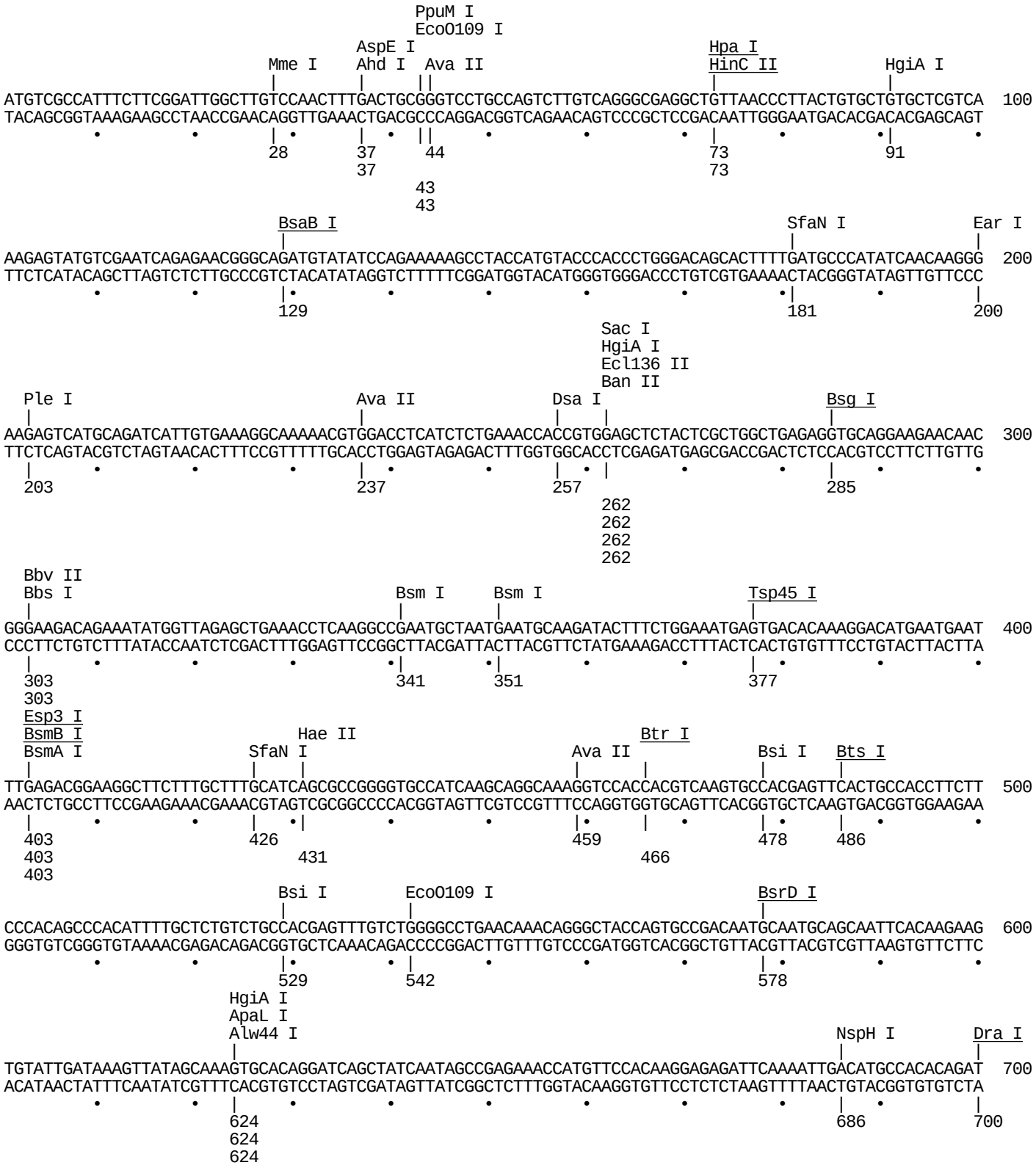
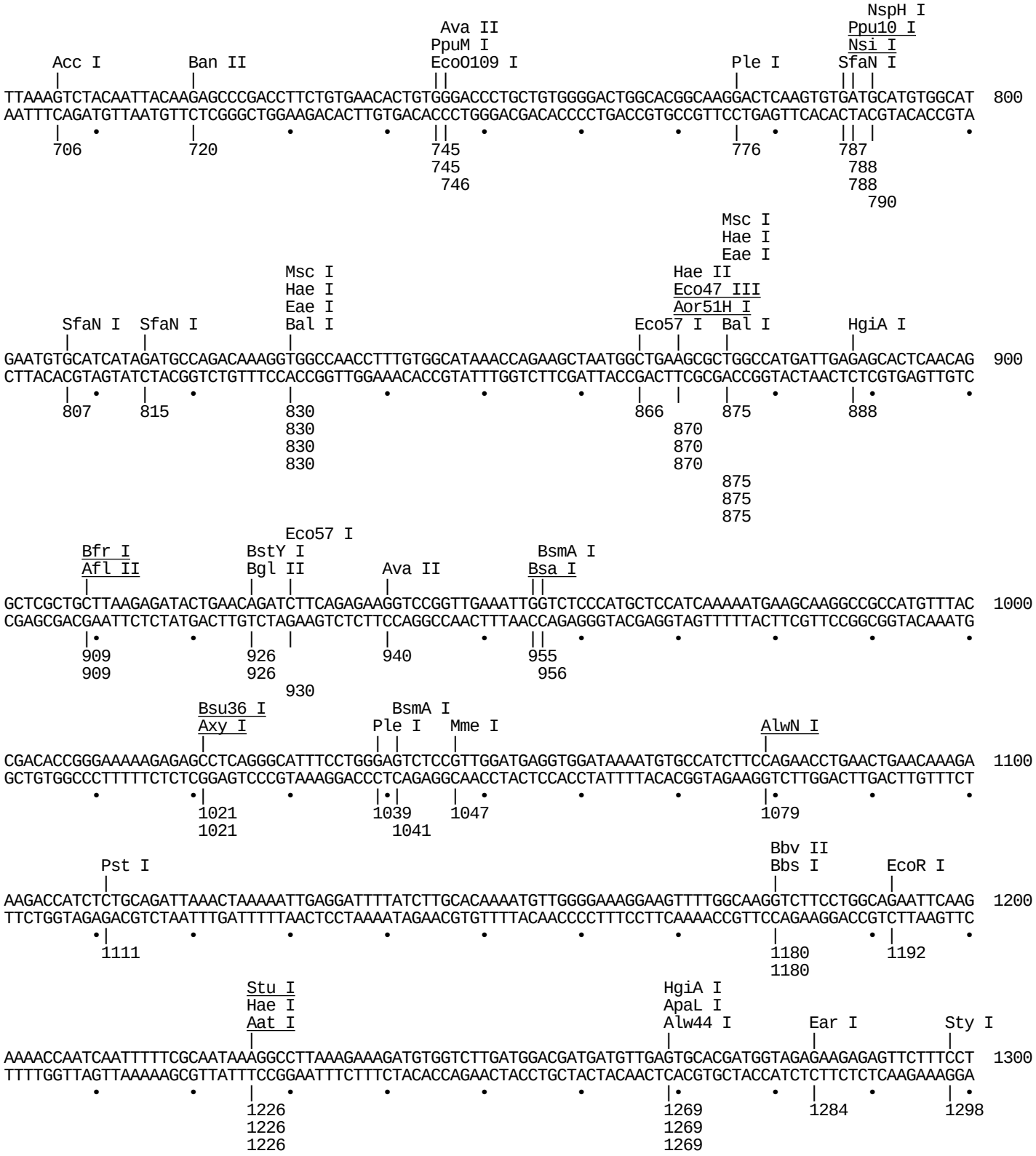
DNA Strider™ 1.2 ### Thursday, November 16, 2000 2:46:53 PM

hPKCtheta_ORF -> Full Restriction Map

DNA sequence 2121 b.p. ATGTCGCCATTT ... CTGATATCCTGA linear

Positions of Restriction Endonucleases sites (unique sites underlined)

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Ava II
Ppu10 I
PpuM I
Nsi I
Acc I
Ban II
EcoO109 I
Ple I
SfaN I
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706 720 745 776 787
745 788
746 788
790
Msc I
Hae I
Eae I
Msc I
Hae I
Eae I
Hae II
Eco47 III
Aor51H I
SfaN I SfaN I
Bal I
Eco57 I Bal I
HgiA I
GAATGTGCATCATAGATGCCAGACAAAGGTGGCCAACCTTTGTGGCATAAACCAGAAGCTAATGGCTGAAGCGCTGGCCATGATTGAGAGCACTCAACAG 900
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807 815 830 866 875 888
830 870
830 870
830 870
875
875
875
Eco57 I
Bfr I
Afl II
BstY I
Bgl II
Ava II
BsmA I
Bsa I
GCTCGCTGCTTAAGAGATACTGAACAGATCTTCAGAGAAGGTCCGGTTGAAATTGGTCTCCCATGCTCCATCAAAAATGAAGCAAGGCCGCCATGTTTAC 1000
CGAGCGACGAATTCTCTATGACTTGTCTAGAAGTCTCTTCCAGGCCAACTTTAACCAGAGGGTACGAGGTAGTTTTTACTTCGTTCCGGCGGTACAAATG
909 926 940 955
909 926 956
930
Bsu36 I
Axy I
BsmA I
Ple I
Mme I
AlwN I
CGACACCGGGAAAAAGAGAGCCTCAGGGCATTTCCTGGGAGTCTCCGTTGGATGAGGTGGATAAAATGTGCCATCTTCCAGAACCTGAACTGAACAAAGA 1100
GCTGTGGCCCTTTTTCTCTCGGAGTCCCGTAAAGGACCCTCAGAGGCAACCTACTCCACCTATTTTACACGGTAGAAGGTCTTGGACTTGACTTGTTTCT
1021 1039 1047 1079
1021 1041
Bbv II
Bbs I
Pst I
EcoR I
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TTCTGGTAGAGACGTCTAATTTGATTTTTAACTCCTAAAATAGAACGTGTTTTACAACCCCTTTCCTTCAAAACCGTTCCAGAAGGACCGTCTTAAGTTC
1111 1180 1192
1180
Stu I
Hae I
Aat I
HgiA I
ApaL I
Alw44 I
Ear I
Sty I
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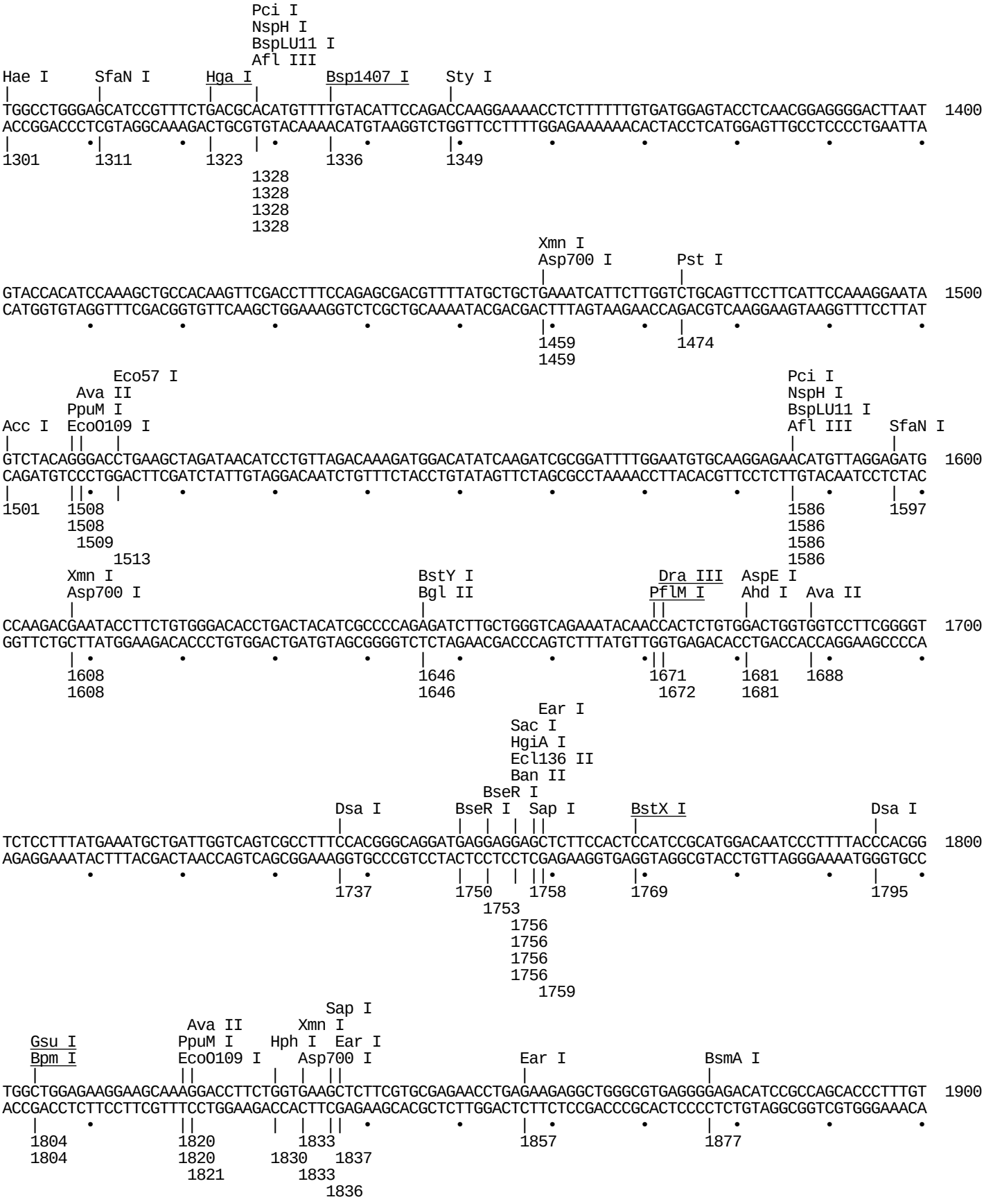
1226 1269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BspLU11 I
Afl III
Hae I
SfaN I
Hga I
Bsp1407 I
Sty I
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1301 1311 1323 1328 1336 1349
1328
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1328
Xmn I
Asp700 I
Pst I
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1459 1474
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Ava II
PpuM I
Acc I
EcoO109 I
Pci I
NspH I
BspLU11 I
Afl III
SfaN I
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1501 1508 1508 1509 1513 1586 1586 1586 1586 1597
Xmn I
Asp700 I
BstY I
Bgl II
Dra III
PflM I
AspE I
Ahd I
Ava II
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1608 1608 1646 1646 1671 1672 1681 1681 1688
Ear I
Sac I
HgiA I
Ecl136 II
Ban II
BseR I
Dsa I
BseR I
Sap I
BstX I
Dsa I
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1737 1750 1753 1756 1756 1756 1756 1758 1759 1769 1795
Sap I
Ava II
Xmn I
Gsu I
Bpm I
PpuM I
Hph I
Ear I
EcoO109 I
Asp700 I
Ear I
BsmA I
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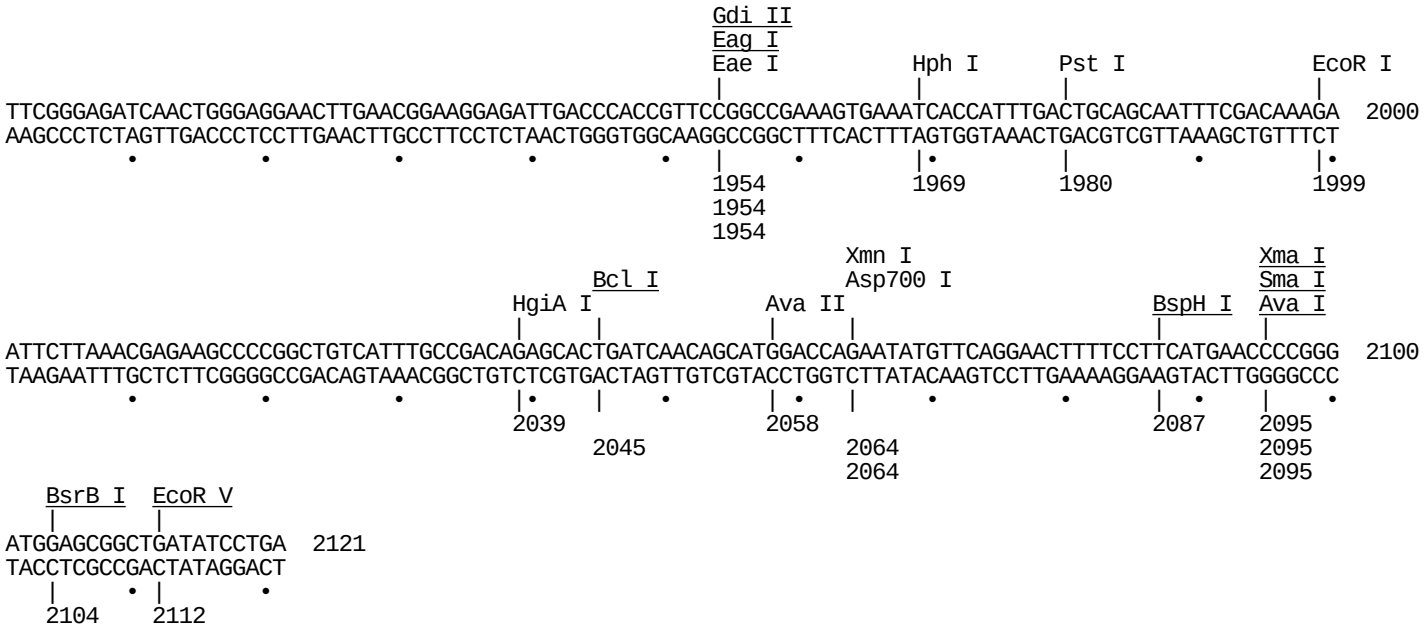

Restriction Endonucleases site usage

Aat I	1	Bbv II	2	BstY I	2	HinD III	-	Psp1406 I	-
Aat II	-	BciV I	-	BstZ17 I	-	Hpa I	1	Pst I	3
Acc65 I	-	Bcl I	1	Bsu36 I	1	Hph I	2	Pvu I	-
Acc I	2	Bfr I	1	Btr I	1	Kas I	-	Pvu II	-
Acl I	-	Bgl I	-	Bts I	1	Kpn I	-	Rsr II	-
Afl II	1	Bgl II	2	Cfr10 I	-	Ksp I	-	Sac I	2
Afl III	2	Bln I	-	Cla I	-	Mfe I	-	Sac II	-
Age I	-	Blp I	-	Dra I	1	Mlu I	-	Sal I	-
Aha II	-	Bpm I	1	Dra III	1	Mme I	2	Sap I	2
Ahd I	2	Bpu1102 I	-	Drd I	-	Msc I	2	Sbf I	-
Alw44 I	2	Bsa I	1	Dsa I	3	Mun I	-	Sca I	-
AlwN I	1	BsaA I	-	Eae I	3	Nae I	-	SfaN I	7
Aor51H I	1	BsaB I	1	Eag I	1	Nar I	-	Sfi I	-
Apa I	-	BseR I	2	Ear I	5	Nco I	-	SgrA I	-
ApaL I	2	Bsg I	1	Ecl136 II	2	Nde I	-	Sma I	1
Asc I	-	Bsi I	2	Eco47 III	1	NgoM I	-	SnaB I	-
Ase I	-	BsiW I	-	Eco57 I	3	Nhe I	-	Spe I	-
Asp700 I	4	Bsm I	2	EcoN I	-	Not I	-	Sph I	-
Asp718	-	BsmA I	4	EcoO109 I	5	Nru I	-	Spl I	-
AspE I	2	BsmB I	1	EcoR I	2	Nsi I	1	Srf I	-
Asp I	-	Bsp120 I	-	EcoR V	1	NspH I	4	Sse8387 I	-
Ava I	1	Bsp1407 I	1	Ehe I	-	Pac I	-	Ssp I	-
Ava II	9	BspE I	-	Esp3 I	1	PaeR7 I	-	Stu I	1
Avi I	-	BspH I	1	Esp I	-	Pci I	2	Sty I	2
Avr II	-	BspM I	-	Fse I	-	PflF I	-	Swa I	-
Axy I	1	BspM II	-	Fsp I	-	PflM I	1	Tsp45 I	1
Bal I	2	BspLU11 I	2	Gdi II	1	Ple I	3	Tth111 I	-
BamH I	-	BsrB I	1	Gsu I	1	Pme I	-	Xba I	-
Ban II	3	BsrD I	1	Hae I	4	Pml I	-	Xca I	-
Ban III	-	BssH II	-	Hae II	2	Ppu10 I	1	Xho I	-
Bbe I	-	Bst1107 I	-	Hga I	1	PpuM I	4	Xcm I	-
BbrP I	-	BstB I	-	HgiA I	7	PshA I	-	Xma I	1
Bbs I	2	BstE II	-	HgiE II	-	Psi I	-	Xmn I	4
Bbu I	-	BstX I	1	HinC II	1				

Enzyme	Site	Use	Site position (Fragment length) Fragment order
Aat I	agg/cct	1	1(1225) 1 1226(896) 2
Afl II	c/ttaag	1	1(908) 2 909(1213) 1
AlwN I	cagnnn/ctg	1	1(1078) 1 1079(1043) 2
Aor51H I	agc/gct	1	1(869) 2 870(1252) 1
Ava I	c/ycgrg	1	1(2094) 1 2095(27) 2
Axy I	cc/tnagg	1	1(1020) 2 1021(1101) 1

Bcl I	t/gatca		1	1(2044) 1	2045(77) 2						
Bfr I	c/ttaag		1	1(908) 2	909(1213) 1						
Bpm I	ctggag	16/14	1	1(1803) 1	1804(318) 2						
Bsa I	ggtctc	1/5	1	1(954) 2	955(1167) 1						
BsaB I	gatnn/nnatc		1	1(128) 2	129(1993) 1						
Bsg I	gtgcag	16/14	1	1(284) 2	285(1837) 1						
BsmB I	cgtctc	1/5	1	1(402) 2	403(1719) 1						
Bsp1407 I	t/gtaca		1	1(1335) 1	1336(786) 2						
BspH I	t/catga		1	1(2086) 1	2087(35) 2						
BsrB I	gagcgg	-3/-3	1	1(2103) 1	2104(18) 2						
BsrD I	gcaatg	2/0	1	1(577) 2	578(1544) 1						
BstX I	ccannnnn/ntgg		1	1(1768) 1	1769(353) 2						
Bsu36 I	cc/tnagg		1	1(1020) 2	1021(1101) 1						
Btr I	cac/gtc		1	1(465) 2	466(1656) 1						
Bts I	gcagtg	2/0	1	1(485) 2	486(1636) 1						
Dra I	ttt/aaa		1	1(699) 2	700(1422) 1						
Dra III	cacnnn/gtg		1	1(1671) 1	1672(450) 2						
Eag I	c/ggccg		1	1(1953) 1	1954(168) 2						
Eco47 III	agc/gct		1	1(869) 2	870(1252) 1						
EcoR V	gat/atc		1	1(2111) 1	2112(10) 2						
Esp3 I	cgtctc	1/5	1	1(402) 2	403(1719) 1						
Gdi II	yggccg	-5/-1	1	1(1953) 1	1954(168) 2						
Gsu I	ctggag	16/14	1	1(1803) 1	1804(318) 2						
Hga I	gacgc	5/10	1	1(1322) 1	1323(799) 2						
HinC II	gty/rac		1	1(72) 2	73(2049) 1						
Hpa I	gtt/aac		1	1(72) 2	73(2049) 1						
Nsi I	atgca/t		1	1(787) 2	788(1334) 1						
PflM I	ccannnn/ntgg		1	1(1670) 1	1671(451) 2						
Ppu10 I	a/tgcat		1	1(787) 2	788(1334) 1						
Sma I	ccc/ggg		1	1(2094) 1	2095(27) 2						
Stu I	agg/cct		1	1(1225) 1	1226(896) 2						
Tsp45 I	/gtsac		1	1(376) 2	377(1745) 1						
Xma I	c/ccggg		1	1(2094) 1	2095(27) 2						
Acc I	gt/mkac		2	1(705) 2	706(795) 1	1501(621) 3					
Afl III	a/crygt		2	1(1327) 1	1328(258) 3	1586(536) 2					
Ahd I	gacnnn/nngtc		2	1(36) 3	37(1644) 1	1681(441) 2					
Alw44 I	g/tgcac		2	1(623) 3	624(645) 2	1269(853) 1					
ApaL I	g/tgcac		2	1(623) 3	624(645) 2	1269(853) 1					
AspE I	gacnnn/nngtc		2	1(36) 3	37(1644) 1	1681(441) 2					
Bal I	tgg/cca		2	1(829) 2	830(45) 3	875(1247) 1					
Bbs I	gaagac	2/6	2	1(302) 3	303(877) 2	1180(942) 1					
Bbv II	gaagac	2/6	2	1(302) 3	303(877) 2	1180(942) 1					
Bgl II	a/gatct		2	1(925) 1	926(720) 2	1646(476) 3					
BseR I	gaggag	10/8	2	1(1749) 1	1750(3) 3	1753(369) 2					
Bsi I	ctcgtg	-5/-1	2	1(477) 2	478(51) 3	529(1593) 1					
Bsm I	gaatgc	1/-1	2	1(340) 2	341(10) 3	351(1771) 1					
BspLU11 I	a/catgt		2	1(1327) 1	1328(258) 3	1586(536) 2					
BstY I	r/gatcy		2	1(925) 1	926(720) 2	1646(476) 3					
Ecl136 II	gag/ctc		2	1(261) 3	262(1494) 1	1756(366) 2					
EcoR I	g/aattc		2	1(1191) 1	1192(807) 2	1999(123) 3					
Hae II	rgcgc/y		2	1(430) 3	431(439) 2	870(1252) 1					
Hph I	ggtga	8/7	2	1(1829) 1	1830(139) 3	1969(153) 2					
Mme I	tccrac	20/18	2	1(27) 3	28(1019) 2	1047(1075) 1					
Msc I	tgg/cca		2	1(829) 2	830(45) 3	875(1247) 1					
Pci I	a/catgt		2	1(1327) 1	1328(258) 3	1586(536) 2					
Sac I	gagct/c		2	1(261) 3	262(1494) 1	1756(366) 2					
Sap I	gctcttc	1/4	2	1(1757) 1	1758(78) 3	1836(286) 2					
Sty I	c/cwwgg		2	1(1297) 1	1298(51) 3	1349(773) 2					
Ban II	grgcy/c		3	1(261) 4	262(458) 2	720(1036) 1	1756(366) 3				
Dsa I	c/crygg		3	1(256) 3	257(1480) 1	1737(58) 4	1795(327) 2				
Eae I	y/ggccr		3	1(829) 2	830(45) 4	875(1079) 1	1954(168) 3				
Eco57 I	ctgaag	16/14	3	1(865) 1	866(64) 4	930(583) 3	1513(609) 2				
Ple I	gagtc	4/5	3	1(202) 4	203(573) 2	776(263) 3	1039(1083) 1				
Pst I	ctgca/g		3	1(1110) 1	1111(363) 3	1474(506) 2	1980(142) 4				
Asp700 I	gaann/nnttc		4	1(1458) 1	1459(149) 4	1608(225) 3	1833(231) 2	2064(58) 5			
BsmA I	gtctc	1/5	4	1(402) 3	403(553) 2	956(85) 5	1041(836) 1	1877(245) 4			
Hae I	wgg/ccw		4	1(829) 1	830(45) 5	875(351) 3					

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                                1226(   75) 4     1301(  821) 2
NspH I     rcatg/y          4       1(  685) 1      686(  104) 5      790(  538) 2
                            1328(  258) 4     1586(  536) 3
PpuM I     rg/gwccy         4       1(   42) 5       43(  702) 2      745(  763) 1
                            1508(  312) 3     1820(  302) 4
Xmn I      gaann/nnttc      4       1( 1458) 1     1459(  149) 4     1608(  225) 3
                            1833(  231) 2     2064(   58) 5

Ear I      ctcttc    1/4    5       1(  199) 4      200( 1084) 1     1284(  475) 2
                            1759(   78) 5     1837(   20) 6     1857(  265) 3
EcoO109 I  rg/gnccy         5       1(   42) 6       43(  499) 2      542(  203) 5
                             745(  763) 1     1508(  312) 3     1820(  302) 4

HgiA I     gwgcw/c          7       1(   90) 7       91(  171) 6      262(  362) 3
                             624(  264) 5      888(  381) 2     1269(  487) 1
                            1756(  283) 4     2039(   83) 8
SfaN I     gcatc     5/9    7       1(  180) 6      181(  245) 5      426(  361) 3
                             787(   20) 7      807(    8) 8      815(  496) 2
                            1311(  286) 4     1597(  525) 1

Ava II     g/gwcc           9       1(   43)10       44(  193) 6      237(  222) 4
                             459(  287) 2      746(  194) 5      940(  569) 1
                            1509(  179) 7     1688(  133) 8     1821(  237) 3
                            2058(   64) 9
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164 sites found

No Sites found for the following Restriction Endonucleases

Aat II	gacgt/c		Bst1107 I	gta/tac		PaeR7 I	c/tcgag				
Acc65 I	g/gtacc		BstB I	tt/cgaa		PflF I	gacn/nngtc				
Acl I	aa/cgtt		BstE II	g/gtnacc		Pme I	gttt/aaac				
Age I	a/ccggt		BstZ17 I	gta/tac		Pml I	cac/gtg				
Aha II	gr/cgyc		Cfr10 I	r/ccggy		PshA I	gacnn/nngtc				
Apa I	gggcc/c		Cla I	at/cgat		Psi I	tta/taa				
Asc I	gg/cgcgcc		Drd I	gacnnnn/nngtc		Psp1406 I	aa/cgtt				
Ase I	at/taat		EcoN I	cctnn/nnnagg		Pvu I	cgat/cg				
Asp718	g/gtacc		Ehe I	ggc/gcc		Pvu II	cag/ctg				
Asp I	gacn/nngtc		Esp I	gc/tnagc		Rsr II	cg/gwccg				
Avi I	tgc/gca		Fse I	ggccgg/cc		Sac II	ccgc/gg				
Avr II	c/ctagg		Fsp I	tgc/gca		Sal I	g/tcgac				
BamH I	g/gatcc		HgiE II	accnnnnnnggt		Sbf I	cctgca/gg				
Ban III	at/cgat		HinD III	a/agctt		Sca I	agt/act				
Bbe I	ggcgc/c		Kas I	g/gcgcc		Sfi I	ggccnnnn/nggcc				
BbrP I	cac/gtg		Kpn I	ggtac/c		SgrA I	cr/ccggyg				
Bbu I	gcatg/c		Ksp I	ccgc/gg		SnaB I	tac/gta				
BciV I	gtatcc	6/5	Mfe I	c/aattg		Spe I	a/ctagt				
Bgl I	gccnnnn/nggc		Mlu I	a/cgcgt		Sph I	gcatg/c				
Bln I	c/ctagg		Mun I	c/aattg		Spl I	c/gtacg				
Blp I	gc/tnagc		Nae I	gcc/ggc		Srf I	gccc/gggc				
Bpu1102 I	gc/tnagc		Nar I	gg/cgcc		Sse8387 I	cctgca/gg				
BsaA I	yac/gtr		Nco I	c/catgg		Ssp I	aat/att				
BsiW I	c/gtacg		Nde I	ca/tatg		Swa I	attt/aaat				
Bsp120 I	g/ggccc		NgoM I	g/ccggc		Tth111 I	gacn/nngtc				
BspE I	t/ccgga		Nhe I	g/ctagc		Xba I	t/ctaga				
BspM I	acctgc	4/8	Not I	gc/ggccgc		Xca I	gta/tac				
BspM II	t/ccgga		Nru I	tcg/cga		Xho I	c/tcgag				
BssH II	g/cgcgc		Pac I	ttaat/taa		Xcm I	ccannnnn/nnnntgg				