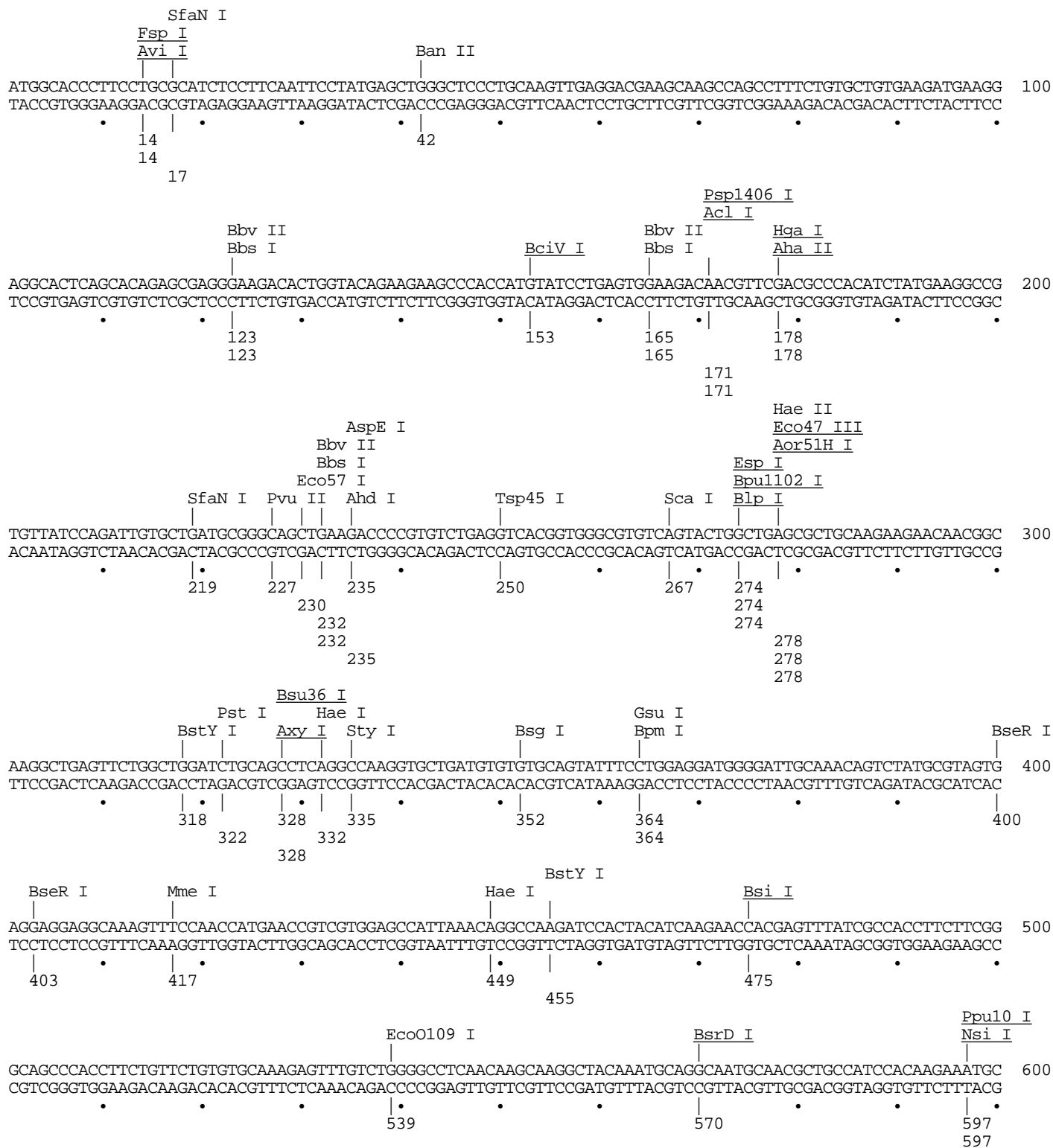
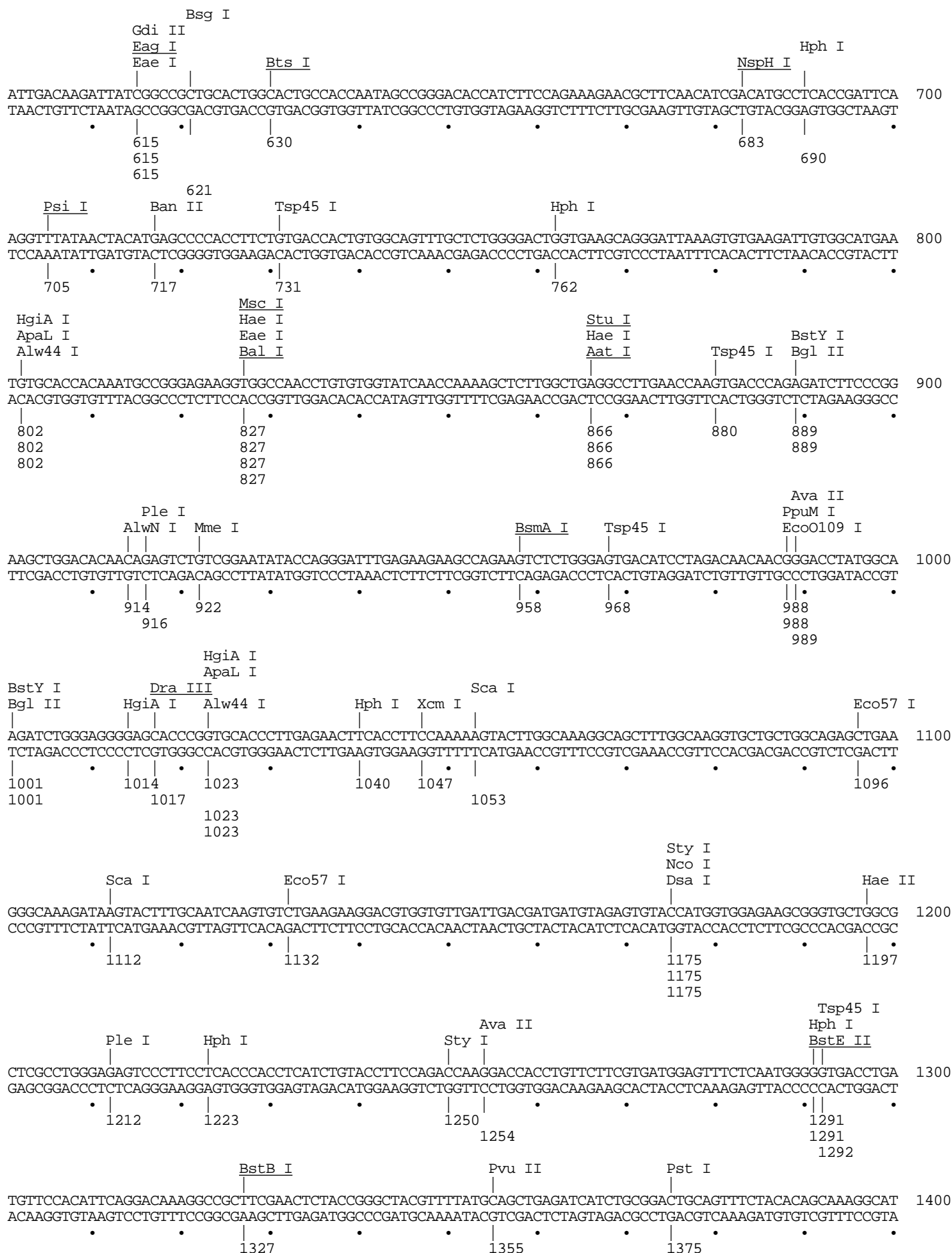


mPKCdelta.ORF.NM_011103 [1 to 252] -> Full Restriction Map

DNA sequence 2025 b.p. ATGGCACCCCTTC ... CTGGACATTTAA linear

Positions of Restriction Endonucleases sites (unique sites underlined)





Afl III	-	Bln I	-	Cla I	-	Mfe I	-	Sac II	-
Age I	-	Blp I	1	Dra I	-	Mlu I	-	Sal I	-
Aha II	1	Bpm I	2	Dra III	1	Mme I	3	Sap I	1
Ahd I	2	Bpu1102 I	1	Drd I	-	Msc I	1	Sbf I	1
Alw44 I	2	Bsa I	-	Dsa I	3	Mun I	-	Sca I	4
AlwN I	2	BsaA I	-	Eae I	4	Nae I	-	SfaN I	3
Aor51H I	1	BsaB I	-	Eag I	1	Nar I	-	Sfi I	-
Apa I	-	BseR I	2	Ear I	1	Nco I	2	SgrA I	-
ApaL I	2	Bsg I	2	Ecl136 II	1	Nde I	-	Sma I	-
Asc I	-	Bsi I	1	Eco47 III	1	NgoM I	-	SnaB I	-
Ase I	-	BsiW I	-	Eco57 I	6	Nhe I	-	Spe I	-
Asp700 I	1	Bsm I	-	EcoN I	-	Not I	-	Sph I	-
Asp718	-	BsmA I	1	EcoO109 I	6	Nru I	-	Spl I	-
AspE I	2	BsmB I	-	EcoR I	-	Nsi I	1	Srf I	-
Asp I	-	Bsp120 I	-	EcoR V	-	NspH I	1	Sse8387 I	1
Ava I	-	Bsp1407 I	-	Ehe I	-	Pac I	-	Ssp I	-
Ava II	7	BspE I	-	Esp3 I	-	Paer7 I	-	Stu I	1
Avi I	1	BspH I	-	Esp I	1	Pci I	-	Sty I	6
Avr II	-	BspM I	-	Fse I	-	PflF I	-	Swa I	-
Axy I	1	BspM II	-	Fsp I	1	PflM I	-	Tsp45 I	6
Bal I	1	BspLU11 I	-	Gdi II	3	Ple I	4	Tth111 I	-
BamH I	-	BsrB I	-	Gsu I	2	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	2
BbrP I	-	BstB I	1	HgiA I	4	PshA I	-	Xma I	-
Bbs I	3	BstE II	1	HgiE II	-	Psi I	1	Xmn I	1
Bbu I	-	BstX I	1	HinC II	-				

Enzyme Site Use Site position (Fragment length) Fragment order

Aat I	agg/cct	1	1(865) 2	866(1160) 1		
Acl I	aa/cggt	1	1(170) 2	171(1855) 1		
Aha II	gr/cgyc	1	1(177) 2	178(1848) 1		
Aor51H I	agc/gct	1	1(277) 2	278(1748) 1		
Asp700 I	gaann/nmttc	1	1(1733) 1	1734(292) 2		
Avi I	tgc/gca	1	1(13) 2	14(2012) 1		
Axy I	cc/tnagg	1	1(327) 2	328(1698) 1		
Bal I	tgg/cca	1	1(826) 2	827(1199) 1		
BciV I	gtatcc	6/5	1(152) 2	153(1873) 1		
Blp I	gc/tnagc	1	1(273) 2	274(1752) 1		
Bpu1102 I	gc/tnagc	1	1(273) 2	274(1752) 1		
Bsi I	ctcgtg	-5/-1	1(474) 2	475(1551) 1		
BsmA I	gtctc	1/5	1(957) 2	958(1068) 1		
BsrD I	gcaatg	2/0	1(569) 2	570(1456) 1		
BstB I	tt/cgaa	1	1(1326) 1	1327(699) 2		
BstE II	g/gtnacc	1	1(1290) 1	1291(735) 2		
BstX I	ccannnn/ntgg	1	1(1669) 1	1670(356) 2		
Bsu36 I	cc/tnagg	1	1(327) 2	328(1698) 1		
Bts I	gcagtg	2/0	1(629) 2	630(1396) 1		
Dra III	cacnnn/gtg	1	1(1016) 1	1017(1009) 2		
Eag I	c/ggccc	1	1(614) 2	615(1411) 1		
Ear I	ctcttc	1/4	1(1659) 1	1660(366) 2		
Ecl136 II	gag/ctc	1	1(1656) 1	1657(369) 2		
Eco47 III	agc/gct	1	1(277) 2	278(1748) 1		
Esp I	gc/tnagc	1	1(273) 2	274(1752) 1		
Fsp I	tgc/gca	1	1(13) 2	14(2012) 1		
Hga I	gacgc	5/10	1(177) 2	178(1848) 1		
Msc I	tgg/cca	1	1(826) 2	827(1199) 1		
Nsi I	atgca/t	1	1(596) 2	597(1429) 1		
NspH I	rcatg/y	1	1(682) 2	683(1343) 1		
Ppu10 I	a/tgcat	1	1(596) 2	597(1429) 1		
Psi I	tta/taa	1	1(704) 2	705(1321) 1		
Psp1406 I	aa/cggt	1	1(170) 2	171(1855) 1		
Sac I	gagct/c	1	1(1656) 1	1657(369) 2		
Sap I	gctcttc	1/4	1(1658) 1	1659(367) 2		
Sbf I	cctgca/gg	1	1(1550) 1	1551(475) 2		
Sse8387 I	cctgca/gg	1	1(1550) 1	1551(475) 2		
Stu I	agg/cct	1	1(865) 2	866(1160) 1		
Xmn I	gaann/nmttc	1	1(1733) 1	1734(292) 2		
Ahd I	gacnnn/nngtc	2	1(234) 3	235(1347) 1	1582(444) 2	
Alw44 I	g/tgcac	2	1(801) 2	802(221) 3	1023(1003) 1	
AlwN I	cagnnn/ctg	2	1(913) 1	914(641) 2	1555(471) 3	
ApaL I	g/tgcac	2	1(801) 2	802(221) 3	1023(1003) 1	
AspE I	gacnnn/nngtc	2	1(234) 3	235(1347) 1	1582(444) 2	
Bgl II	a/gatct	2	1(888) 2	889(112) 3	1001(1025) 1	
Bpm I	ctggag	16/14	1(363) 2	364(1461) 1	1825(201) 3	
BseR I	gaggag	10/8	1(399) 2	400(3) 3	403(1623) 1	

Bsg I	gtgcag	16/14	2	1(351) 2	352(269) 3	621(1405) 1
Gsu I	ctggag	16/14	2	1(363) 2	364(1461) 1	1825(201) 3
Hae II	rgcgc/y		2	1(277) 3	278(919) 1	1197(829) 2
Nco I	c/catgg		2	1(1174) 1	1175(799) 2	1974(52) 3
Pvu II	cag/ctg		2	1(226) 3	227(1128) 1	1355(671) 2
Xcm I	ccannnn/nnntgg		2	1(1046) 1	1047(671) 2	1718(308) 3
Ban II	grgcy/c		3	1(41) 4	42(675) 2	717(940) 1
Bbs I	gaagac	2/6	3	1(122) 2	123(42) 4	165(67) 3
Bbv II	gaagac	2/6	3	1(122) 2	123(42) 4	165(67) 3
Dsa I	c/crygg		3	1(1174) 1	1175(463) 2	1638(336) 3
Gdi II	yggccg	-5/-1	3	1(614) 2	615(831) 1	1446(177) 4
Mme I	tccrac	20/18	3	1(416) 3	417(505) 2	922(778) 1
Pst I	ctgca/g		3	1(321) 3	322(1053) 1	1375(177) 4
SfaN I	gcatc	5/9	3	1(16) 4	17(202) 3	219(1212) 1
Eae I	y/ggCCR		4	1(614) 2	615(212) 4	827(619) 1
Hae I	wgg/ccw		4	1(331) 3	332(117) 4	449(378) 2
HgiA I	gwgw/c		4	1(801) 1	802(212) 4	1014(9) 5
Ple I	gagtc	4/5	4	1(915) 1	916(296) 3	1212(454) 2
PpuM I	rg/gwccy		4	1(987) 1	988(421) 2	1409(189) 4
Sca I	agt/act		4	1(266) 4	267(786) 1	1053(59) 5
BstY I	r/gatcy		5	1(317) 4	318(137) 5	455(434) 3
Eco57 I	ctgaag	16/14	6	1(229) 4	230(866) 1	1096(36) 7
Eco0109 I	rg/gnccy		6	1(538) 1	539(449) 2	988(421) 3
Sty I	c/cwwgg		6	1(334) 3	335(840) 1	1175(75) 5
Tsp45 I	/gtsac		6	1(249) 4	250(481) 2	731(149) 5
Ava II	g/gwcc		7	1(988) 1	989(265) 2	1254(156) 4
Hph I	ggtga	8/7	7	1(689) 1	690(72) 7	762(278) 3

158 sites found

No Sites found for the following Restriction Endonucleases

Aat II	gacgt/c	BspM I	acctgc	4/8	NgoM I	g/ccggc
Acc65 I	g/gtacc	BspM II	t/ccgga		Nhe I	g/ctagc
Acc I	gt/mkac	BspLU11 I	a/catgt		Not I	gc/ggccgc
Afl II	c/ttaag	BsrB I	gagcgg	-3/-3	Nru I	tcg/cga
Afl III	a/crygt	BssH II	g/cgcgc		Pac I	ttaat/taa
Age I	a/ccggt	Bst1107 I	gta/tac		Paer7 I	c/tcgag
Apa I	gggcc/c	BstZ17 I	gta/tac		Pci I	a/catgt
Asc I	gg/cgcgcc	Btr I	cac/gtc		PflF I	gacn/nngtc
Ase I	at/taat	Cfr10 I	r/ccggy		Pf1M I	ccannnn/ntgg
Asp718	g/gtacc	Cla I	at/cgat		Pme I	gttt/aaac
Asp I	gacn/nngtc	Dra I	ttt/aaa		Pml I	cac/gtg
Ava I	c/ycgrg	Drd I	gacnnnn/nngtc		PshA I	gacnn/nngtc
Avr II	c/ctagg	EcoN I	cctnn/nnnagg		Pvu I	cgat/cg
BamH I	g/gatcc	EcoR I	g/aattc		Rsr II	cg/gwccg
Ban III	at/cgat	EcoR V	gat/atc		Sac II	ccgc/gg
Bbe I	ggcgc/c	Ehe I	ggc/gcc		Sal I	g/tcgac

BbrP I	cac/gtg	Esp3 I	cgtctc	1/5	Sfi I	ggcnnnn/nggcc
Bbu I	gcatg/c	Fse I	ggccgg/cc		SgrA I	cr/ccggyg
Bcl I	t/gatca	HgiE II	accnnnnnnggt		Sma I	ccc/ggg
Bfr I	c/ttaag	HinC II	gty/rac		SnaB I	tac/gta
Bgl I	gcnnnn/nggc	HinD III	a/agctt		Spe I	a/ctagt
Bln I	c/ctagg	Hpa I	gtt/aac		Sph I	gcatg/c
Bsa I	ggtctc	Kas I	g/gcgcc		SpI I	c/gtacg
BsaA I	yac/gtr	Kpn I	ggtac/c		Srf I	gccc/gggc
BsaB I	gatnn/natc	Ksp I	ccgc/gg		Ssp I	aat/att
BsiW I	c/gtacg	Mfe I	c/aattg		Swa I	attt/aaat
Bsm I	gaatgc	Mlu I	a/cgctt		Tth111 I	gacn/nngtc
BsmB I	cgtctc	Mun I	c/aattg		Xba I	t/ctaga
Bsp120 I	g/ggccc	Nae I	gcc/ggc		Xca I	gta/tac
Bsp1407 I	t/gtaca	Nar I	gg/cgcc		Xho I	c/tcgag
BspE I	t/ccgga	Nde I	ca/tatg		Xma I	c/ccggg
BspH I	t/catga					