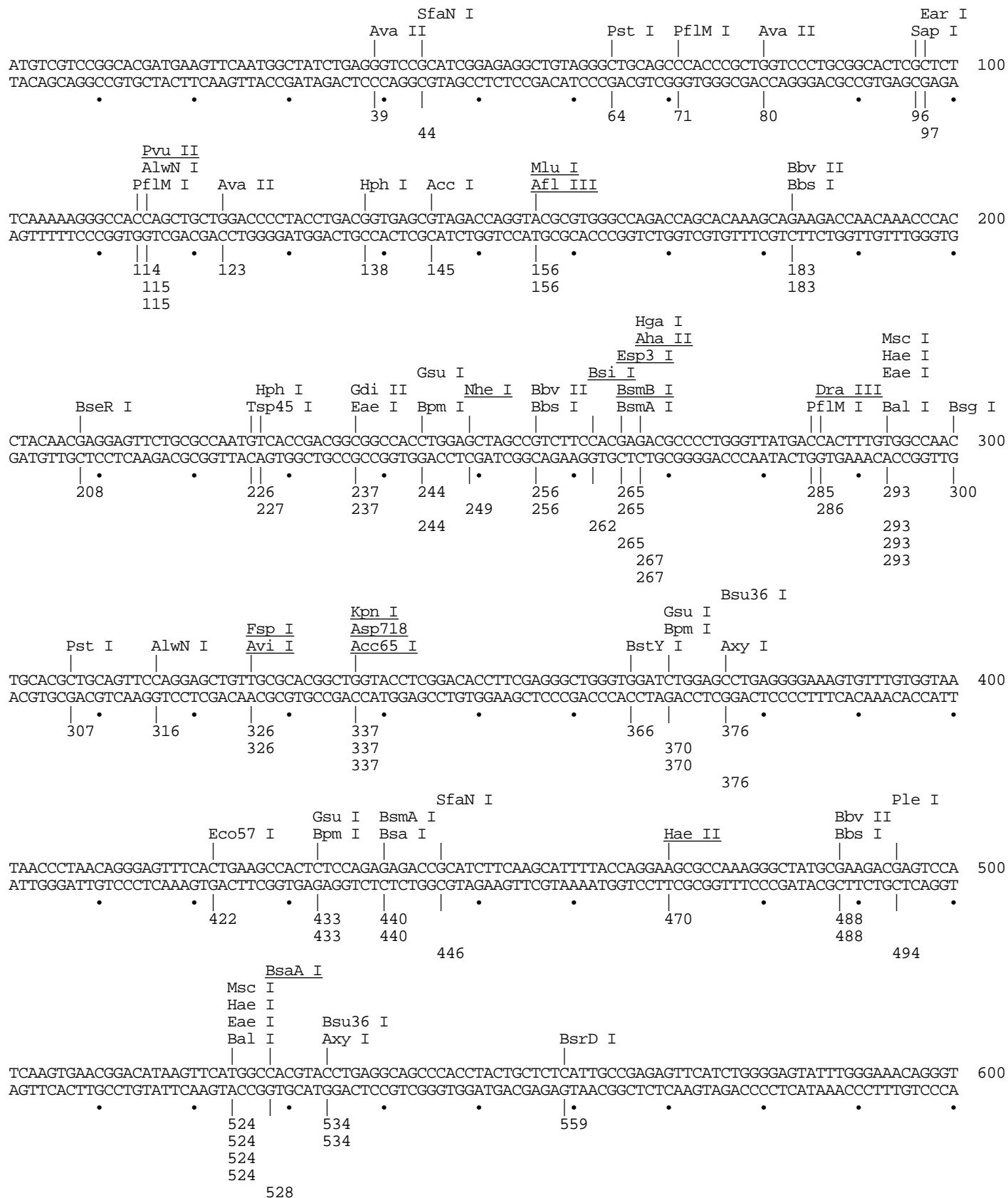
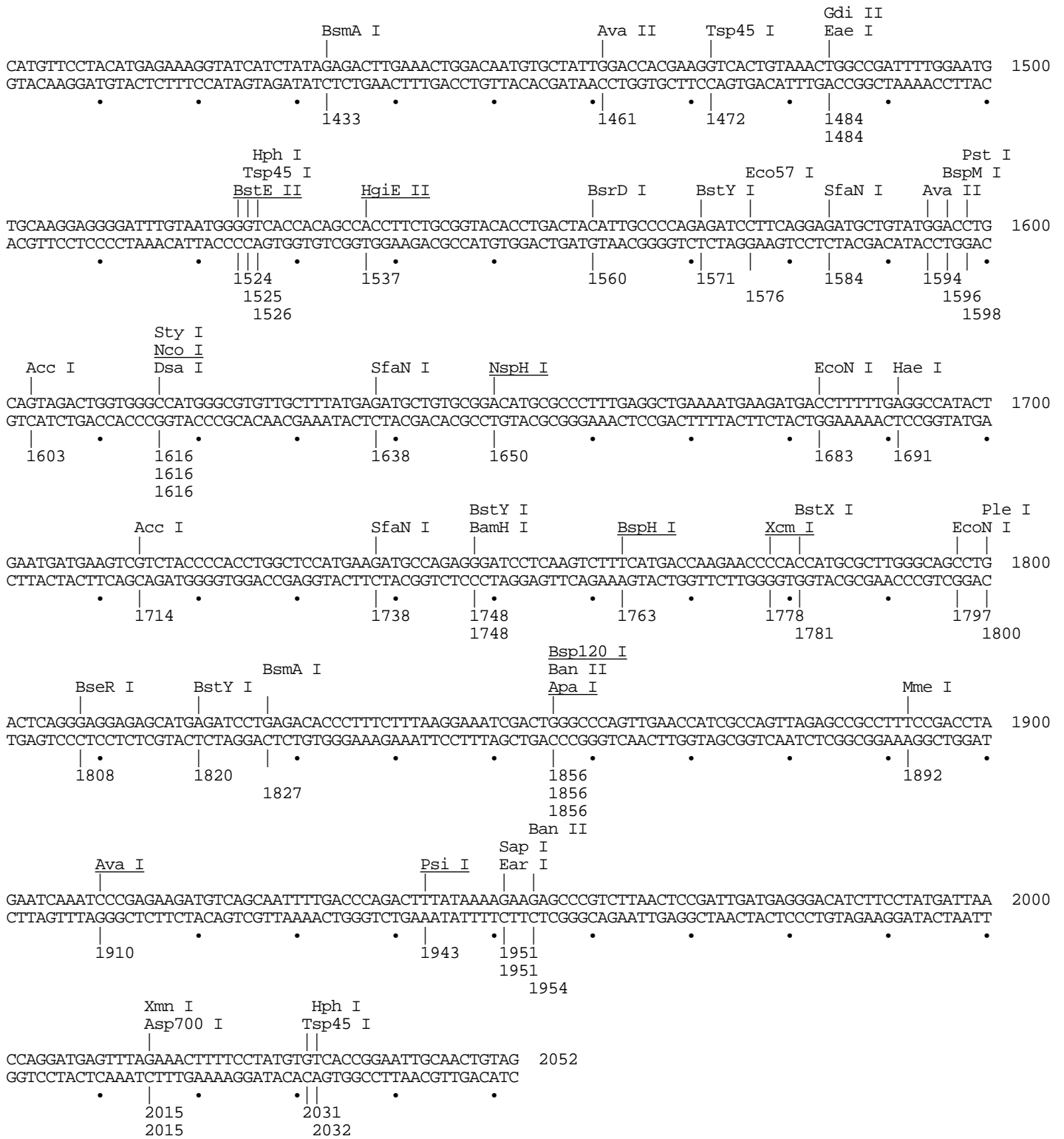


mPKCeta_ORF -> Full Restriction Map

DNA sequence 2052 b.p. ATGTCGTCCGGC ... TTGCAACTGTAG linear

Positions of Restriction Endonucleases sites (unique sites underlined)





Restriction Endonucleases site usage

Aat I	-	Bbv II	3	BstY I	5	HinD III	-	Psp1406 I	1
Aat II	-	BciV I	-	BstZ17 I	-	Hpa I	1	Pst I	4
Acc65 I	1	Bcl I	-	Bsu36 I	2	Hph I	7	Pvu I	-
Acc I	4	Bfr I	-	Btr I	-	Kas I	-	Pvu II	1
Acl I	1	Bgl I	-	Bts I	-	Kpn I	1	Rsr II	-
Afl II	-	Bgl II	-	Cfr10 I	-	Ksp I	1	Sac I	-
Afl III	1	Bln I	-	Cla I	-	Mfe I	-	Sac II	1
Age I	-	Blp I	-	Dra I	-	Mlu I	1	Sal I	1
Aha II	1	Bpm I	4	Dra III	1	Mne I	3	Sap I	3

Ahd I	-	Bpu1102 I	-	Drd I	-	Msc I	2	Sbf I	-
Alw44 I	2	Bsa I	2	Dsa I	3	Mun I	-	Sca I	-
AlwN I	2	BsaA I	1	Eae I	4	Nae I	-	SfaN I	9
Aor51H I	-	BsaB I	-	Eag I	-	Nar I	-	Sfi I	-
Apa I	1	BseR I	2	Ear I	5	Nco I	1	SgrA I	-
ApaL I	2	Bsg I	3	Ecl136 II	-	Nde I	-	Sma I	-
Asc I	-	Bsi I	1	Eco47 III	-	NgoM I	-	SnaB I	-
Ase I	-	BsiW I	-	Eco57 I	4	Nhe I	1	Spe I	-
Asp700 I	2	Bsm I	1	EcoN I	2	Not I	-	Sph I	-
Asp718	1	BsmA I	6	EcoO109 I	-	Nru I	-	Spl I	-
AspE I	-	BsmB I	1	EcoR I	-	Nsi I	-	Srf I	-
Asp I	-	Bsp120 I	1	EcoR V	-	NspH I	1	Sse8387 I	-
Ava I	1	Bsp1407 I	1	Ehe I	-	Pac I	-	Ssp I	2
Ava II	5	BspE I	-	Esp3 I	1	Paer7 I	-	Stu I	-
Avi I	1	BspH I	1	Esp I	-	Pci I	-	Sty I	2
Avr II	-	BspM I	2	Fse I	-	PflF I	-	Swa I	-
Axy I	2	BspM II	-	Fsp I	1	PflM I	3	Tsp45 I	5
Bal I	2	BspLU11 I	-	Gdi II	2	Ple I	3	Tth111 I	-
BamH I	2	BsrB I	-	Gsu I	4	Pme I	-	Xba I	-
Ban II	3	BsrD I	2	Hae I	3	Pml I	-	Xca I	-
Ban III	-	BssH II	-	Hae II	1	Ppu10 I	-	Xho I	-
Bbe I	-	Bst1107 I	-	Hga I	2	PpuM I	-	Xcm I	1
BbrP I	-	BstB I	-	HgiA I	3	PshA I	-	Xma I	-
Bbs I	3	BstE II	1	HgiE II	1	Psi I	1	Xmn I	2
Bbu I	-	BstX I	2	HinC II	2				

Enzyme	Site	Use	Site position (Fragment length)	Fragment order	
Acc65 I	g/gtacc	1	1(336) 2	337(1716) 1	
Acl I	aa/cggt	1	1(744) 2	745(1308) 1	
Afl III	a/crygt	1	1(155) 2	156(1897) 1	
Aha II	gr/cgyc	1	1(266) 2	267(1786) 1	
Apa I	gggcc/c	1	1(1855) 1	1856(197) 2	
Asp718	g/gtacc	1	1(336) 2	337(1716) 1	
Ava I	c/ycgrg	1	1(1909) 1	1910(143) 2	
Avi I	tgc/gca	1	1(325) 2	326(1727) 1	
BsaA I	yac/gtr	1	1(527) 2	528(1525) 1	
Bsi I	ctcgtg	-5/-1	1(261) 2	262(1791) 1	
Bsm I	gaatgc	1/-1	1(890) 2	891(1162) 1	
BsmB I	cgtctc	1/5	1(264) 2	265(1788) 1	
Bsp120 I	g/ggccc	1	1(1855) 1	1856(197) 2	
Bsp1407 I	t/gtaca	1	1(845) 2	846(1207) 1	
BspH I	t/catga	1	1(1762) 1	1763(290) 2	
BstE II	g/gtnacc	1	1(1523) 1	1524(529) 2	
Dra III	cacnnn/gtgc	1	1(285) 2	286(1767) 1	
Esp3 I	cgtctc	1/5	1(264) 2	265(1788) 1	
Fsp I	tgc/gca	1	1(325) 2	326(1727) 1	
Hae II	rgcgc/y	1	1(469) 2	470(1583) 1	
HgiE II	accnnnnnggt	1	1(1536) 1	1537(516) 2	
Hpa I	ggt/aac	1	1(1029) 1	1030(1023) 2	
Kpn I	ggtac/c	1	1(336) 2	337(1716) 1	
Ksp I	ccgc/gg	1	1(1378) 1	1379(674) 2	
Mlu I	a/cgcgt	1	1(155) 2	156(1897) 1	
Nco I	c/catgg	1	1(1615) 1	1616(437) 2	
Nhe I	g/ctagc	1	1(248) 2	249(1804) 1	
NspH I	rcatg/y	1	1(1649) 1	1650(403) 2	
Psi I	tta/taa	1	1(1942) 1	1943(110) 2	
Psp1406 I	aa/cggt	1	1(744) 2	745(1308) 1	
Pvu II	cag/ctg	1	1(114) 2	115(1938) 1	
Sac II	ccgc/gg	1	1(1378) 1	1379(674) 2	
Sal I	g/tcgac	1	1(974) 2	975(1078) 1	
Xcm I	ccannnnn/nnmtgg	1	1(1777) 1	1778(275) 2	
Alw44 I	g/tgcac	2	1(614) 2	615(579) 3	1194(859) 1
AlwN I	cagnnn/ctgc	2	1(114) 3	115(201) 2	316(1737) 1
ApaL I	g/tgcac	2	1(614) 2	615(579) 3	1194(859) 1
Asp700 I	gaann/nttc	2	1(940) 2	941(1074) 1	2015(38) 3
Axy I	cc/tnagg	2	1(375) 2	376(158) 3	534(1519) 1
Bal I	tgg/cca	2	1(292) 2	293(231) 3	524(1529) 1
BamH I	g/gatcc	2	1(1213) 1	1214(534) 2	1748(305) 3
Bsa I	ggtctc	1/5	1(439) 3	440(488) 2	928(1125) 1
BseR I	gaggag	10/8	1(207) 3	208(1600) 1	1808(245) 2
BspM I	acctgc	4/8	1(618) 2	619(977) 1	1596(457) 3
BsrD I	gcaatg	2/0	1(558) 2	559(1001) 1	1560(493) 3

BstX I	ccannnn/ntgg	2	1(907) 1	908(873) 2	1781(272) 3
Bsu36 I	cc/tnagg	2	1(375) 2	376(158) 3	534(1519) 1
EcoN I	cctnn/nnnagg	2	1(1682) 1	1683(114) 3	1797(256) 2
Gdi II	yggccg -5/-1	2	1(236) 3	237(1247) 1	1484(569) 2
Hga I	gacgc 5/10	2	1(266) 3	267(356) 2	623(1430) 1
HinC II	gty/rac	2	1(974) 2	975(55) 3	1030(1023) 1
Msc I	tgg/cca	2	1(292) 2	293(231) 3	524(1529) 1
Ssp I	aat/att	2	1(678) 2	679(264) 3	943(1110) 1
Sty I	c/cwggg	2	1(1222) 1	1223(393) 3	1616(437) 2
Xmn I	gaann/nnttc	2	1(940) 2	941(1074) 1	2015(38) 3
Ban II	grgcy/c	3	1(1001) 1 1954(99) 3	1002(854) 2	1856(98) 4
Bbs I	gaagac 2/6	3	1(182) 3 488(1565) 1	183(73) 4	256(232) 2
Bbv II	gaagac 2/6	3	1(182) 3 488(1565) 1	183(73) 4	256(232) 2
Bsg I	gtgcag 16/14	3	1(299) 4 1394(659) 2	300(363) 3	663(731) 1
Dsa I	c/crygg	3	1(895) 1 1616(437) 3	896(483) 2	1379(237) 4
Hae I	wgg/ccw	3	1(292) 3 1691(362) 2	293(231) 4	524(1167) 1
HgiA I	gwgcw/c	3	1(614) 2 1364(689) 1	615(579) 3	1194(170) 4
Mme I	tccrac 20/18	3	1(931) 2 1892(161) 3	932(19) 4	951(941) 1
PflM I	ccannnn/ntgg	3	1(70) 3 285(1768) 1	71(43) 4	114(171) 2
Ple I	gagtc 4/5	3	1(493) 3 1800(253) 4	494(778) 1	1272(528) 2
Sap I	gctcttc 1/4	3	1(95) 4 1951(102) 3	96(1158) 1	1254(697) 2
Acc I	gt/mkac	4	1(144) 4 1603(111) 5	145(830) 1 1714(339) 3	975(628) 2
Bpm I	ctggag 16/14	4	1(243) 3 433(841) 1	244(126) 4 1274(779) 2	370(63) 5
Eae I	y/ggccr	4	1(236) 3 524(960) 1	237(56) 5 1484(569) 2	293(231) 4
Eco57 I	ctgaag 16/14	4	1(421) 2 1156(420) 3	422(398) 4 1576(477) 1	820(336) 5
Gsu I	ctggag 16/14	4	1(243) 3 433(841) 1	244(126) 4 1274(779) 2	370(63) 5
Pst I	ctgca/g	4	1(63) 5 1174(424) 3	64(243) 4 1598(455) 2	307(867) 1
Ava II	g/gwcc	5	1(38) 6 123(1338) 1	39(41) 5 1461(133) 3	80(43) 4 1594(459) 2
BstY I	r/gatcy	5	1(365) 2 1571(177) 5	366(848) 1 1748(72) 6	1214(357) 3 1820(233) 4
Ear I	ctcttc 1/4	5	1(96) 5 1209(46) 6	97(938) 1 1255(696) 2	1035(174) 3 1951(102) 4
Tsp45 I	/gtsac	5	1(225) 4 1472(53) 5	226(550) 2 1525(506) 3	776(696) 1 2031(22) 6
BsmA I	gtctc 1/5	6	1(264) 4 929(197) 6 1827(226) 5	265(175) 7 1126(307) 3	440(489) 1 1433(394) 2
Hph I	ggtga 8/7	7	1(137) 6 888(216) 4 1526(506) 2	138(89) 7 1104(143) 5 2032(21) 8	227(661) 1 1247(279) 3
SfaN I	gcatc 5/9	9	1(43) 9 694(28) 10 1107(477) 1 1738(315) 4	44(402) 2 722(330) 3 1584(54) 8	446(248) 5 1052(55) 7 1638(100) 6

175 sites found

No Sites found for the following Restriction Endonucleases

Aat I	agg/cct	Bst1107 I	gta/tac	PaeR7 I	c/tcgag
Aat II	gacgt/c	BstB I	tt/cgaa	Pci I	a/catgt

Afl II	c/ttaag	BstZ17 I	gta/tac	PflF I	gacn/nngtc
Age I	a/ccggt	Btr I	cac/gtc	Pme I	gttt/aaac
Ahd I	gacnnn/nngtc	Bts I	gcagtg 2/0	Pml I	cac/gtg
Aor51H I	agc/gct	Cfr10 I	r/ccggy	Ppu10 I	a/tgcat
Asc I	gg/cgcgcc	Cla I	at/cgat	PpuM I	rg/gwccy
Ase I	at/taat	Dra I	ttt/aaa	PshA I	gacnn/nngtc
AspE I	gacnnn/nngtc	Drd I	gacnnnn/nngtc	Pvu I	cgat/cg
Asp I	gacn/nngtc	Eag I	c/ggccg	Rsr II	cg/gwccg
Avr II	c/ctagg	Ecl136 II	gag/ctc	Sac I	gagct/c
Ban III	at/cgat	Eco47 III	agc/gct	Sbf I	cctgca/gg
Bbe I	ggcgc/c	EcoO109 I	rg/gnccy	Sca I	agt/act
BbrP I	cac/gtg	EcoR I	g/aattc	Sfi I	ggccnnnn/nggcc
Bbu I	gcatg/c	EcoR V	gat/atc	SgrA I	cr/ccggyg
BciV I	gtatcc 6/5	Ehe I	ggc/gcc	Sma I	ccc/ggg
Bcl I	t/gatca	Esp I	gc/tnagc	SnaB I	tac/gta
Bfr I	c/ttaag	Fse I	ggccgg/cc	Spe I	a/ctagt
Bgl I	gccnnnn/nggc	HinD III	a/agctt	Sph I	gcatg/c
Bgl II	a/gatct	Kas I	g/gcgcc	Spl I	c/gtacg
Bln I	c/ctagg	Mfe I	c/aattg	Srf I	gccc/gggc
Blp I	gc/tnagc	Mun I	c/aattg	Sse8387 I	cctgca/gg
Bpu1102 I	gc/tnagc	Nae I	gcc/ggc	Stu I	agg/cct
BsaB I	gatnn/nnatc	Nar I	gg/cgcc	Swa I	attt/aaat
BsiW I	c/gtacg	Nde I	ca/tatg	Tth111 I	gacn/nngtc
BspE I	t/ccgga	NgoM I	g/ccggc	Xba I	t/ctaga
BspM II	t/ccgga	Not I	gc/ggccgc	Xca I	gta/tac
BspLU11 I	a/catgt	Nru I	tcg/cga	Xho I	c/tcgag
BsrB I	gagcgg -3/-3	Nsi I	atgca/t	Xma I	c/ccggg
BssH II	g/cgcgc	Pac I	ttaat/taa		