Vector: **pCAT**

Antibiotic Selection: **Cam** (**Chloramphenicol**)

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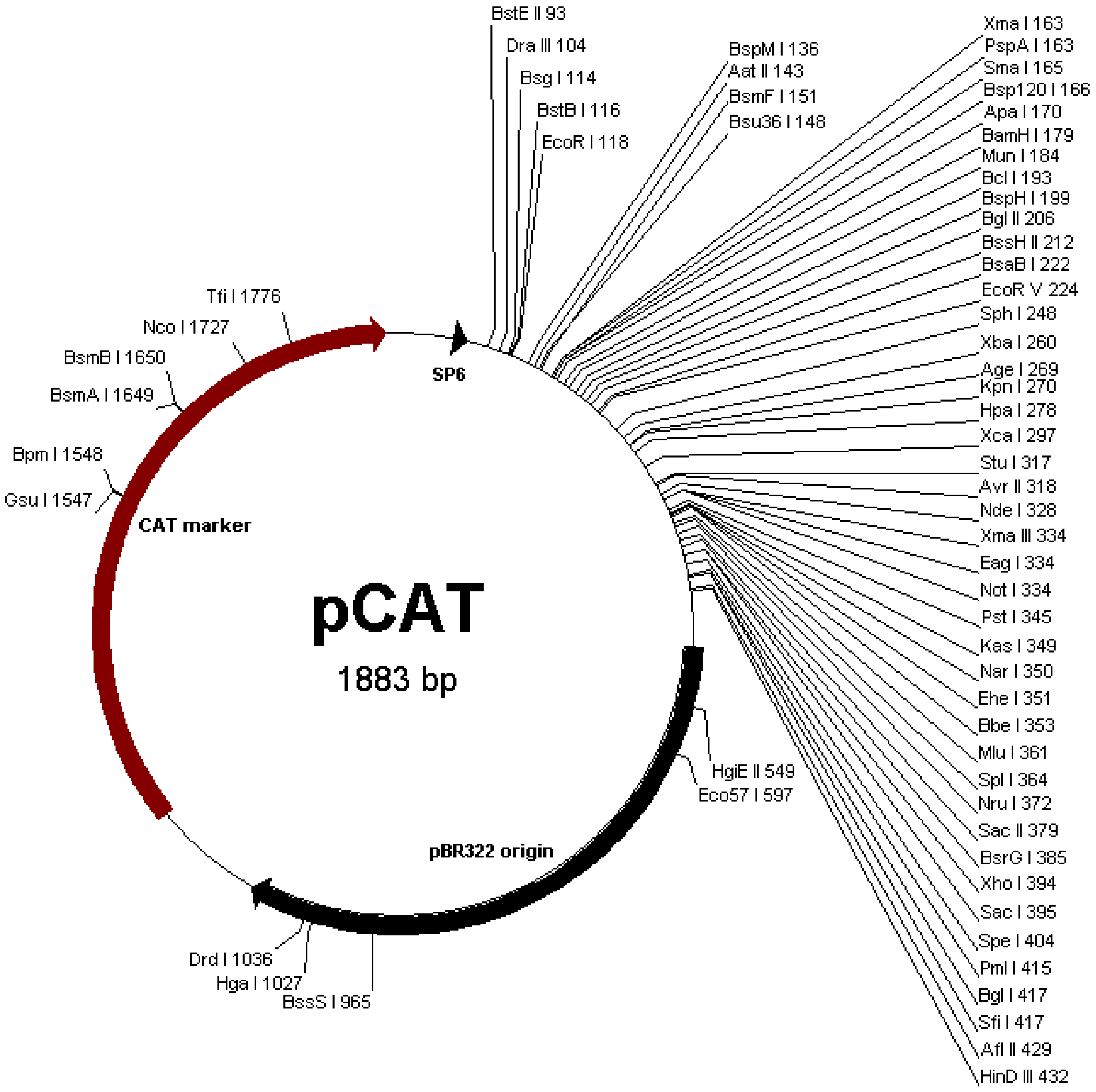
Date of Construction: January, 2014

CATendFwd: `5′-CGGCAGAATGCTTAATGAATTAC-3′`

CATmidFwd: `5′-CGCAAGATGTGGCGTGTTACGGTG-3′`

BR322Ori 5′-endRev: `5′-GTTTGCAAGCAGCAGATTACGCGC-3′`



pCAT Full-length Sequence

(assembled, not fully sequenced)

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CGTTAGAACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAGAACT
CGAAGgatctCATGGCTGGTGACCACGTCGTGGAATGCCTTCGAATTCAGCACCTGCACATGGGACGTCGACCT
GAGGTAATTATAACCCGGGCCCTATATATGGATCCAATTGCAATGATCATCATGACAGATCTGCGCGCGATCGA
TATCAGCGCTTTAAATTTGCGCATGCTAGCTATAGTTCTAGAGGTACCGGTTGTTAACGTTAGCCGGCTACGTA
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TCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTT
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CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTG
GCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACG
GGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATG
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TTGTTACACCGTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGC
AGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATT
GAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGA
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TTCAGGTTCATCATGCCGTTTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGAT
GAGTGGCAGGGCGGGGCGTAATTGGTACGTCGA
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Unique enzymes in pCAT:

BstE II	G\`GTNAC,C	93
Tth111 I	GACN\`N,NGTC	99
Dra III	CAC,NNN\`GTG	104
Xmn I	GAANN|NNTTC	112
Bsg I	GTGCAG 22/20	114
BsiC I	TT\`CG,AA	116
BstB I	TT\`CG,AA	116
EcoR I	G\`AATT,C	118
BspM I	ACCTGC 10/14	136
Aat II	G,ACGT\`C	143
Bsu36 I	CC\`TNA,GG	148
BsmF I	GGGAC 15/19	151
PspA I	C\`CCGG,G	163
Xma I	C\`CCGG,G	163
Sma I	CCC|GGG	165
Bsp120 I	G\`GGCC,C	166
EcoO109 I	RG\`GNC,CY	167
Apa I	G,GGCC\`C	170
BamH I	G\`GATC,C	179
Mun I	C\`AATT,G	184
Bcl I	T\`GATC,A	193
BspH I	T\`CATG,A	199
Bgl II	A\`GATC,T	206
BssH II	G\`CGCG,C	212
Pvu I	CG,AT\`CG	220
BsaB I	GATNN|NNATC	222
EcoR V	GAT|ATC	224
Afe I	AGC|GCT	230
Eco47 III	AGC|GCT	230
Fsp I	TGC|GCA	243
Sph I	G,CATG\`C	248
Xba I	T\`CTAG,A	260
Acc65 I	G\`GTAC,C	266
Asp718	G\`GTAC,C	266
Age I	A\`CCGG,T	269
Kpn I	G,GTAC\`C	270
Hpa I	GTT|AAC	278
NgoM I	G\`CCGG,C	286
Nae I	GCC|GGC	288
SnaB I	TAC|GTA	294
Bst1107 I	GTA|TAC	297
Xca I	GTA|TAC	297
Stu I	AGG|CCT	317
Avr II	C\`CTAG,G	318
Nsi I	A,TGCA\`T	328
Nde I	CA\`TA,TG	328
Not I	GC\`GGCC,GC	334
Eag I	C\`GGCC,G	334
Xma III	C\`GGCC,G	334
Pst I	C,TGCA\`G	345

Kas I	G\`GCGC,C	349
Nar I	GG\`CG,CC	350
Ehe I	GGC|GCC	351
Bbe I	G,GCGC\`C	353
Mlu I	A\`CGCG,T	361
BsiW I	C\`GTAC,G	364
Spl I	C\`GTAC,G	364
Nru I	TCG|CGA	372
Sac II	CC,GC\`GG	379
BsrG I	T\`GTAC,A	385
PaeR7 I	C\`TCGA,G	394
Xho I	C\`TCGA,G	394
Sac I	G,AGCT\`C	395
Spe I	A\`CTAG,T	404
Eco72 I	CAC|GTG	415
Pml I	CAC|GTG	415
Sfi I	GGCCN,NNN\`NGGCC	417
Bgl I	GCCN,NNN\`NGGC	417
Afl II	C\`TTAA,G	429
HinD III	A\`AGCT,T	432
HgiE II	ACCNNNNNNGGT	-1/13549
Eco57 I	CTGAAG 21/19	597
BssS I	C\`TCGT,G	965
Hga I	GACGC 9/14	1027
Drd I	GACNN,NN\`NNGTC	1036
Gsu I	CTGGAG 21/19	1547
Bpm I	CTGGAG 22/20	1548
BsmA I	GTCTC\`/9	1649
BsmB I	CGTCTC 7/11	1650
Nco I	C\`CATG,G	1727
Tfi I	G\`AWT,C	1776

Number of enzymes = 81

The following enzymes do not cut in pCAT:

Ahd I Asc I Ava II Bbs I Bbv II
Blp I Bsa I BseR I Bsp1286 I BstX I
Ear I EcoN I Esp I Fse I Msl I
Pac I Ple I Pme I PpuM I Rsr II

pCAT: sites sorted by name:

Aat II	(1)	143			
Acc I	(3)	143	296	1881	
Acc65 I	(1)	266			
Aci I	(21)	11	333	337	376
		378	451	462	546
		555	690	800	921
		940	1067	1095	1114
		1125	1163	1404	1768
		1862			
Afe I	(1)	230			
Afl II	(1)	429			
Afl III	(2)	361	382		
Age I	(1)	269			
Aha II	(2)	140	350		
Alu I	(14)	252	346	393	434
		581	838	884	974
		1150	1169	1198	1207
		1326	1455		
Alw I	(8)	87	175	186	473
		493	493	579	1104
AlwN I	(2)	128	729		
Apa I	(1)	170			
ApaL I	(2)	423	824		
Apo I	(4)	118	236	442	1132
Ase I	(2)	21	310		
Asp718	(1)	266			
Ava I	(2)	163	394		
Avr II	(1)	318			
BamH I	(1)	179			
Ban I	(2)	266	349		
Ban II	(2)	170	395		
Bbe I	(1)	353			
Bbv I	(2)	355	809		
Bcl I	(1)	193			
Bcn I	(4)	165	166	440	762
Bfa I	(6)	249	261	319	405
		645	1166		
Bgl I	(1)	417			
Bgl II	(1)	206			
Bpm I	(1)	1548			
BsaA I	(2)	294	415		
BsaB I	(1)	222			
BsaH I	(2)	140	350		
BsaJ I	(7)	163	318	376	978
		1657	1658	1727	
BsaW I	(5)	269	301	785	932
		1422			
Bsg I	(1)	114			
BsiC I	(1)	116			
BsiE I	(4)	220	337	376	804
BsiHKA I	(3)	395	427	828	
BsiW I	(1)	364			
Bsm I	(3)	114	1419	1826	
BsmA I	(1)	1649			
BsmB I	(1)	1650			
BsmF I	(1)	151			
BsoF I	(11)	12	334	337	344
		524	730	733	798
		941	1163	1768	
Bsp120 I	(1)	166			
BspH I	(1)	199			
BspM I	(1)	136			
BspM II	(2)	301	1422		
Bsr I	(5)	610	724	737	1232
		1674			
BsrB I	(2)	462	1116		
BsrD I	(2)	196	1445		
BsrG I	(1)	385			
BssH II	(1)	212			
BssS I	(1)	965			
Bst1107 I	(1)	297			
BstB I	(1)	116			
BstE II	(1)	93			
BstN I	(4)	979	992	1603	1659
BstU I	(8)	11	214	216	363
		372	378	514	1095
BstY I	(5)	80	179	206	486
		497			

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Bsu36 I     (1)   148
Cac8 I      (14)  214     246     250     288
                  341     348     464     528
                  1088    1114    1127    1167
                  1404    1772
Cfr10 I     (2)   269     286
Cla I       (2)   220     356
Csp6 I      (7)   267     365     386     402
                  1304    1842    1876
Dde I       (4)   148     864     1199    1647
Dpn I       (10)  82      181     195     208
                  219     479     488     499
                  574     1099
DpnII       (10)  80      179     193     206
                  217     477     486     497
                  572     1097
Dra I       (3)   235     1346    1685
Dra III     (1)   104
Drd I       (1)   1036
Dsa I       (2)   376     1727
Eae I       (3)   334     409     1691
Eag I       (1)   334
Eco47 III   (1)   230
Eco57 I     (1)   597
Eco72 I     (1)   415
EcoO109 I   (1)   167
EcoR I      (1)   118
EcoR II     (4)   977     990     1601    1657
EcoR V      (1)   224
Ehe I       (1)   351
Fnu4H I     (11)  12      334     337     344
                  524     730     733     798
                  941     1163    1768
Fok I       (2)   335     1406
Fsp I       (1)   243
Gdi II      (2)   333     335
Gsu I       (1)   1547
Hae I       (5)   317     411     664     1606
                  1693
Hae II      (3)   232     353     898
Hae III     (11)  168     317     336     411
                  420     664     1162    1339
                  1384    1606    1693
Hga I       (1)   1027
HgiA I      (3)   395     427     828
HgiE II     (1)   549
Hha I       (10)  214     216     231     244
                  352     514     623     797
                  897     964
HinC II     (3)   144     278     1882
Hind II     (3)   144     278     1882
HinD III    (1)   432
Hinf I      (2)   768     1776
HinI I      (2)   140     350
HinP I      (10)  212     214     229     242
                  350     512     621     795
                  895     962
Hpa I       (1)   278
Hpa II      (12)  164     270     287     302
                  438     570     760     786
                  933     1381    1423    1551
Hph I       (9)   70      104     1461    1469
                  1469    1605    1663    1673
                  1717
Kas I       (1)   349
Kpn I       (1)   270
Mae I       (6)   249     261     319     405
                  645     1166
Mae II      (9)   100     140     280     293
                  367     414     1513    1688
                  1878
Mae III     (7)   59      93      602     718
                  781     1483    1588
Mbo I       (10)  80      179     193     206
                  217     477     486     497
                  572     1097
Mbo II      (3)   482     634     1702
Mlu I       (1)   361
Mme I       (2)   746     930
Mnl I       (6)   143     257     710     961
                  1034    1272
Msc I       (2)   411     1693
Mse I       (10)  21      234     277     310
                  430     446     1172    1345
                  1684    1826
Msp I       (12)  164     270     287     302
                  438     570     760     786
                  933     1381    1423    1551
MspA1 I     (6)   346     378     555     800
                  1326    1770
Mun I       (1)   184
Nae I       (1)   288
Nar I       (1)   350
Nci I       (4)   164     165     439     761
Nco I       (1)   1727
Nde I       (1)   328
NgoM I      (1)   286
Nhe I       (2)   248     1165
Nla III     (10)  89      137     203     248
                  386     1142    1501    1731
                  1792    1813
Nla IV      (5)   168     181     268     351
                  1071
Not I       (1)   334
Nru I       (1)   372
Nsi I       (1)   328
Nsp7524 I   (2)   244     382
NspB II     (6)   346     378     555     800
                  1326    1770
NspH I      (2)   248     386
PaeR7 I     (1)   394
Pal I       (11)  168     317     336     411
                  420     664     1162    1339
                  1384    1606    1693
PflM I      (2)   104     1658
Pml I       (1)   415
Psp1406 I   (2)   280     1513
PspA I      (1)   163
Pst I       (1)   345
Pvu I       (1)   220
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Pvu II	(2)	346	1326		
Rsa I	(7)	268	366	387	403
		1305	1843	1877	
Sac I	(1)	395			
Sac II	(1)	379			
Sal I	(2)	142	1880		
Sau3A I	(10)	80	179	193	206
		217	477	486	497
		572	1097		
Sau96 I	(4)	166	167	418	1160
Sca I	(2)	403	1843		
ScrF I	(8)	164	165	439	761
		979	992	1603	1659
Sec I	(7)	163	318	376	978
		1657	1658	1727	
SfaN I	(4)	314	1042	1268	1755
Sfc I	(5)	66	253	341	682
		873			
Sfi I	(1)	417			
Sma I	(1)	165			
SnaB I	(1)	294			
Spe I	(1)	404			
Sph I	(1)	248			
Spl I	(1)	364			
Ssp I	(2)	308	1738		
Stu I	(1)	317			
Sty I	(2)	318	1727		
Taq I	(9)	75	116	143	220
		356	395	1040	1183
		1881			
Tfi I	(1)	1776			
Tsp45 I	(2)	59	93		
Tth111 I	(1)	99			
Tth111 II	(4)	516	546	555	1132
Vsp I	(2)	21	310		
Xba I	(1)	260			
Xca I	(1)	297			
Xho I	(1)	394			
Xho II	(5)	80	179	206	486
		497			
Xma I	(1)	163			
Xma III	(1)	334			
Xmn I	(1)	112			

Site usage in pCAT:

Aat II	G,ACGT`C	1	Acc I	GT`MK,AC	3
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	21
Afe I	AGC|GCT	1	Afl II	C`TTAA,G	1
Afl III	A`CRYG,T	2	Age I	A`CCGG,T	1
Aha II	GR`CG,YC	2	Ahd I	GACNN,N`NNGTC	-
Alu I	AG|CT	14	Alw I	GGATC 8/9	8
AlwN I	CAG,NNN`CTG	2	Apa I	G,GGCC`C	1
ApaL I	G`TGCA,C	2	Apo I	R`AATT,Y	4
Asc I	GG`CGCG,CC	-	Ase I	AT`TA,AT	2
Asp718	G`GTAC,C	1	Ava I	C`YCGR,G	2
Ava II	G`GWC,C	-	Avr II	C`CTAG,G	1
BamH I	G`GATC,C	1	Ban I	G`GYRC,C	2
Ban II	G,RGCY`C	2	Bbe I	G,GCGC`C	1
Bbs I	GAAGAC 8/12	-	Bbv I	GCAGC 13/17	2
Bbv II	GAAGAC 7/11	-	Bcl I	T`GATC,A	1
Bcn I	CC,S`GG	4	Bfa I	C`TA,G	6
Bgl I	GCCN,NNN`NGGC	1	Bgl II	A`GATC,T	1
Blp I	GC`TNA,GC	-	Bpm I	CTGGAG 22/20	1
Bsa I	GGTCTC 7/11	-	BsaA I	YAC|GTR	2
BsaB I	GATNN|NNATC	1	BsaH I	GR`CG,YC	2
BsaJ I	C`CNNG,G	7	BsaW I	W`CCGG,W	5
BseR I	GAGGAG 16/14	-	Bsg I	GTGCAG 22/20	1
BsiC I	TT`CG,AA	1	BsiE I	CG,RY`CG	4
BsiHKA I	G,WGCW`C	3	BsiW I	C`GTAC,G	1
Bsm I	GAATG,C 7	3	BsmA I	GTCTC`/9	1
BsmB I	CGTCTC 7/11	1	BsmF I	GGGAC 15/19	1
BsoF I	GC`N,GC	11	Bsp120 I	G`GGCC,C	1
Bsp1286 I	G,DGCH`C	-	BspH I	T`CATG,A	1
BspM I	ACCTGC 10/14	1	BspM II	T`CCGG,A	2
Bsr I	ACT,GG`	5	BsrB I	GAG|CGG	2
BsrD I	GCAATG, 8	2	BsrG I	T`GTAC,A	1
BssH II	G`CGCG,C	1	BssS I	C`TCGT,G	1
Bst1107 I	GTA|TAC	1	BstB I	TT`CG,AA	1
BstE II	G`GTNAC,C	1	BstN I	CC`W,GG	4
BstU I	CG|CG	8	BstX I	CCAN,NNNN`NTGG	-
BstY I	R`GATC,Y	5	Bsu36 I	CC`TNA,GG	1
Cac8 I	GCN|NGC	14	Cfr10 I	R`CCGG,Y	2
Cla I	AT`CG,AT	2	Csp6 I	G`TA,C	7
Dde I	C`TNA,G	4	Dpn I	GA|TC	10
DpnII	`GATC,	10	Dra I	TTT|AAA	3
Dra III	CAC,NNN`GTG	1	Drd I	GACNN,NN`NNGTC	1
Dsa I	C`CRYG,G	2	Eae I	Y`GGCC,R	3
Eag I	C`GGCC,G	1	Ear I	CTCTTC 7/10	-
Eco47 III	AGC|GCT	1	Eco57 I	CTGAAG 21/19	1
Eco72 I	CAC|GTG	1	EcoN I	CCTNN`N,NNAGG	-
EcoO109 I	RG`GNC,CY	1	EcoR I	G`AATT,C	1
EcoR II	`CCWGG,	4	EcoR V	GAT|ATC	1
Ehe I	GGC|GCC	1	Esp I	GC`TNA,GC	-
Fnu4H I	GC`N,GC	11	Fok I	GGATG 14/18	2
Fse I	GG,CCGG`CC	-	Fsp I	TGC|GCA	1
Gdi II	`YGGC,CG	2	Gsu I	CTGGAG 21/19	1
Hae I	WGG|CCW	5	Hae II	R,GCGC`Y	3
Hae III	GG|CC	11	Hga I	GACGC 9/14	1
HgiA I	G,WGCW`C	3	HgiE II	ACCNNNNNNGGT -1/131	
Hha I	G,CG`C	10	HinC II	GTY|RAC	3
Hind II	GTY|RAC	3	HinD III	A`AGCT,T	1
Hinf I	G`ANT,C	2	HinI I	GR`CG,YC	2
HinP I	G`CG,C	10	Hpa I	GTT|AAC	1
Hpa II	C`CG,G	12	Hph I	GGTGA 12/11	9
Kas I	G`GCGC,C	1	Kpn I	G,GTAC`C	1
Mae I	C`TA,G	6	Mae II	A`CG,T	9
Mae III	`GTNAC,	7	Mbo I	`GATC,	10
Mbo II	GAAGA 12/11	3	Mlu I	A`CGCG,T	1
Mme I	TCCRAC 25/23	2	Mnl I	CCTC 10/10	6
Msc I	TGG|CCA	2	Mse I	T`TA,A	10
Msl I	CAYNN|NNRTG	-	Msp I	C`CG,G	12
MspA1 I	CMG|CKG	6	Mun I	C`AATT,G	1
Nae I	GCC|GGC	1	Nar I	GG`CG,CC	1
Nci I	CC`S,GG	4	Nco I	C`CATG,G	1
Nde I	CA`TA,TG	1	NgoM I	G`CCGG,C	1
Nhe I	G`CTAG,C	2	Nla III	,CATG`	10
Nla IV	GGN|NCC	5	Not I	GC`GGCC,GC	1

Nru I	TCG|CGA	1	Nsi I	A,TGCA`T	1
Nsp7524 I	R`CATG,Y	2	NspB II	CMG|CKG	6
NspH I	R,CATG`Y	2	Pac I	TTA,AT`TAA	-
PaeR7 I	C`TCGA,G	1	Pal I	GG|CC	11
PflM I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	-
Pme I	CTTT|AAAC	-	Pml I	CAC|GTG	1
PpuM I	RG`GWC,CY	-	Psp1406 I	AA`CG,TT	2
PspA I	C`CCGG,G	1	Pst I	C,TGCA`G	1
Pvu I	CG,AT`CG	1	Pvu II	CAG|CTG	2
Rsa I	GT|AC	7	Rsr II	CG`GWC,CG	-
Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
Sal I	G`TCGA,C	2	Sap I	GCTCTTC 8/11	-
Sau3A I	`GATC,	10	Sau96 I	G`GNC,C	4
Sca I	AGT|ACT	2	ScrF I	CC`N,GG	8
Sec I	C`CNNG,G	7	SfaN I	GCATC 9/13	4
Sfc I	C`TRYA,G	5	Sfi I	GGCCN,NNN`NGGCC	1
Sma I	CCC|GGG	1	SnaB I	TAC|GTA	1
Spe I	A`CTAG,T	1	Sph I	G,CATG`C	1
Spl I	C`GTAC,G	1	Srf I	GCCC|GGGC	-
Ssp I	AAT|ATT	2	Stu I	AGG|CCT	1
Sty I	C`CWWG,G	2	Swa I	ATTT|AAAT	-
Taq I	T`CG,A	9	Tfi I	G`AWT,C	1
Tsp45 I	`GTSAC,	2	Tth111 I	GACN`N,NGTC	1
Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	2
Xba I	T`CTAG,A	1	Xca I	GTA|TAC	1
Xcm I	CCANNNN,N`NNNNTGG	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	5	Xma I	C`CCGG,G	1
Xma III	C`GGCC,G	1	Xmn I	GAANN|NNTTC	1