC	5	3	1	0	154; 115; 57; 57
<i>Bacillus amyloliquefaciens</i> K	T. Kaneko	<u>BamKI</u> (<u>BamHI</u>)	GGATCC	5	3	1	0	129
<i>Bacillus amyloliquefaciens</i> N	T. Ando	<u>BamNI</u> (<u>BamHI</u>)	GGATCC	5	3	1	0	128
<i>Bacillus brevis</i> S	A.P. Zarubina	<u>BamN_x</u> (<u>AvaII</u>)	G+G(A)CC	>17	>30	6	1	127, 128; 67
<i>Bacillus brevis</i>	ATCC 9999	<u>BbvSI</u>	GC(A)GC	---	specific methylase---			151
<i>Bacillus caldolyticus</i>	A. Atkinson	<u>BbvI</u>	GC(A)GC	>30	>30	23	14	46; 45; 57; 57
<i>Bacillus cereus</i>	ATCC 14579	<u>BclI</u>	T+GATCA	7 ^d	5	1	0	10
<i>Bacillus cereus</i>	IAM 1229	<u>BceI4579</u>	?	>10	?	?	?	129
<i>Bacillus cereus</i>	T. Ando	<u>BceI229</u>	?	>10	?	?	?	129
<i>Bacillus cereus</i> Rf sm st	T. Ando	<u>BceI170</u> (<u>PstI</u>)	CTGCAG	18	25	2	1	129
<i>Bacillus globigii</i>	G.A. Wilson	<u>BceR</u> (<u>EnuDI</u>)	CGCG	>50	>50	0	14	129
<i>Bacillus megaterium</i> 899	B899	<u>BglI</u>	GCCNNNN+NGGC	22	12	1	0	31, 155; 6
<i>Bacillus megaterium</i> B205-3	T. Kaneko	<u>BglII</u>	A+GATCT	6	12	0	0	31, 155; 105
<i>Bacillus megaterium</i>	J. Upcroft	<u>Bme899</u>	?	>5	?	?	?	129
<i>Bacillus pumilus</i> AHU1387A	T. Ando	<u>Bme205</u>	?	>10	?	?	?	129
<i>Bacillus sphaericus</i>	IAM 1286	<u>BmeI</u>	?	>10	>20	4	?	42
		<u>BpuI</u>	?	6	>30	2	?	66
		<u>BspI286</u>	?	?	?	?	?	129

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References
				$\frac{\lambda}{\Delta}$	Ad2	SV40 9X174	
<i>Bacillus sphaericus</i> R	P. Venetianer	<u>BspRI</u> (<u>HaeIII</u>)	GGCC	>50	>50	19 11	71
<i>Bacillus stearothermophilus</i> 1503-4R	N. Welker	<u>BstI</u> (<u>BamHI</u>)	G+GATCC	5	3	1 0	23; 24a
<i>Bacillus stearothermophilus</i> 240	A. Atkinson	<u>BstAI</u>	?	?	?	?	12
<i>Bacillus stearothermophilus</i> ET	N. Welker	<u>BstEI</u>	?	?	?	?	93
		<u>BstEII</u>	G+GTNACC	11	8	0 0	93
		<u>BstEIII</u>	?	> 7	?	?	93
<i>Bacillus stearothermophilus</i> ATCC 12980	ATCC 12980	<u>BstPI</u> (<u>BstEII</u>)	G+GTNACC	11	8	0 0	107
<i>Bacillus stearothermophilus</i>	D. Comb	<u>BstNI</u> (<u>EcoRII</u>)	CC+(A)GG	>35 ^d	>35	16 2	124
<i>Bacillus subtilis</i> strain X5	T. Trautner	<u>BsuRI</u> (<u>HaeIII</u>)	GG+CC	>50	>50	19 11	16; 17; 51
<i>Bacillus subtilis</i> Marburg 168	T. Ando	<u>BsuM</u>	?	>10	?	?	129
<i>Bacillus subtilis</i>	ATCC 6633	<u>Bsu6663</u>	?	>20	?	?	129
<i>Bacillus subtilis</i>	IAM 1076	<u>Bsu1076</u> (<u>HaeIII</u>)	GGCC	>50	>50	19 11	129
<i>Bacillus subtilis</i>	IAM 1114	<u>Bsu1114</u> (<u>HaeIII</u>)	GGCC	>50	>50	19 11	129
<i>Bacillus subtilis</i>	IAM 1247	<u>Bsu1247</u> (<u>PstI</u>)	CTGCAG	18	25	2 1	129; 61
<i>Bacillus subtilis</i>	ATCC 14593	<u>Bsu1145</u>	?	>20	?	?	129
<i>Bacillus subtilis</i>	IAM 1192	<u>Bsu1192</u>	?	>10	?	?	129
<i>Bacillus subtilis</i>	IAM 1193	<u>Bsu1193</u>	?	>30	?	?	129
<i>Bacillus subtilis</i>	IAM 1231	<u>Bsu1231</u>	?	>20	?	?	129
<i>Bacillus subtilis</i>	IAM 1259	<u>Bsu1259</u>	?	> 8	?	?	129
<i>Bordetella bronchiseptica</i>	ATCC 19395	<u>BbrI</u> (<u>HindIII</u>)	AAAGCTT	6	11	6 0	112

Microorganism	Source	Enzyme ^a	Sequence ^b	$\frac{\text{Number of cleavage sites}^c}{\lambda}$	$\frac{\text{SV40}}{\Phi X174}$	References		
<i>Brevibacterium albidum</i>	ATCC 15831	<u>BalI</u>	TGG+CCA	15	17	0	0	43
<i>Brevibacterium luteum</i>	ATCC 15830	<u>BluI</u> (<u>XhoI</u>)	C+TCGAG	1	6	0	1	47
<i>Caryophanon latum</i> L	H. Mayer	<u>BluII</u> (<u>HaeIII</u>)	GGCC	>50	>50	19	11	148
<i>Caryophanon latum</i>	DSM 494	<u>ClgI</u>	AT+CGAT	12	?	0	0	88
<i>Chloroflexus aurantiacus</i>	A. Bingham	<u>CltI</u> (<u>HaeIII</u>)	GG+CC	>50	>50	19	11	90
		<u>CauI</u> (<u>AvaII</u>)	GG(^A)CC	>30	>30	6	1	11
		<u>CauII</u>	?	>30	>30	0	?	11
<i>Chromobacterium violaceum</i>	ATCC 12472	<u>CviI</u>	?	?	?	?	?	33
<i>Clostridium formicoaceticum</i>	ATCC 23439	<u>CfoI</u> (<u>HhaI</u>)	GGGC	>50	>50	2	18	84
<i>Corynebacterium humiferum</i>	ATCC 21108	<u>ChuI</u> (<u>HindIII</u>)	AAGCTT	6	11	6	0	33
		<u>ChuII</u> (<u>HindII</u>)	GTPyPuAC	34	>20	7	13	33
<i>Corynebacterium petrophilum</i>	ATCC 19080	<u>CpeI</u> (<u>BclI</u>)	TGATCA	7 ^d	5	1	0	36
<i>Desulfovibrio desulfuricans</i> Norway strain	H. Peck	<u>DdeI</u>	C+TNAG	>50	>50	19	14	84; 44
<i>Diplococcus pneumoniae</i>	S. Lacks	<u>DpnI</u>	G ^A +TC	--only cleaves methylated DNA--	0			74; 40, 75
<i>Diplococcus pneumoniae</i>	S. Lacks	<u>DpnII</u> (<u>MboI</u>)	GATC	>50 ^d	>50	8	0	74; 75
<i>Enterobacter cloacae</i>	H. Hartmann	<u>EclI</u>	?	14	?	?	?	55
		<u>EclIII</u> (<u>EcoRII</u>)	CC(^A)GG	>35 ^d	>35	16	2	55
<i>Enterobacter cloacae</i>	DSM 30056	<u>EcaI</u> (<u>BstEII</u>)	G+GTNACC	11	8	0	0	60
<i>Enterobacter cloacae</i>	DSM 30060	<u>EccI</u> (<u>SacII</u>)	CCGCGG	3	>25	0	1	89; 112
<i>Escherichia coli</i> RV13	R.N. Yoshimori	<u>EcoRI</u>	G+ATTC	5	5	1	0	50; 58; 50; 30
		<u>EcoRI'</u>	PuPuA+TPyPy	>10	>10	24	16	99

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c Ad2 SV40 gA174	References
<i>Haemophilus suis</i>	ATCC 19417	<u>HsuI</u> (<u>HindIII</u>)	A+AGCTT	6 11 6 0	112
<i>Herpetosiphon giganteus</i> HP1023	J. H. Parish	<u>HgiAI</u>	G(↓)GC(↓)+C	20 ? 0 3	22
<i>Herpetosiphon giganteus</i> Hpg 5	H. Reichenbach	<u>HgiBI</u> (<u>AvaII</u>)	G+G(↓)CC	>17 >30 6 1	91
<i>Herpetosiphon giganteus</i> Hpg 9	H. Reichenbach	<u>HgiCI</u>	?	? ? ? ?	91
		<u>HgiCII</u> (<u>AvaII</u>)	G+G(↓)CC	>17 >30 6 1	91
		<u>HgiCIII</u> (<u>SalI</u>)	G+TCGAC	2 3 0 0	91
<i>Herpetosiphon giganteus</i> Hpa2	H. Reichenbach	<u>HgiDI</u>	?	? ? ? ?	91
		<u>HgiDII</u> (<u>SalI</u>)	G+TCGAC	2 3 0 0	91
<i>Herpetosiphon giganteus</i> Hpg 24	H. Reichenbach	<u>HgiEI</u> (<u>AvaII</u>)	G+G(↓)CC	>17 >30 6 1	91
		<u>HgiEII</u>	?	? ? ? ?	91
<i>Klebsiella pneumoniae</i> OK8	J. Davies	<u>KpnI</u>	GGTAC+C	2 8 1 0	131; 145
<i>Microcoleus</i> species	D. Comb	<u>MstI</u>	TCGCGA	>10 >15 0 1	25; 45
		<u>MstII</u>	?	2 > 6 0 0	123
<i>Moraxella bovis</i>	ATCC 10390	<u>MboI</u>	+GATC	>50 ^d >50 8 0	41
		<u>MboII</u>	GAAGA ^g	>50 >50 16 11	41; 19, 32
<i>Moraxella glueidii</i> LG1	J. Davies	<u>MglI</u>	?	? ? ? ?	131
<i>Moraxella glueidii</i> LG2	J. Davies	<u>MglII</u>	?	? ? ? ?	131
<i>Moraxella nonliquefaciens</i>	ATCC 19975	<u>MnoI</u> (<u>HpaII</u>)	C+CGG	>50 >50 1 5	112; 5
		<u>MnoII</u> (<u>MmnIII</u>)	?	>10 > 6 3 ?	112
		<u>MnoIII</u> (<u>MboI</u>)	GATC	>50 ^d >50 8 0	112

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References	
				$\frac{\Delta}{\Delta}$	$\frac{SV40}{SV40}$	$\frac{\Phi X174}{\Phi X174}$		
<i>Escherichia coli</i> R245	R. N. Yoshimori	<i>EcoRII</i>	\downarrow CC(\uparrow)GG	>35 ^d	>35	16	2	158; 8, 13; 158; 13
<i>Escherichia coli</i> B	W. Arber	<i>EcoB</i>	TGA(N) ₈ TGCT		---	Type I---		35; 77, 108; 78; 150
<i>Escherichia coli</i> K	M. Meselson	<i>EcoK</i>	AAC(N) ₆ GTGC		---	Type I---		94; 7, 68; 53
<i>Escherichia coli</i> (PI)	K. Murray	<i>EcoPI</i>	AGACC	--Type III ¹ --	4	7		52; 4; 14, 15; 4, 56
<i>Escherichia coli</i> P15	W. Arber	<i>EcoP15</i>	CAGCAG	--Type III ¹ --	12	5		109; 3
<i>Flavobacterium</i> species	N. Brown	<i>FspAI</i> (<i>BstEII</i>)	G+GTNACC	11	8	0	0	18
<i>Fusobacterium nucleatum</i> A	M. Smith	<i>FnuAI</i> (<i>HinfI</i>)	G+ANTC	>50	>50	10	21	82
		<i>FnuAII</i> (<i>MboI</i>)	GATC	>50 ^d	>50	8	0	82; 112
<i>Fusobacterium nucleatum</i> C	M. Smith	<i>FnuCI</i> (<i>MboI</i>)	\downarrow GATC	>50 ^d	>50	8	0	82
<i>Fusobacterium nucleatum</i> D	M. Smith	<i>FnuDI</i> (<i>HaeIII</i>)	GG+CC	>50	>50	19	11	82
		<i>FnuDII</i>	CG+CG	>50	>50	0	14	82
		<i>FnuDIII</i> (<i>HhaI</i>)	GCG+G	>50	>50	2	18	82
<i>Fusobacterium nucleatum</i> E	M. Smith	<i>FnuEI</i> (<i>MboI</i>)	\downarrow GATC	>50 ^d	>50	8	0	82
<i>Fusobacterium nucleatum</i> 48	M. Smith	<i>Fnu48 I</i>	?	>50	?	?	>10	81
<i>Fusobacterium nucleatum</i> 4H	M. Smith	<i>Fnu4H I</i>	GC+NGC	>50	>50	25	31	80
<i>Haemophilus aegyptius</i>	ATCC 11116	<i>HaeI</i>	(\uparrow)GG+CC(\uparrow)	?	?	11	6	102
		<i>HaeII</i>	PUGCGC+Py	>30	>30	1	8	111; 147
		<i>HaeIII</i>	GG+CC	>50	>50	19	11	95; 17; 86; 86
<i>Haemophilus aphrophilus</i>	ATCC 19415	<i>HapI</i>	?	>30	?	?	?	112
		<i>HapII</i> (<i>HpaII</i>)	C+CGG	>50	>50	1	5	143; 137
<i>Haemophilus gallinarum</i>	ATCC 14385	<i>HgaI</i>	GAGGC ^e	>50	>50	0	14	143; 20, 136

<u>Microorganism</u>	<u>Source</u>	<u>Enzyme^a</u>	<u>Sequence^b</u>	<u>Number of cleavage sites^c</u>	<u>References</u>
				$\frac{\lambda}{\text{Ad2}}$ $\frac{\text{SV40}}{\phi\text{X174}}$	
Haemophilus haemo- globinophilus	ATCC 19416	<u>HhgI</u> (<u>HaeIII</u>)	GGCC	>50 19 11	112
Haemophilus haemolyticus	ATCC 10014	<u>HhaI</u>	GCG+C	>50 2 18	114; 114; 87
		<u>HhaII</u> (<u>HinfI</u>)	GANTC	>50 10 21	85
Haemophilus influenzae 1056	J. Stuy	<u>Hin1056I</u> (<u>FnulII</u>)	CGGG	>50 0 14	104
		<u>Hin1056II</u>	?	>30 >30 0 5	104
Haemophilus influenzae serotype b, 1076	J. Stuy	<u>HinbIII</u> (<u>HindIII</u>)	AAGCTT	6 11 6 0	104
Haemophilus influenzae R _b	C. A. Hutchison	<u>HinbIII</u> (<u>HindIII</u>)	AAGCTT	6 11 6 0	96, 112
Haemophilus influenzae serotype c, 1160	J. Stuy	<u>HincII</u> (<u>HindII</u>)	GTPyPuAC	34 >20 7 13	104
Haemophilus influenzae serotype c, 1161	J. Stuy	<u>HincII</u> (<u>HindII</u>)	GTPyPuAC	34 >20 7 13	104
Haemophilus influenzae R _c	A. Landy, G. Leidy	<u>HincII</u> (<u>HindII</u>)	GTPyPuAC	34 >20 7 13	76
Haemophilus influenzae R _d	S. H. Goodgal (exo mutant)	<u>HindI</u>	CAC	---specific methylase---	120; 121
		<u>HindII</u>	GTPy+PuAC	34 >20 7 13	133, 70, 120, 121
		<u>HindIII</u>	AAGCTT	6 11 6 0	103; 103; 120; 121
		<u>HindIV</u>	GAC	---specific methylase---	120; 121
Haemophilus influenzae R _f	C. A. Hutchison	<u>HinfI</u>	G+ANTC	>50 >50 10 21	96; 65, 101
		<u>HinfII</u> (<u>HindIII</u>)	AAGCTT	6 11 6 0	87
		<u>HinfIII</u>	?	---Type III ^f ---	69
Haemophilus influenzae H-1	M. Takanami	<u>HinhI</u> (<u>HaeII</u>)	PuGGCGPy	>30 >30 1 8	143
Haemophilus parahaemolyticus	C. A. Hutchison	<u>HphI</u>	GGTGA ^f	>50 >50 4 9	96; 72
Haemophilus parainfluenzae	J. Setlow	<u>HpaI</u>	GTT+AAC	13 6 4 3	126; 39
		<u>HpaII</u>	C+CGG	>50 >50 1 5	126; 39; 86; 86

Microorganism	Source	Enzyme ^a	Sequence ^b	$\frac{\lambda}{\text{Ad2}}$	Number of cleavage sites ^c $\frac{\text{SV40}}{\text{9XI174}}$	References		
Moraxella nonliquefaciens	ATCC 17953	<u>MnlI</u>	CCTC ^h	>50	>51	34	160	
Moraxella nonliquefaciens	ATCC 17954	<u>MnnI</u> (<u>HindII</u>)	GTPyPuAC	34	>20	7	13	54
		<u>MnnII</u> (<u>HaeIII</u>)	GGCC	>50	>50	19	11	54
		<u>MnnIII</u>	?	>10	>6	3	?	54
		<u>MnnIV</u> (<u>HhaI</u>)	GGCC	>50	>50	2	18	54
Moraxella osloensis	ATCC 19976	<u>MosI</u> (<u>MboI</u>)	GATC	>50 ^d	>50	8	0	41
Moraxella species	R. J. Roberts	<u>MspI</u> (<u>HpaII</u>)	CCGG	>50	>50	1	5	149
Myxococcus stipitatus Mxs2H	H. Reichenbach	<u>MsII</u> (<u>XhoI</u>)	CTCGAG	1	6	0	1	96, 112
Myxococcus virescens V-2	H. Reichenbach	<u>MvII</u>	?	1	?	?	?	98
		<u>MvIII</u>	?	?	?	?	?	98
Neisseria gonorrhoea	G. Wilson	<u>NgOI</u> (<u>HaeII</u>)	PuGGGCPy	>30	>30	1	8	156
Neisseria gonorrhoea	CDC 66	<u>NgpII</u> (<u>HaeIII</u>)	GGCC	>50	>50	19	11	26
Oerskovia xanthineolytica	R. Shekman	<u>OxaI</u> (<u>AluI</u>)	AGCT	>50	>50	35	24	135
		<u>OxaII</u>	?	?	?	?	?	135
Proteus vulgaris	ATCC 13315	<u>PvuI</u>	CGATCG	4	7	0	0	46
		<u>PvuII</u>	CAG+CTG	15	22	3	0	46
Providencia alcalifaciens	ATCC 9886	<u>PalI</u> (<u>HaeIII</u>)	GGCC	>50	>50	19	11	42
Providencia stuartii 164	J. Davies	<u>PstI</u>	CTGCA+G	18	25	2	1	131; 21
Pseudomonas aeruginosa	G. A. Jacoby	<u>PaeR7</u>	?	1	?	0	0	59
Pseudomonas facilis	M. VanMontagu	<u>PfaI</u> (<u>MboI</u>)	GATC	>50 ^d	>50	8	0	149
Pseudomonas maltophilia	D. Comb	<u>PmaI</u> (<u>PstI</u>)	CTGCAG	18	25	2	1	123

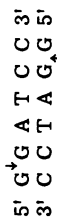
Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c		References
				$\frac{\lambda}{\text{AgZ}}$	$\frac{\text{SV40 } \phi\text{X174}}{\phi\text{X174}}$	
Rhodopseudomonas sphaeroides	R. Lascelles	<u>RspI</u>	CGATCG	4	7 0 0	9
Rhodopseudomonas sphaeroides	S. Kaplan	<u>RshI (PvuI)</u>	CGAT+CG	4	7 0 0	83
Rhodopseudomonas sphaeroides	S. Kaplan	<u>RsaI</u>	GT+AC	>50	>50 11 17	38
Rhodopseudomonas sphaeroides	S. Kaplan	<u>RsrI (EcoRI)</u>	GAATTC	5	5 1 0	38
Serratia marcescens S _b	C. Muider	<u>SmaI</u>	CCC+GGG	3	12 0 0	49; 34
Serratia species SAI	B. Torheim	<u>SspI</u>	?	?	? ? ?	146
Sphaerotilus natans C	A. Pope	<u>SnaI</u>	?	2	? ? ?	106
Staphylococcus aureus 3A	E.E. Stobberingh	<u>Sau3A (MboI)</u>	+GATC	>50 ^d	>50 8 0	138
Staphylococcus aureus P596	E.E. Stobberingh	<u>Sau96I (AsuI)</u>	G+GNCC	>30	>30 11 2	139
Streptococcus faecalis var. zymogenes	R. Wu	<u>SfaI (HaeIII)</u>	GG+CC	>50	>50 19 11	157
Streptococcus faecalis ND547	D. Clewell	<u>SfaNI</u>	GATGC	>50 ^h	>30 6 12	125
Streptomyces achromogenes	ATCC 12767	<u>SacI</u>	GAGCT+C	2	7 0 0	1
		<u>SacII</u>	CCGC+GG	3	>25 0 1	1
		<u>SacIII</u>	?	>100	>100 ? ?	1
Streptomyces albus	CM1 52766	<u>SaIPI (PstI)</u>	CTGCAG	18	25 2 1	24
Streptomyces albus subspecies pathocidicus	KCC S0166	<u>SpaI (XhoI)</u>	CTCGAG	1	6 0 1	142
Streptomyces albus G	J.M. Ghuyssen	<u>SalI</u>	G+TCGAC	2	3 0 0	2
		<u>SalIII</u>	?	>20	? ? ?	2
Streptomyces aureofaciens IKA 18/4	?	<u>SauI</u>	?	2	? ? ?	144
Streptomyces bobilliae	ATCC 3310	<u>SboI (SacII)</u>	CCCGCG	3	>25 0 1	141

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c			References	
				$\frac{\lambda}{\lambda}$	$\frac{\text{AgZ}}{\text{SV40}}$	$\frac{\phi\text{X174}}{\phi\text{X174}}$		
<i>Streptomyces bradiae</i>	ATCC 3535	<u>SbrI</u> (<u>SacII</u>)	CCGCGG	3	>25	0	1	141
<i>Streptomyces cupidosporus</i>	KCC S0316	<u>ScuI</u> (<u>XhoI</u>)	CTCGAG	1	6	0	1	141
<i>Streptomyces exfoliatus</i>	KCC S0030	<u>SexI</u> (<u>XhoI</u>)	CTCGAG	1	6	0	1	142
<i>Streptomyces goshikiensis</i>	KCC S0294	<u>SgoI</u> (<u>XhoI</u>)	CTCGAG	1	6	0	1	142
<i>Streptomyces griseus</i>	ATCC 23345	<u>SgrI</u>	?	0	7	0	?	1
<i>Streptomyces hygroscopicus</i>	F. Walter	<u>ShyI</u> (<u>SacII</u>)	CCGCGG	3	>25	0	1	152
<i>Streptomyces lavendulae</i>	ATCC 8644	<u>SlaI</u> (<u>XhoI</u>)	C+TCGAG	1	6	0	1	141
<i>Streptomyces luteoreticulii</i>	KCC S0788	<u>SluI</u> (<u>XhoI</u>)	CTCGAG	1	6	0	1	142
<i>Streptomyces phaeochromogenes</i>	F. Bolivar	<u>SphI</u>	GCATG+C	4	?	2	0	162
<i>Streptomyces stanford</i>	S. Goff, A. Rambach	<u>SstI</u> (<u>SacI</u>)	GAGCT+C	2	7	0	0	48; 97
		<u>SstII</u> (<u>SacII</u>)	CCGC+GG	3	>25	0	1	48
		<u>SstIII</u> (<u>SacIII</u>)	?	>100	>100	?	?	48
<i>Thermoplasma acidophilum</i>	D. Searcy	<u>ThaI</u> (<u>FnuDII</u>)	CG+CG	>50	>50	0	14	92
<i>Thermoplyspora glauca</i>	ATCC 15345	<u>IglI</u> (<u>SacII</u>)	CCGCGG	3	>25	0	1	46
<i>Thermus aquaticus</i> YTI	J.I. Harris	<u>TagI</u>	T+CGA	>50	>50	1	10	122
		<u>TagII</u>	?	>30	>30	4	6	112
<i>Xanthomonas amaranthicola</i>	ATCC 11645	<u>XamI</u> (<u>SalI</u>)	GTCGAC	2	3	0	0	2
<i>Xanthomonas badrii</i>	ATCC 11672	<u>XbaI</u>	T+CTAGA	1 ^d	4	0	0	161
<i>Xanthomonas holcicola</i>	ATCC 13461	<u>XhoI</u>	C+TCGAG	1	6	0	1	47
		<u>XhoII</u>	Pu+GATCPy	>20	>20	3	0	104; 46

Microorganism	Source	Enzyme ^a	Sequence ^b	Number of cleavage sites ^c				References
				λ	Ad2	SV40	ϕ X174	
Xanthomonas malvacearum	ATCC 9924	<u>Xma</u> I	C+CCGGG	3	12	0	0	34
		<u>Xma</u> II (<u>Pst</u> I)	CTGCAG	18	25	2	1	34
		<u>Xma</u> III	C+GGCCG	2	10	0	0	73
Xanthomonas nigromaculans	ATCC 23390	<u>Xin</u> II (<u>Pvu</u> I)	CGATCG	4	7	0	0	54
Xanthomonas oryzae	M. Ehrlich	<u>Xor</u> I (<u>Pst</u> I)	CTGCAG	18	25	2	1	153
Xanthomonas papavericola	ATCC 14180	<u>Xor</u> II (<u>Pvu</u> I)	CGATC+G	4	7	0	0	153
		<u>Xpa</u> I (<u>Xho</u> I)	C+TCGAG	1	6	0	1	47

Footnotes to Table

- a. When two enzymes recognize the same sequence, i.e., are isoschizomers, the prototype (i.e., the first example isolated) is indicated in parentheses.
- 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



Bases appearing in parentheses signify that either base may occupy that position in the recognition sequence. Thus, AccI cleaves the sequence GTAGAC, GTATAC, GTCGAC, and GTCATC. Where known, the base modified by the corresponding specific methylase is indicated by an asterisk. *A is N⁶-methyladenosine. *C 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), and φX174 Rf DNA (φX174). In the latter two cases, the sites were checked by computer search of the published sequences.

d. In most *E. coli* strains, bacteriophage lambda DNA is partially modified against the action of AtuBI, AtuII, AtuCI, BclI, CpeI, DpnII, EclII, EcoRII, FnuAII, FnuCI, MboI, MnoIII, MosI, and XbaI. It should be noted that FnuE I, Pfal and Sau3A are not inhibited by dam methylation; BstNI and ApyI are not inhibited by mec methylation.

e. HgaI cleaves as indicated:

$$\begin{array}{r} 5' \text{ GACGCNNNNN}^{\dagger} \\ 3' \text{ CTGCGNNNNNNNNNN}^{\dagger} \end{array}$$

f. HphI cleaves as indicated:

$$\begin{array}{r} 5' \text{ GGTGANNNNNNNN}^{\dagger} \\ 3' \text{ CCACTNNNNNNNN}^{\dagger} \end{array}$$

g. MboII cleaves as indicated:

$$\begin{array}{r} 5' \text{ GAAGANNNNNNNN}^{\dagger} \\ 3' \text{ CTTCTNNNNNNNN}^{\dagger} \end{array}$$

h. MnII cleaves 5 to 10 bases in the 3' direction from the recognition sequence. SfaNI cleaves an unknown number of nucleotides away from the recognition sequence.

i. EcoPI, EcoP15, and HinfIII 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 Piekarowicz (69).

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