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Restriction and modification enzymes and their recognition sequences

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Introduction

Since the last compilation of Type II restriction endonucleases (133), more than 45 new enzymes have been discovered. Among the valuable new specificities are GdiI and its isoschizomer StuI (AGGCCT), GdiII (PyGGCCG), HgiEII (ACC[N]$_6$GGT), RruI (AGTACT), Tth111 I and its isoschizomers TtrI and TteI (GACNNNGTC), and Tth111 II (CAAPuCA). The new enzyme NciI (CC[G/C]GG) turns out to be an isoschizomer of CauII whose recognition has recently been determined. The recognition sequences of SnaI (GTATAC) and SauI (CCTNAGG) have also been newly determined. Among the 258 enzymes listed, there are at least 69 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 (161). 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case, refers to the purification procedure for the restriction enzyme, or from the individuals who have provided their unpublished results.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] λ	Ad2	SV40	φX174	References
§ Acetobacter aceti sub. liquefaciens	IFO 12388	AacI (BamHI)	GGATCC	5	3	1	0	150
§ Acetobacter aceti sub. liquefaciens	M. Van Montagu	AaeI (BamHI)	GGATCC	5	3	1	0	150
Achromobacter immobilis	ATCC 15934	AimI	?	?	?	?	?	40
Acinetobacter calcoaceticus	R.J. Roberts	AccI	GT↓($\frac{A}{C}$)($\frac{G}{T}$)AC	7	8	1	2	197
		AccII (FnuDII)	CGCG	>50	>50	0	14	197
§		AccIII	?	>10	> 6	?	?	124
Agrobacterium tumefaciens	ATCC 15955	AtuAI	?	>30	>30	?	?	149
Agrobacterium tumefaciens B6806	E. Nester	AtuBI (EcoRII)	CC($\frac{A}{T}$)GG	>35[d]	>35	16	2	140
Agrobacterium tumefaciens IIBV7	G. Roizes	AtuBVI	?	>14	?	1	0	139
Agrobacterium tumefaciens ID 135	C. Kado	AtuII (EcoRII)	CC($\frac{A}{T}$)GG	>35[d]	>35	16	2	97
Agrobacterium tumefaciens C58	E. Nester	AtuCI (BclI)	TGATCA	7[d]	5	1	0	149
Anabaena catanula	CCAP 1403/1	AcaI	?	?	?	?	?	77
Anabaena cylindrica	ATCC 27899	AcyI	GPu↓CGPyC	>14	>14	0	7	33
Anabaena oscillarioides	CCAP 1403/11	AosI (MstI)	TGC↓GCA	>10	>15	0	1	34
		AosII (AcyI)	GPu↓CGPyC	>14	>14	0	7	34
§ Anabaena strain Waterbury	ATCC 29208	AstWI (AcyI)	GPu↓CGPyC	>14	>14	0	7	32
Anabaena subcylindrica	CCAP 1043/4b	AsuI	G↓GNCC	>30	>30	11	2	78
		AsuII	TT↓CGAA	7	1	0	0	124, 32; 32
§		AsuIII (AcyI)	GPu↓CGPyC	>14	>14	0	7	32

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Anabaena variabilis	ATCC 27892	AvaI	C↓PyCGPuG	8	15	0	1	121; 79
		AvaII	G↓G($\frac{A}{T}$)CC	>17	>30	6	1	121; 173, 79, 45
		AvaIII	ATGCAT	?	?	3	0	138; 138, 155
Anabaena variabilis[uw]	E.C. Rosenvold	AvrI (AvaI)	CPyCGPuG	8	15	0	1	141
		AvrII	CCTAGG	2	2	2	0	141
Arthrobacter luteus	ATCC 21606	AluI	AG↓CT	>50	>50	35	24	135
Arthrobacter pyridinolis	R. DiLauro	ApyI (EcoRII)	CC↓($\frac{A}{T}$)GG	>35[d]	>35	16	2	35
Bacillus acidocaldarius	ATCC 27009	BacI (SacII)	CCGCGG	4	>25	0	1	112, 124
Bacillus amyloliquefaciens F	ATCC 23350	BamFI (BamHI)	GGATCC	5	3	1	0	154
Bacillus amyloliquefaciens H	F.E. Young	BamHI	G↓GAT$\overset{*}{C}$C	5	3	1	0	190; 137; 69; 69
Bacillus amyloliquefaciens K	T. Kaneko	BamKI (BamHI)	GGATCC	5	3	1	0	154
Bacillus amyloliquefaciens N	T. Ando	BamNI (BamHI)	GGATCC	5	3	1	0	153
		$BamN_x$ (AvaII)	G↓G($\frac{A}{T}$)CC	>17	>30	6	1	152, 153; 82
Bacillus brevis S	A.P. Zarubina	BbvSI	$G\overset{*}{C}$($\frac{A}{T}$)GC	---specific methylase---				185
Bacillus brevis	ATCC 9999	BbvI	$G\overset{*}{C}$($\frac{A}{T}$)GC	>30	>30	23	14	54; 53; 69; 69
Bacillus caldolyticus	A. Atkinson	BclI	T↓GATCA	7[d]	5	1	0	10
Bacillus cereus	ATCC 14579	Bce14579	?	>10	?	?	?	154
Bacillus cereus	IAM 1229	Bce1229	?	>10	?	?	?	154
Bacillus cereus	T. Ando	Bce170 (PstI)	CTGCAG	18	25	2	1	154
Bacillus cereus Rf sm st	T. Ando	BceR (FnuDII)	CGCG	>50	>50	0	14	154

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Bacillus globigii	G.A. Wilson	BglI	GCCNNNN↓NGGC	22	12	1	0	37, 191; 6, 96, 181
		BglII	A↓GATCT	6	12	0	0	37, 191; 128
Bacillus megaterium 899	B899	Bme899	?	> 5	?	?	?	154
Bacillus megaterium B205-3	T. Kaneko	Bme205	?	>10	?	?	?	154
Bacillus megaterium	J. Upcroft	BmeI	?	>10	>20	4	?	50
Bacillus pumilus AHU1387A	T. Ando	BpuI	?	6	>30	2	?	81
Bacillus sphaericus	IAM 1286	Bsp1286	?	?	?	?	?	154
Bacillus sphaericus R	P. Venetianer	BspRI (HaeIII)	GGCC	>50	>50	19	11	87
Bacillus stearothermophilus 1503-4R	N. Welker	BstI (BamHI)	G↓GATCC	5	3	1	0	23; 26
Bacillus stearothermophilus 240	A. Atkinson	BstAI	?	?	?	?	?	12
Bacillus stearothermophilus ET	N. Welker	BstEI	?	?	?	?	?	114
		BstEII	G↓GTNACC	11	8	0	0	114
		BstEIII (MboI)	GATC	>50[d]	>50	> 8	0	114; 58; 124
Bacillus stearothermophilus	ATCC 12980	BstPI (BstEII)	G↓GTNACC	11	8	0	0	130
Bacillus stearothermophilus	D. Comb	BstNI (EcoRII)	CC↓(A/T)GG	>35[d]	>35	16	2	148
§ Bacillus stearothermophilus strain 822	T. Oshima	BseI (HaeIII)	GGCC	>50	>50	19	11	157
§		BseII (HpaI)	GTTAAC	13	6	4	3	157
Bacillus subtilis strain X5	T. Trautner	BsuRI (HaeIII)	GG↓*CC	>50	>50	19	11	16; 17; 62
Bacillus subtilis Marburg 168	T. Ando	BsuM	?	>10	?	?	?	154
Bacillus subtilis	ATCC 6633	Bsu6663	?	>20	?	?	?	154

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Bacillus subtilis	IAM 1076	Bsu1076 (HaeIII)	GGCC	>50	>50	19	11	154
Bacillus subtilis	IAM 1114	Bsu1114 (HaeIII)	GGCC	>50	>50	19	11	154
Bacillus subtilis	IAM 1247	Bsu1247 (PstI)	CTGCAG	18	25	2	1	154; 75
Bacillus subtilis	ATCC 14593	Bsu1145	?	>20	?	?	?	154
Bacillus subtilis	IAM 1192	Bsu1192	?	>10	?	?	?	154
Bacillus subtilis	IAM 1193	Bsu1193	?	>30	?	?	?	154
Bacillus subtilis	IAM 1231	Bsu1231	?	>20	?	?	?	154
Bacillus subtilis	IAM 1259	Bsu1259	?	> 8	?	?	?	154
Bordetella bronchiseptica	ATCC 19395	BbrI (HindIII)	AAGCTT	6	11	6	0	124
§ Bordetella pertussis	P. Novotny	BpeI (HindIII)	AAGCTT	6	11	6	0	59
Brevibacterium albidum	ATCC 15831	BalI	TGG↓CCA	15	17	0	0	51
Brevibacterium luteum	ATCC 15830	BluI (XhoI)	C↓TCGAG	1	6	0	1	55
		BluII (HaeIII)	GGCC	>50	>50	19	11	182
Caryophanon latum L	H. Mayer	ClaI	AT↓CGAT	12	2	0	0	110
§ Caryophanon latum	ATCC 15219	ClmI (HaeIII)	GGCC	>50	>50	19	11	164
		ClmII (AvaII)	GG($\frac{A}{T}$)CC	>17	>30	6	1	164
Caryophanon latum	DSM 484	CltI (HaeIII)	GG↓CC	>50	>50	19	11	112
Chloroflexus aurantiacus	A. Bingham	CauI (AvaII)	GG($\frac{A}{T}$)CC	>30	>30	6	1	11
§		CauII	CC↓($\frac{G}{C}$)GG	>30	>30	0	1	11, 100
Chromobacterium violaceum	ATCC 12472	CviI	?	?	?	?	?	40
Clostridium formicoaceticum	ATCC 23439	CfoI (HhaI)	GCGC	>50	>50	2	18	106

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	ϕX174	References
Corynebacterium humiferum	ATCC 21108	ChuI (HindIII)	AAGCTT	6	11	6	0	40
		ChuII (HindII)	GTPyPuAC	34	>20	7	13	40
Corynebacterium petrophilum	ATCC 19080	CpeI (BclI)	TGATCA	7[d]	5	1	0	43
Desulfovibrio desulfuricans Norway strain	H. Peck	DdeI	C↓TNAG	>50	>50	19	14	106; 52
§		DdeII (XhoI)	CTCGAG	1	6	0	1	124
§ Desulfovibrio desulfuricans	ATCC 27774	DdsI (BamHI)	GGATCC	5	3	1	0	105
Diplococcus pneumoniae	S. Lacks	DpnI	G$\overset{*}{A}$↓TC	--only cleaves methylated DNA--				91; 48, 92
Diplbcoccus pneumoniae	S. Lacks	DpnII (MboI)	GATC	>50[d]	>50	8	0	91; 92
Enterobacter cloacae	H. Hartmann	EclI	?	14	?	?	?	67
		EclII (EcoRII)	CC($\frac{A}{T}$)GG	>35[d]	>35	16	2	67
Enterobacter cloacae	DSM 30056	EcaI (BstEII)	G↓GTNACC	11	8	0	0	74
§		EcaII (EcoRII)	CC($\frac{A}{T}$)GG	>35[d]	>35	16	2	124
Enterobacter cloacae	DSM 30060	EccI (SacII)	CCGCGG	4	>25	0	1	111; 124
Escherichia coli RY13	R.N. Yoshimori	EcoRI	G↓$\overset{*}{A}$ATTC	5	5	1	0	61; 70; 61; 36
		EcoRI'	PuPuA↓TPyPy	>10	>10	24	16	120
Escherichia coli R245	R.N. Yoshimori	EcoRII	↓C$\overset{*}{C}$($\frac{A}{T}$)GG	>35[d]	>35	16	2	196; 8, 13; 196; 13
Escherichia coli B	W. Arber	EcoB	TG$\overset{*}{A}$(N)$_8$TGCT	---Type I---		1	0	42; 94, 131; 95; 184
Escherichia coli K	M. Meselson	EcoK	AAC(N)$_6$GTGC	---Type I---		0	0	115; 7, 84; 64
Escherichia coli (PI)	K. Murray	EcoPI	AG$\overset{*}{A}$CC	--Type III[i]--		4	7	63; 4; 14, 15; 4, 68
Escherichia coli P15	W. Arber	EcoP15	CAGCAG	--Type III[i]--		12	5	132; 65
Flavobacterium species	N. Brown	FspAI (BstEII)	G↓GTNACC	11	8	0	0	18

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	ϕX174	References
Fusobacterium nucleatum A	M. Smith	FnuAI (HinfI)	G↓ANTC	>50	>50	10	21	102
		FnuAII (MboI)	GATC	>50[d]	>50	8	0	102; 124
Fusobacterium nucleatum C	M. Smith	FnuCI (MboI)	↓GATC	>50[d]	>50	8	0	102
Fusobacterium nucleatum D	M. Smith	FnuDI (HaeIII)	GG↓CC	>50	>50	19	11	102
		FnuDII	CG↓CG	>50	>50	0	14	102
		FnuDIII (HhaI)	GCG↓C	>50	>50	2	18	102
Fusobacterium nucleatum E	M. Smith	FnuEI (MboI)	↓GATC	>50[d]	>50	8	0	102
Fusobacterium nucleatum 48	M. Smith	Fnu48 I	?	>50	?	?	>10	101
Fusobacterium nucleatum 4H	M. Smith	Fnu4H I	GC↓NGC	>50	>50	25	31	99
§ Gluconobacter dioxyacetonicus	IAM 1814	GdiI (StuI)	AGG↓CCT	>10	> 6	7	1	182
§		GdiII	Py↓GGCCG	>10	?	0	2	182
§ Gluconobacter dioxyacetonicus	IAM 1840	GdoI (BamHI)	GGATCC	5	3	1	0	150
§ Gluconobacter oxydans sub. melonogenes	IAM 1836	GoxI (BamHI)	GGATCC	5	3	1	0	150
Haemophilus aegyptius	ATCC 11116	HaeI	$(^{A}_{T})$GG↓CC$(^{A}_{T})$	?	?	11	6	123
		HaeII	PuGCGC↓Py	>30	>30	1	8	134; 180
		HaeIII	GG↓$\overset{*}{C}$C	>50	>50	19	11	116; 17; 108; 108
Haemophilus aphrophilus	ATCC 19415	HapI	?	>30	?	?	?	124
		HapII (HpaII)	C↓CGG	>50	>50	1	5	176; 170
Haemophilus gallinarum	ATCC 14385	HgaI	GACGC[e]	>50	>50	0	14	176; 20, 169

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Haemophilus haemoglobinophilus	ATCC 19416	HhgI (HaeIII)	GGCC	>50	>50	19	11	124
Haemophilus haemolyticus	ATCC 10014	HhaI	G*CG↓C	>50	>50	2	18	136; 136; 109
		HhaII (HinfI)	GANTC	>50	>50	10	21	107
§ Haemophilus influenzae GU	J. Chirikjian	HinGU I (HhaI)	GCGC	>50	>50	2	18	165 and 25
§		HinGU II	?	>50	>50	12	> 8	165
§ Haemophilus influenzae 173	J. Chirikjian	Hin173 (HindIII)	AAGCTT	6	11	6	0	165
Haemophilus influenzae 1056	J. Stuy	Hin1056I (FnuDII)	CGCG	>50	>50	0	14	126
		Hin1056II	?	>30	>30	0	5	126
Haemophilus influenzae serotype b, 1076	J. Stuy	HinbIII (HindIII)	AAGCTT	6	11	6	0	126
Haemophilus influenzae R_b	C.A. Hutchison	HinbIII (HindIII)	AAGCTT	6	11	6	0	117, 124
Haemophilus influenzae serotype c, 1160	J. Stuy	HincII (HindII)	GTPyPuAC	34	>20	7	13	126
Haemophilus influenzae serotype c, 1161	J. Stuy	HincII (HindII)	GTPyPuAC	34	>20	7	13	126
Haemophilus influenzae R_c	A. Landy, G. Leidy	HincII (HindII)	GTPyPuAC	34	>20	7	13	93
Haemophilus influenzae R_d	S.H. Goodgal (exo mutant)	HindI	C*AC	---specific methylase---				142; 143
		HindII	GTPy↓Pu*AC	34	>20	7	13	162, 86, 142, 143
		HindIII	*A↓AGCTT	6	11	6	0	125; 125; 142; 143
		HindIV	G*AC	---specific methylase---				142; 143
Haemophilus influenzae R_f	C.A. Hutchison	HinfI	G↓ANTC	>50	>50	10	21	117; 80, 122
		HinfII (HindIII)	AAGCTT	6	11	6	0	109
		HinfIII	CGAAT[k]	---Type III[i]---		0	5	85, 127

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Haemophilus influenzae H-1	M. Takanami	HinHI (HaeII)	PuGCGCPy	>30	>30	1	8	176
Haemophilus parahaemolyticus	C.A. Hutchison	HphI	GGTGA[f]	>50	>50	4	9	117; 88
Haemophilus parainfluenzae	J. Setlow	HpaI	GTT↓AAC	13	6	4	3	151; 47, 2
		HpaII	C↓CGG	>50	>50	1	5	151; 47; 108; 108
Haemophilus suis	ATCC 19417	HsuI (HindIII)	A↓AGCTT	6	11	6	0	124
Herpetosiphon giganteus HP1023	J.H. Parish	HgiAI	G(A/T)GC(A/T)↓C	24	>20	0	3	22
Herpetosiphon giganteus Hpg 5	H. Reichenbach	HgiBI (AvaII)	G↓G(A/T)CC	>17	>30	6	1	73
Herpetosiphon giganteus Hpg 9	H. Reichenbach	HgiCI	G↓GPyPuCC	?	?	?	?	73, 89
		HgiCII (AvaII)	G↓G(A/T)CC	>17	>30	6	1	73
		HgiCIII (SalI)	G↓TCGAC	2	3	0	0	73
Herpetosiphon giganteus Hpa2	H. Reichenbach	HgiDI (AcyI)	GPu↓CGPyC	>14	>14	0	7	73, 89
		HgiDII (SalI)	G↓TCGAC	2	3	0	0	73
Herpetosiphon giganteus Hpg 24	H. Reichenbach	HgiEI (AvaII)	G↓G(A/T)CC	>17	>30	6	1	73
§		HgiEII	ACC(N)$_6$GGT	?	?	1	1	73
§ Herptosiphon giganteus Hpa 1	H. Reichenbach	HgiGI (AcyI)	GPu↓CGPyC	>14	>14	0	7	89
Klebsiella pneumoniae OK8	J. Davies	KpnI	GGTAC↓C	2	8	1	0	160; 178
§ Mastigocladus laminosus	CCAP 1447/1	MlaI (AsuII)	TT↓CGAA	7	1	0	0	38
Microcoleus species	D. Comb	MstI	TGCGCA	>10	>15	0	1	28; 53
		MstII	?	2	> 6	0	0	147
Moraxella bovis	ATCC 10900	MboI	↓GATC	>50[d]	>50	8	0	49
		MboII	GAAGA[g]	>50	>50	16	11	49; 19, 39

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
§ Moraxella bovis	ATCC 17947	MbvI	?	?	?	?	?	83
Moraxella glueidi LG1	J. Davies	MglI	?	?	?	?	?	160
Moraxella glueidi LG2	J. Davies	MglII	?	?	?	?	?	160
§ Moraxella kingae	ATCC 23331	MkiI (HindIII)	AAGCTT	6	11	6	0	83
Moraxella nonliquefaciens	ATCC 19975	MnoI (HpaII)	C↓CGG	>50	>50	1	5	124; 5
		MnoII (MnnIII)	?	>10	> 6	3	?	124
		MnoIII (MboI)	GATC	>50[d]	>50	8	0	124
Moraxella nonliquefaciens	ATCC 17953	MnlI	CCTC[h]	>50	>50	51	34	198
Moraxella nonliquefaciens	ATCC 17954	MnnI (HindII)	GTPyPuAC	34	>20	7	13	66
		MnnII (HaeIII)	GGCC	>50	>50	19	11	66
		MnnIII	?	>10	> 6	3	?	66
		MnnIV (HhaI)	GCGC	>50	>50	2	18	66
§ Moraxella nonliquefaciens	ATCC 19996	MniI (HaeIII)	GGCC	>50	>50	19	11	83
		MniII (HpaII)	CCGG	>50	>50	1	5	83
Moraxella osloensis	ATCC 19976	MosI (MboI)	GATC	>50[d]	>50	8	0	49
§ Moraxella phenylpyruvica	ATCC 17955	MphI (EcoRII)	CC($\frac{A}{T}$)GG	>35[d]	>35	16	2	83
Moraxella species	R.J. Roberts	MspI (HpaII)	C↓CGG	>50	>50	1	5	183, 147
Myxococcus stipitatus Mxs2H	H. Reichenbach	MsiI (XhoI)	CTCGAG	1	6	0	1	117, 124
Myxococcus virescens V-2	H. Reichenbach	MviI	?	1	?	?	?	119
		MviII	?	?	?	?	?	119
§ Neisseria cinerea	NRCC 31006	NciI (CauII)	CC($\frac{C}{G}$)GG	>15	>15	0	1	189

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Neisseria gonorrhoea	G. Wilson	NgoI (HaeII)	PuGCGCPy	>30	>30	1	8	192
Neisseria gonorrhoea	CDC 66	NgoII (HaeIII)	GGCC	>50	>50	19	11	29, 30
Oerskovia xanthineolytica	R. Shekman	OxaI (AluI)	AGCT	>50	>50	35	24	167
		OxaII	?	?	?	?	?	167
Proteus vulgaris	ATCC 13315	PvuI	CGAT↓CG	3	7	0	0	56
		PvuII	CAG↓CTG	15	22	3	0	56
Providencia alcalifaciens	ATCC 9886	PalI (HaeIII)	GGCC	>50	>50	19	11	50
Providencia stuartii 164	J. Davies	PstI	CTGCA↓G	18	25	2	1	160; 21
Pseudomonas aeruginosa	G.A. Jacoby	PaeR7	?	1	?	0	0	72
Pseudomonas facilis	M. VanMontagu	PfaI (MboI)	GATC	>50[d]	>50	8	0	183
Pseudomonas maltophila	D. Comb	PmaI (PstI)	CTGCAG	18	25	2	1	147
§ Rhizobium leguminosarum 300	J. Beringer	RleI	?	6	>10	?	?	194
§ Rhizobium lupini #1	W. Heumann	RluI	?	1	8	?	?	193, 71
§ Rhizobium meliloti	J.L. Denarié	RmeI	?	8	>10	?	?	71
§ Rhodospirillum rubrum	A. deWaard	RruI	AGT↓ACT	?	?	0	0	31
§		RruII (EcoRII)	CC↓($\frac{A}{T}$)GG	>35	>35	16	2	31
§ Rhodospirillum rubrum	J. Chirikjian	RrbI	?	?	4	5	1	98
Rhodopseudomonas sphaeroides	R. Lascelles	RspI (PvuI)	CGATCG	3	7	0	0	9
Rhodopseudomonas sphaeroides	S. Kaplan	RshI (PvuI)	CGAT↓CG	3	7	0	0	103
Rhodopseudomonas sphaeroides	S. Kaplan	RsaI	GT↓AC	>50	>50	11	11	104
Rhodopseudomonas sphaeroides	S. Kaplan	RsrI (EcoRI)	GAATTC	5	5	1	0	46

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Serratia marcescens S_b	C. Mulder	SmaI	CCC↓GGG	3	12	0	0	60; 41
Serratia species SAI	B. Torheim	SspI	?	?	?	?	?	179
§ Sphaerotilus natans C	A. Pope	SnaI	GTATAC	2	?	0	0	129
§ Spiroplasma citri ASP2	M.A. Stephens	SciNI (HhaI)	G↓CGC	>50	>50	2	18	163
Staphylococcus aureus 3A	E.E. Stobberingh	Sau3A (MboI)	↓GATC	>50[d]	>50	8	0	171
Staphylococcus aureus PS96	E.E. Stobberingh	Sau96I (AsuI)	G↓GNCC	>30	>30	11	2	172
Streptococcus faecalis var. zymogenes	R. Wu	SfaI (HaeIII)	GG↓CC	>50	>50	19	11	195
§ Streptococcus faecalis GU	J. Chirikjian	SfaGU I (HpaII)	CCGG	>50	>50	1	5	27
Streptococcus faecalis ND547	D. Clewell	SfaNI	GATGC[h]	>50	>30	6	12	149
Streptomyces achromogenes	ATCC 12767	SacI	GAGCT↓C	2	7	0	0	1
		SacII	CCGC↓GG	4	>25	0	1	1
		SacIII	?	>100	>100	?	?	1
Streptomyces albus	CM1 52766	SalPI (PstI)	CTGCAG	18	25	2	1	24
Streptomyces albus subspecies pathocidicus	KCC S0166	SpaI (XhoI)	CTCGAG	1	6	0	1	175
Streptomyces albus G	J.M. Ghuysen	SalI	G↓TCGAC	2	3	0	0	3
		SalII	?	>20	?	?	?	3
§ Streptomyces aureofaciens IKA 18/4	J. Timko	SauI	CC↓TNAGG	2	7	0	0	177
Streptomyces bobili	ATCC 3310	SboI (SacII)	CCGCGG	4	>25	0	1	174
Streptomyces cupidosporus	KCC S0316	ScuI (XhoI)	CTCGAG	1	6	0	1	174
Streptomyces exfoliatus	KCC S0030	SexI (XhoI)	CTCGAG	1	6	0	1	175

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
Streptomyces fradiae	ATCC 3355	SfrI (SacII)	CCGCGG	4	>25	0	1	174
Streptomyces goshikiensis	KCC S0294	SgoI (XhoI)	CTCGAG	1	6	0	1	175
Streptomyces griseus	ATCC 23345	SgrI	?	0	7	0	?	1
Streptomyces hygroscopicus	F. Walter	ShyI (SacII)	CCGCGG	4	>25	0	1	187
Streptomyces lavendulae	ATCC 8664	SlaI (XhoI)	C↓TCGAG	1	6	0	1	174
Streptomyces luteoreticuli	KCC S0788	SluI (XhoI)	CTCGAG	1	6	0	1	175
Streptomyces phaeochromogenes	F. Bolivar	SphI	GCATG↓C	4	9	2	0	44
Streptomyces stanford	S. Goff, A. Rambach	SstI (SacI)	GAGCT↓C	2	7	0	0	57; 118
		SstII (SacII)	CCGC↓GG	4	>25	0	1	57
		SstIII (SacIII)	?	>100	>100	?	?	57
§		SstIV (BclI)	TGATCA	7	5	1	0	76
§ Streptomyces tubercidicus	S. Takahashi	StuI	AGG↓CCT	>10	> 6	7	1	156
Thermoplasma acidophilum	D. Searcy	ThaI (FnuDII)	CG↓CG	>50	>50	0	14	113
Thermopolyspora glauca	ATCC 15345	TglI (SacII)	CCGCGG	3	>25	0	1	54
Thermus aquaticus YTI	J.I. Harris	TaqI	T↓CGA*	>50	>50	1	10	144; 144; -; 145
		TaqII	?	>30	>30	4	6	124
§ Thermus flavus AT62	T. Oshima	TflI (TaqI)	TCGA	>50	>50	1	10	145
§ Thermus thermophilus HB8	T. Oshima	TthHB8 I (TaqI)	TCGA*	>50	>50	1	10	146, 186; 146, 186; 145; 145
§ Thermus thermophilus strain 23	T. Oshima	TtrI (Tth111 I)	GACNNNGTC	2	?	0	0	159
§ Thermus thermophilus strain 110	T. Oshima	TteI (Tth111 I)	GACNNNGTC	2	?	0	0	159

Microorganism	Source	Enzyme[a]	Sequence[b]	Number of cleavage sites[c] λ	Ad2	SV40	φX174	References
§ Thermus thermophilus strain 111	T. Oshima	Tth111 I	GACN↓NNGTC	2	?	0	0	159, 159
§		Tth111 II	CAAPuCA[j]	>30	>30	12	11	158, 158
§		Tth111 III	?	?	?	?	?	157
§ Tolypothrix tenuis	W. Siegelman	TtnI (HaeIII)	GGCC	>50	>50	19	11	168
Xanthomonas amaranthicola	ATCC 11645	XamI (SalI)	GTCGAC	2	3	0	0	3
Xanthomonas badrii	ATCC 11672	XbaI	T↓CTAGA	1[d]	4	0	0	199
Xanthomonas holcicola	ATCC 13461	XhoI	C↓TCGAG	1	6	0	1	55
		XhoII	Pu↓GATCPy	>20	>20	3	0	126; 54
Xanthomonas malvacearum	ATCC 9924	XmaI (SmaI)	C↓CCGGG	3	12	0	0	41
		XmaII (PstI)	CTGCAG	18	25	2	1	41
		XmaIII	C↓GGCCG	2	10	0	0	90
Xanthomonas nigromaculans	ATCC 23390	XniI (PvuI)	CGATCG	3	7	0	0	66
Xanthomonas oryzae	M. Ehrlich	XorI (PstI)	CTGCAG	18	25	2	1	188
		XorII (PvuI)	CGATC↓G	3	7	0	0	188
Xanthomonas papavericola	ATCC 14180	XpaI (XhoI)	C↓TCGAG	1	6	0	1	55

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

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

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 GTCTAC. Where known, the base modified by the corresponding specific methylase is indicated by an asterisk. $\overset{*}{A}$ is N^6-methyladenosine. $\overset{*}{C}$ 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, BstEIII, CpeI, DpnII, EcaII, EclII, EcoRII, FnuAII, FnuCI, MboI, MnoIII, MosI, MphI, and XbaI. It should be noted that FnuE I, PfaI and Sau3A are not inhibited by dam methylation; BstNI and ApyI are not inhibited by mec methylation.

e. HgaI cleaves as indicated:

$$\begin{array}{ll} 5'\ GACGCNNNNN^{\downarrow} & 3' \\ 3'\ CTGCGNNNNNNNNNN_{\uparrow} & 5' \end{array}$$

f. HphI cleaves as indicated:

$$\begin{array}{ll} 5'\ GGTGANNNNNNNN^{\downarrow} & 3' \\ 3'\ CCACTNNNNNNN_{\uparrow} & 5' \end{array}$$

g. MboII cleaves as indicated:

$$\begin{array}{ll} 5'\ GAAGANNNNNNNN^{\downarrow} & 3' \\ 3'\ CTTCTNNNNNNN_{\uparrow} & 5' \end{array}$$

h. MnlI 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 (85).

j. Tth111 II cleaves as indicated:

$$\begin{array}{ll} 5'\ CAAPuCA\ (N)_{11}{}^{\downarrow} & 3' \\ 3'\ GTTPyGT\ (N)_{9}{}^{\uparrow} & 5' \end{array}$$

k. HinfIII cleaves about 25 bases 3' of the recognition sequence.

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