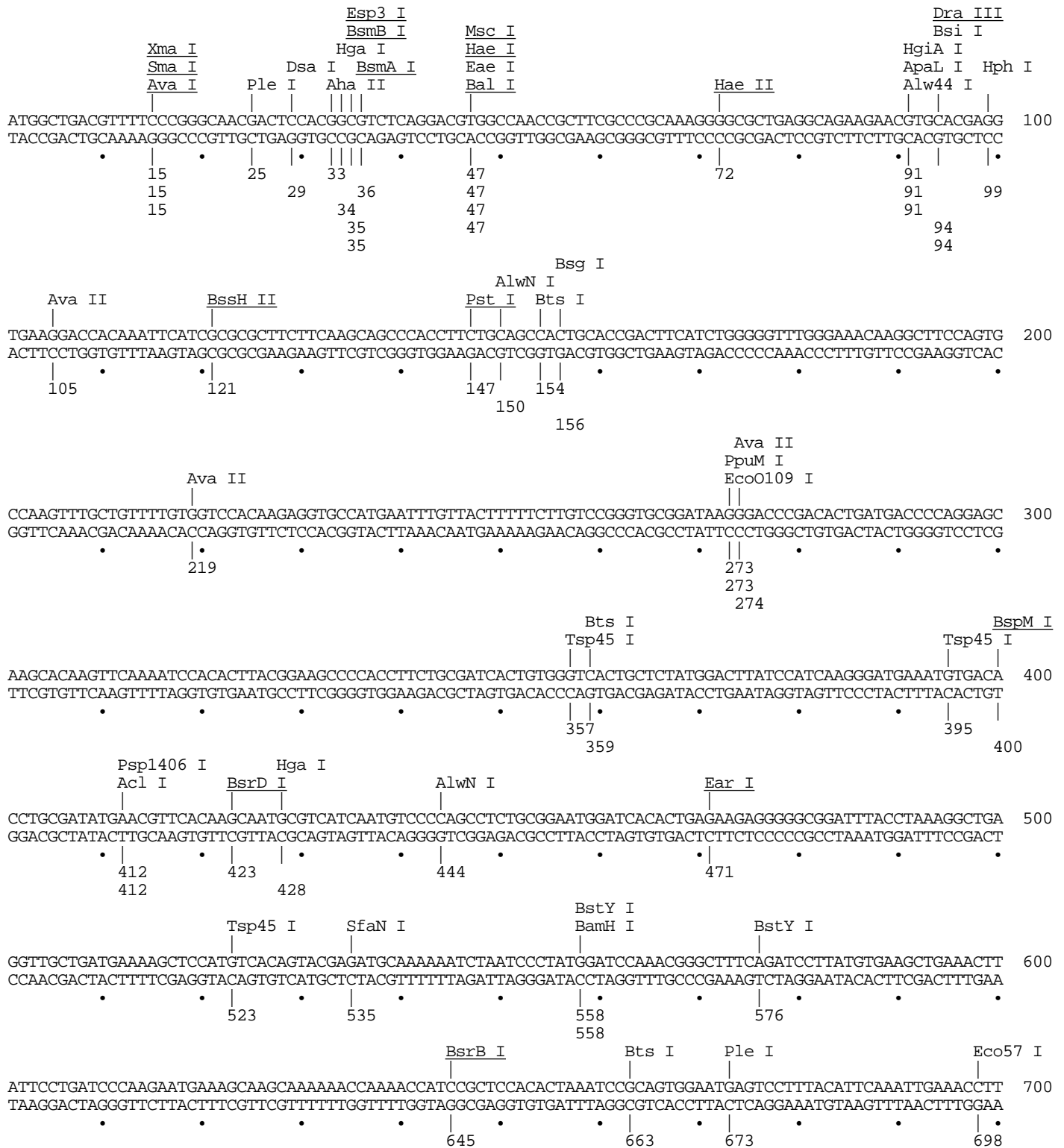
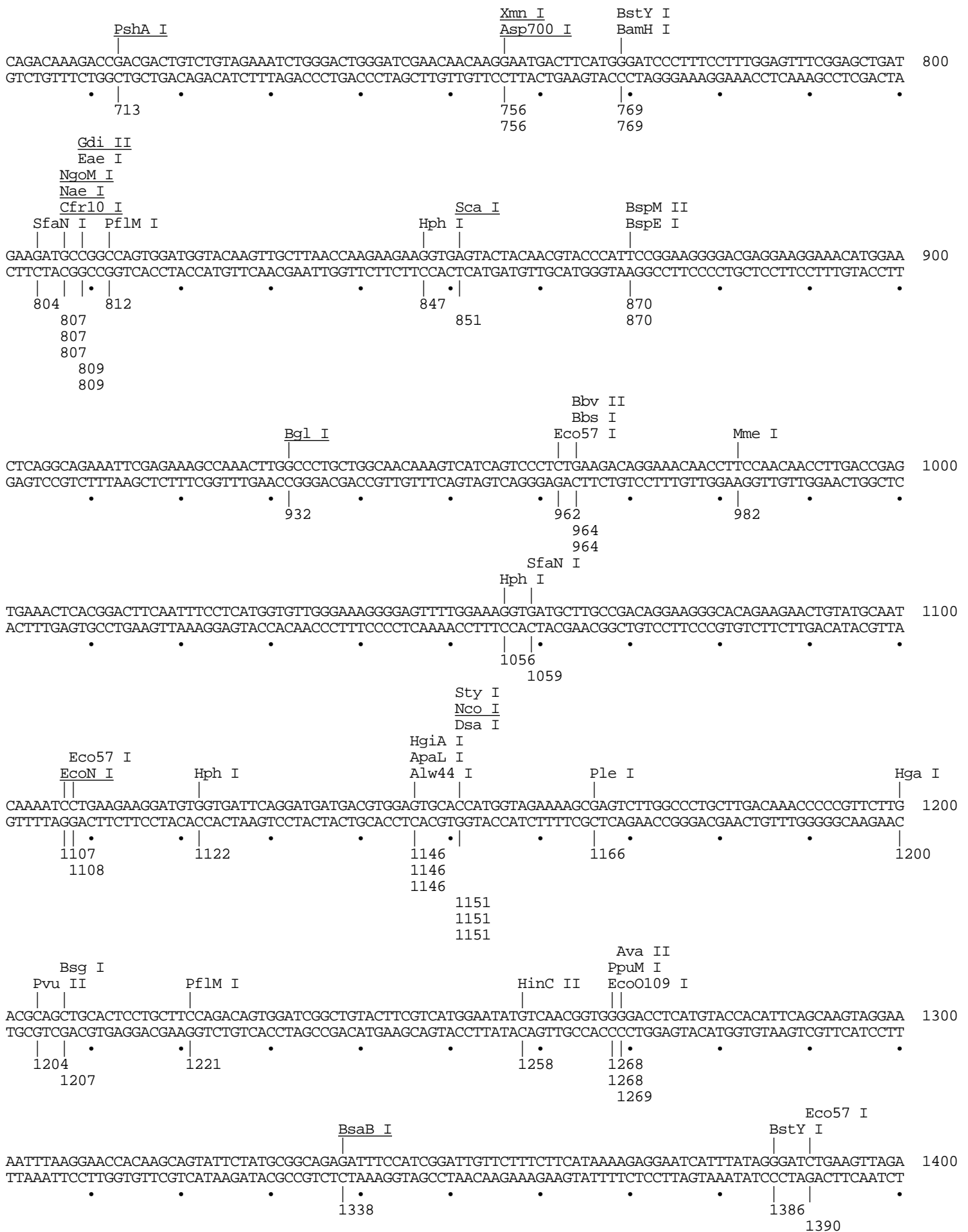


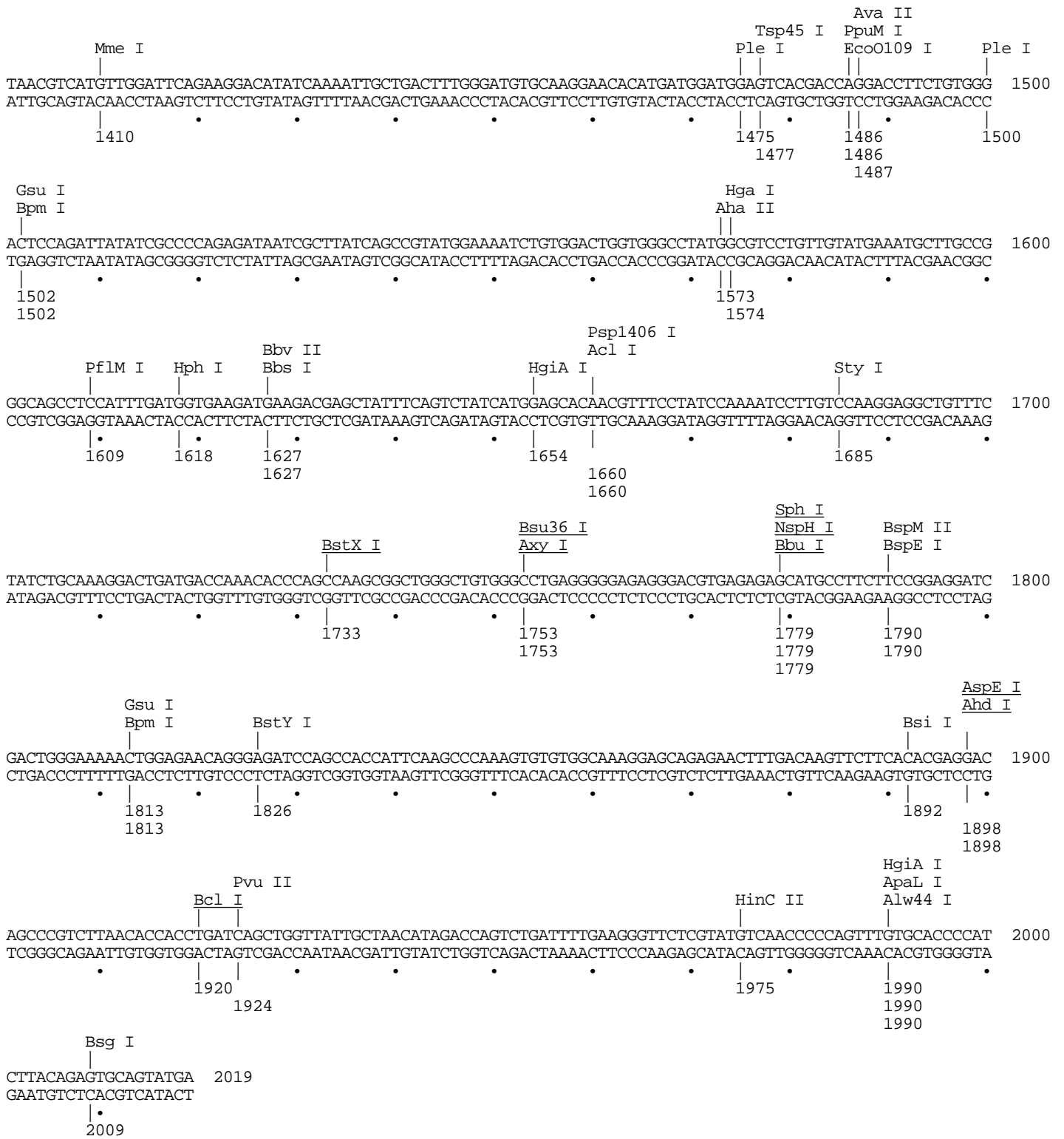
hPKCalpha_ORF -> Full Restriction Map

DNA sequence 2019 b.p. ATGGCTGACGTT ... AGTGCAGTATGA linear

Positions of Restriction Endonucleases sites (unique sites underlined)







Restriction Endonucleases site usage

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

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

Enzyme	Site	Use	Site position (Fragment length)		Fragment order
Ahd I	gacnnn/nngtc	1	1(1897)	1	1898(122) 2
Asp700 I	gaann/nnttc	1	1(755)	2	756(1264) 1
AspE I	gacnnn/nngtc	1	1(1897)	1	1898(122) 2
Ava I	c/ycgrg	1	1(14)	2	15(2005) 1
Axy I	cc/tnagg	1	1(1752)	1	1753(267) 2
Bal I	tgg/cca	1	1(46)	2	47(1973) 1
Bbu I	gcatg/c	1	1(1778)	1	1779(241) 2
Bcl I	t/gatca	1	1(1919)	1	1920(100) 2
Bgl I	gccnnnn/nggc	1	1(931)	2	932(1088) 1
BsaB I	gatnn/nnatc	1	1(1337)	1	1338(682) 2
BsmA I	gtctc 1/5	1	1(35)	2	36(1984) 1
BsmB I	cgtctc 1/5	1	1(34)	2	35(1985) 1
BspM I	acctgc 4/8	1	1(399)	2	400(1620) 1
BsrB I	gagcgg -3/-3	1	1(644)	2	645(1375) 1
BsrD I	gcaatg 2/0	1	1(422)	2	423(1597) 1
BssH II	g/cgcgc	1	1(120)	2	121(1899) 1
BstX I	ccannnn/ntgg	1	1(1732)	1	1733(287) 2
Bsu36 I	cc/tnagg	1	1(1752)	1	1753(267) 2
Cfr10 I	r/ccggy	1	1(806)	2	807(1213) 1
Dra III	cacnnn/gtg	1	1(93)	2	94(1926) 1
Ear I	ctcttc 1/4	1	1(470)	2	471(1549) 1
EcoN I	cctnn/mnagg	1	1(1106)	1	1107(913) 2
Esp3 I	cgtctc 1/5	1	1(34)	2	35(1985) 1
Gdi II	yggccg -5/-1	1	1(808)	2	809(1211) 1
Hae I	wgg/ccw	1	1(46)	2	47(1973) 1
Hae II	rgcgc/y	1	1(71)	2	72(1948) 1
Msc I	tgg/cca	1	1(46)	2	47(1973) 1
Nae I	gcc/ggc	1	1(806)	2	807(1213) 1
Nco I	c/catgg	1	1(1150)	1	1151(869) 2
NgoM I	g/ccggc	1	1(806)	2	807(1213) 1
NspH I	rcaatg/y	1	1(1778)	1	1779(241) 2
PshA I	gacnn/nngtc	1	1(712)	2	713(1307) 1
Pst I	ctgca/g	1	1(146)	2	147(1873) 1
Sca I	agt/act	1	1(850)	2	851(1169) 1
Sma I	ccc/ggg	1	1(14)	2	15(2005) 1
Sph I	gcatg/c	1	1(1778)	1	1779(241) 2
Xma I	c/ccggy	1	1(14)	2	15(2005) 1
Xmn I	gaann/nnttc	1	1(755)	2	756(1264) 1
Acl I	aa/cggt	2	1(411)	2	412(1248) 1
Aha II	gr/cgyc	2	1(32)	3	33(1540) 1
AlwN I	cagnnn/ctg	2	1(149)	3	150(294) 2
BamH I	g/gatcc	2	1(557)	2	558(211) 3
Bbs I	gaagac 2/6	2	1(963)	1	964(663) 2
Bbv II	gaagac 2/6	2	1(963)	1	964(663) 2
Bpm I	ctggag 16/14	2	1(1501)	1	1502(311) 2

Bsi I	ctcgtg	-5/-1	2	1(93) 3	94(1798) 1	1892(128) 2
BspE I	t/ccgga		2	1(869) 2	870(920) 1	1790(230) 3
BspM II	t/ccgga		2	1(869) 2	870(920) 1	1790(230) 3
Dsa I	c/crygg		2	1(28) 3	29(1122) 1	1151(869) 2
Eae I	y/ggccr		2	1(46) 3	47(762) 2	809(1211) 1
Gsu I	ctggag	16/14	2	1(1501) 1	1502(311) 2	1813(207) 3
HinC II	gty/rac		2	1(1257) 1	1258(717) 2	1975(45) 3
Mme I	tccrac	20/18	2	1(981) 1	982(428) 3	1410(610) 2
Psp1406 I	aa/cggt		2	1(411) 2	412(1248) 1	1660(360) 3
Pvu II	cag/ctg		2	1(1203) 1	1204(720) 2	1924(96) 3
Sty I	c/cwwgg		2	1(1150) 1	1151(534) 2	1685(335) 3
Alw44 I	g/tgcac		3	1(90) 3	91(1055) 1	1146(844) 2
ApaL I	g/tgcac		3	1(90) 3	91(1055) 1	1146(844) 2
Bsg I	gtgcag	16/14	3	1(155) 3	156(1051) 1	1207(802) 2
Bts I	gcagtg	2/0	3	1(153) 4	154(205) 3	359(304) 2
Eco0109 I	rg/gnccy		3	1(272) 3	273(995) 1	1268(218) 4
PflM I	ccannnn/ntgg		3	1(811) 1	812(409) 3	1221(388) 4
PpuM I	rg/gwccy		3	1(272) 3	273(995) 1	1268(218) 4
SfaN I	gcatc	5/9	3	1(534) 2	535(269) 3	804(255) 4
Eco57 I	ctgaag	16/14	4	1(697) 1	698(264) 4	962(146) 5
Hga I	gacgc	5/10	4	1(33) 5	34(394) 3	428(772) 1
HgiA I	gwgcw/c		4	1(90) 4	91(1055) 1	1146(508) 2
Tsp45 I	/gtsac		4	1(356) 3	357(38) 5	395(128) 4
Ava II	g/gwcc		5	1(104) 5	105(114) 4	219(55) 6
BstY I	r/gatcy		5	1(557) 2	558(18) 6	576(193) 5
Hph I	ggtga	8/7	5	1(98) 5	99(748) 1	847(209) 4
Ple I	gagtc	4/5	5	1(24) 6	25(648) 1	673(493) 3

134 sites found

No Sites found for the following Restriction Endonucleases

Aat I	agg/cct			BspH I	t/catga	Nru I	tcg/cga
Aat II	gacgt/c			BspLU11 I	a/catgt	Nsi I	atgca/t
Acc65 I	g/gtacc			Bst1107 I	gta/tac	Pac I	ttaat/taa
Acc I	gt/mkac			BstB I	tt/cgaa	Paer7 I	c/tcgag
Afl II	c/ttaag			BstE II	g/gtnacc	Pci I	a/catgt
Afl III	a/crygt			BstZ17 I	gta/tac	PflF I	gacn/nngtc
Age I	a/cgggt			Btr I	cac/gtc	Pme I	gttt/aaac
Aor51H I	agc/gct			Cla I	at/cgat	Pml I	cac/gtg
Apa I	gggcc/c			Dra I	ttt/aaa	Ppu10 I	a/tgcat
Asc I	gg/cgcgcc			Drd I	gacnnnn/nngtc	Psi I	tta/taa
Ase I	at/taat			Eag I	c/ggccg	Pvu I	cgat/cg
Asp718	g/gtacc			Ecl136 II	gag/ctc	Rsr II	cg/gwccg
Asp I	gacn/nngtc			Eco47 III	agc/gct	Sac I	gagct/c
Avi I	tgc/gca			EcoR I	g/aattc	Sac II	ccgc/gg
Avr II	c/ctagg			EcoR V	gat/atc	Sal I	g/tcgac
Ban II	grgcy/c			Ehe I	ggc/gcc	Sap I	gctcttc 1/4
Ban III	at/cgat			Esp I	gc/tnagc	Sbf I	cctgca/gg
Bbe I	ggcgc/c			Fse I	ggccgg/cc	Sfi I	ggccnnnn/nggcc
BbrP I	cac/gtg			Fsp I	tgc/gca	SgrA I	cr/ccggyg
BciV I	gtatcc	6/5		HgiE II	accnnnnnnggt	SnaB I	tac/gta
Bfr I	c/ttaag			HinD III	a/agctt	Spe I	a/ctagt
Bgl II	a/gatct			Hpa I	gtt/aac	Spl I	c/gtacg
Bln I	c/ctagg			Kas I	g/gcgcc	Srf I	gccc/gggc
Blp I	gc/tnagc			Kpn I	ggtac/c	Sse8387 I	cctgca/gg

Bpu1102 I	gc/tnagc		Ksp I	ccgc/gg	Ssp I	aat/att
Bsa I	ggtctc	1/5	Mfe I	c/aattg	Stu I	agg/cct
BsaA I	yac/gtr		Mlu I	a/cgctg	Swa I	attt/aaat
BseR I	gaggag	10/8	Mun I	c/aattg	Tth111 I	gacn/nngtc
BsiW I	c/gtacg		Nar I	gg/cgcc	Xba I	t/ctaga
Bsm I	gaatgc	1/-1	Nde I	ca/tatg	Xca I	gta/tac
Bsp120 I	g/ggccc		Nhe I	g/ctagc	Xho I	c/tcgag
Bsp1407 I	t/gtaca		Not I	gc/ggccgc	Xcm I	ccannnnn/nnmntgg