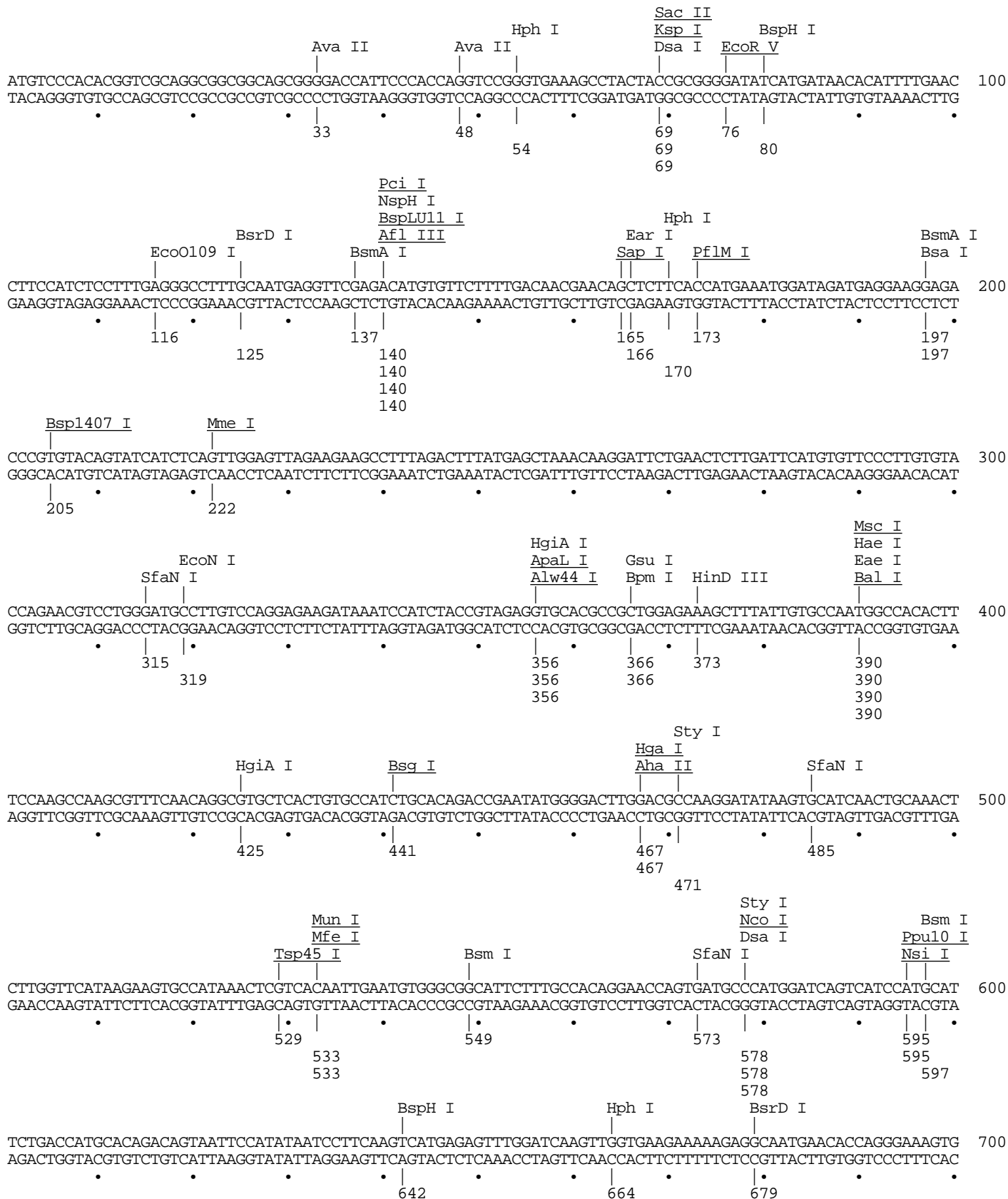
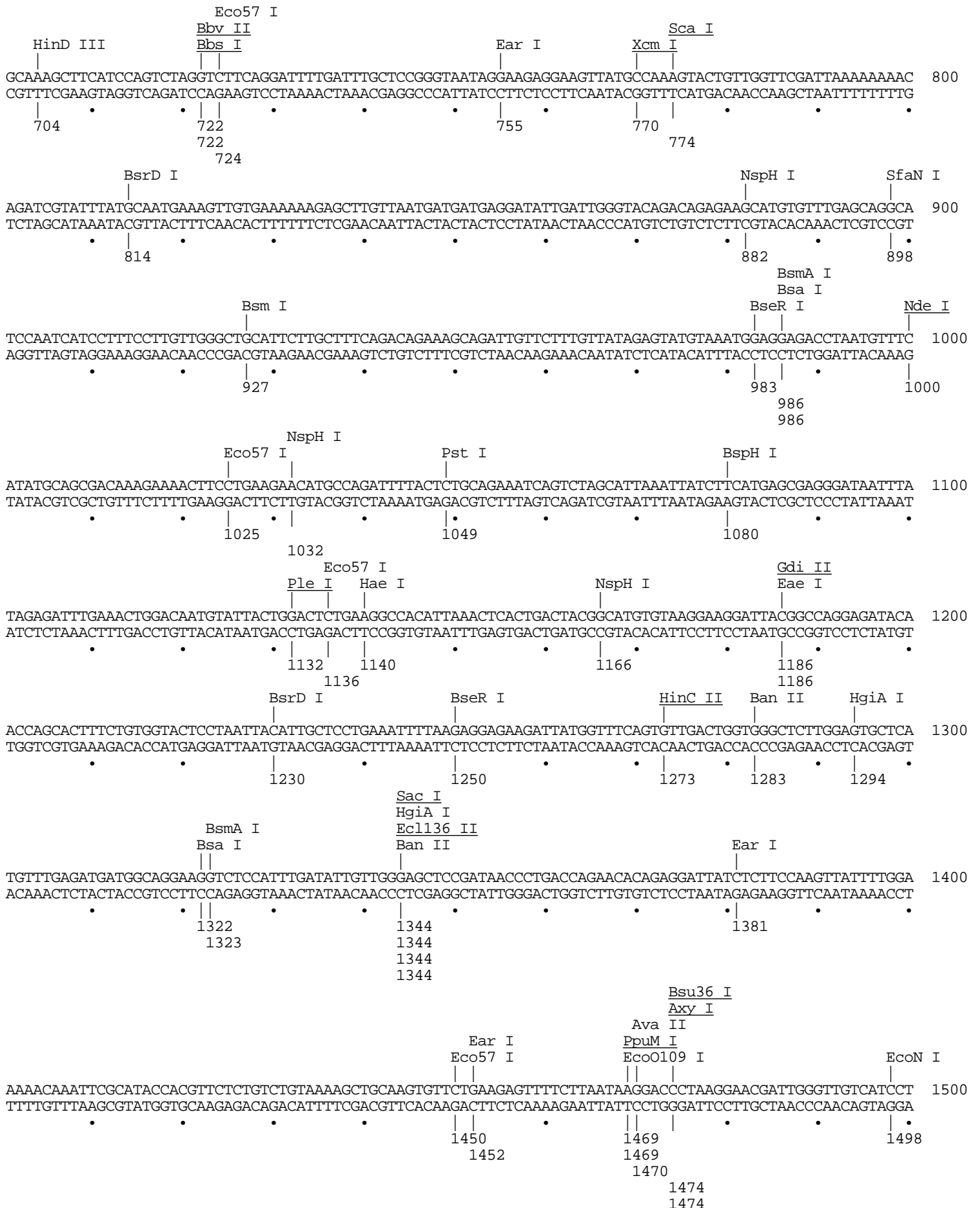


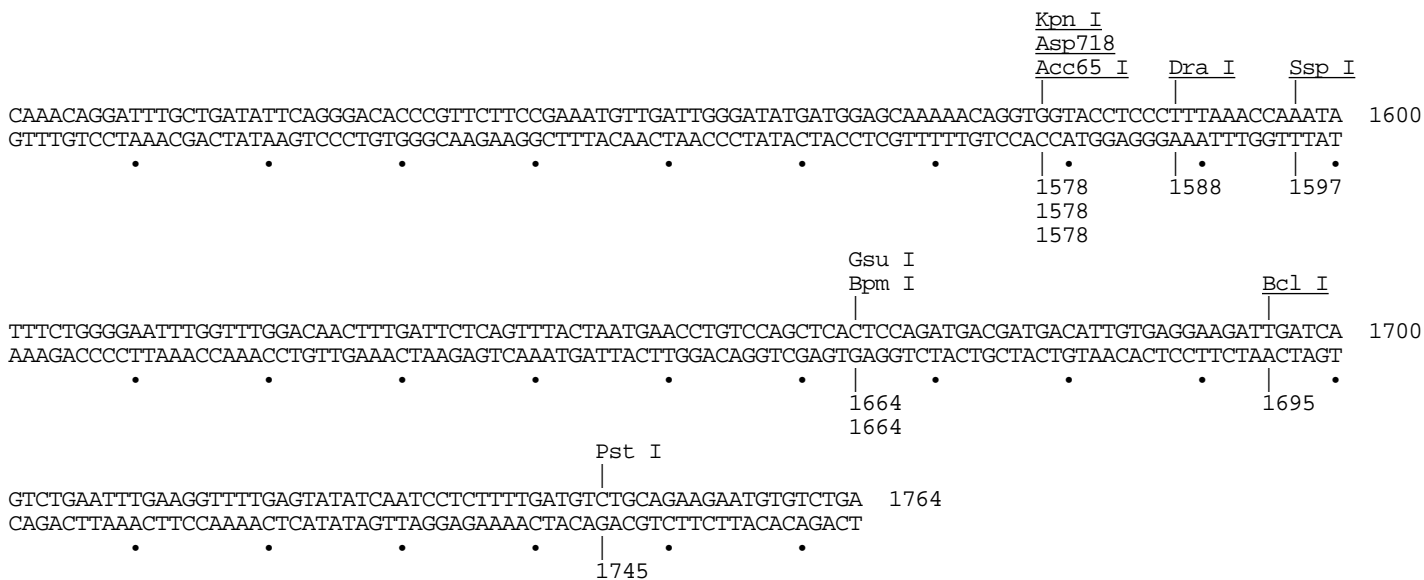
hPKCiota_ORF -> Full Restriction Map

DNA sequence 1764 b.p. ATGTCCACACG ... GAATGTGTCTGA linear

Positions of Restriction Endonucleases sites (unique sites underlined)







Restriction Endonucleases site usage

Aat I	-	Bbv II	1	BstY I	-	HinD III	2	Psp1406 I	-
Aat II	-	BciV I	-	BstZ17 I	-	Hpa I	-	Pst I	2
Acc65 I	1	Bcl I	1	Bsu36 I	1	Hph I	3	Pvu I	-
Acc I	-	Bfr I	-	Btr I	-	Kas I	-	Pvu II	-
Acl I	-	Bgl I	-	Bts I	-	Kpn I	1	Rsr II	-
Afl II	-	Bgl II	-	Cfr10 I	-	Ksp I	1	Sac I	1
Afl III	1	Bln I	-	Cla I	-	Mfe I	1	Sac II	1
Age I	-	Blp I	-	Dra I	1	Mlu I	-	Sal I	-
Aha II	1	Bpm I	2	Dra III	-	Mme I	1	Sap I	1
Ahd I	-	Bpu1102 I	-	Drd I	-	Msc I	1	Sbf I	-
Alw44 I	1	Bsa I	3	Dsa I	2	Mun I	1	Sca I	1
AlwN I	-	BsaA I	-	Eae I	2	Nae I	-	SfaN I	4
Aor51H I	-	BsaB I	-	Eag I	-	Nar I	-	Sfi I	-
Apa I	-	BseR I	2	Ear I	4	Nco I	1	SgrA I	-
ApaL I	1	Bsg I	1	Ecl136 II	1	Nde I	1	Sma I	-
Asc I	-	Bsi I	-	Eco47 III	-	NgoM I	-	SnaB I	-
Ase I	-	BsiW I	-	Eco57 I	4	Nhe I	-	Spe I	-
Asp700 I	-	Bsm I	3	EcoN I	2	Not I	-	Sph I	-
Asp718	1	BsmA I	4	EcoO109 I	2	Nru I	-	Spl I	-
AspE I	-	BsmB I	-	EcoR I	-	Nsi I	1	Srf I	-
Asp I	-	Bsp120 I	-	EcoR V	1	NspH I	4	Sse8387 I	-
Ava I	-	Bsp1407 I	1	Ehe I	-	Pac I	-	Ssp I	1
Ava II	3	BspE I	-	Esp3 I	-	Paer7 I	-	Stu I	-
Avi I	-	BspH I	3	Esp I	-	Pci I	1	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	1	BspLU11 I	1	Gdi II	1	Ple I	1	Tth111 I	-
BamH I	-	BsrB I	-	Gsu I	2	Pme I	-	Xba I	-
Ban II	2	BsrD I	4	Hae I	2	Pml I	-	Xca I	-
Ban III	-	BssH II	-	Hae II	-	Ppu10 I	1	Xho I	-
Bbe I	-	Bst1107 I	-	Hga I	1	PpuM I	1	Xcm I	1
BbrP I	-	BstB I	-	HgiA I	4	PshA I	-	Xma I	-
Bbs I	1	BstE II	-	HgiE II	-	Psi I	-	Xmn I	-
Bbu I	-	BstX I	-	HinC II	1				

Enzyme	Site	Use	Site position (Fragment length)	Fragment order
Acc65 I	g/gtacc	1	1(1577) 1	1578(187) 2
Afl III	a/crygt	1	1(139) 2	140(1625) 1
Aha II	gr/cgyc	1	1(466) 2	467(1298) 1
Alw44 I	g/tgcac	1	1(355) 2	356(1409) 1
ApaL I	g/tgcac	1	1(355) 2	356(1409) 1
Asp718	g/gtacc	1	1(1577) 1	1578(187) 2
Axy I	cc/tnagg	1	1(1473) 1	1474(291) 2
Bal I	tgg/cca	1	1(389) 2	390(1375) 1

Bbs I	gaagac	2/6	1	1(721) 2	722(1043) 1		
Bbv II	gaagac	2/6	1	1(721) 2	722(1043) 1		
Bcl I	t/gatca		1	1(1694) 1	1695(70) 2		
Bsg I	gtgcag	16/14	1	1(440) 2	441(1324) 1		
Bsp1407 I	t/gtaca		1	1(204) 2	205(1560) 1		
BspLU11 I	a/catgt		1	1(139) 2	140(1625) 1		
Bsu36 I	cc/tnagg		1	1(1473) 1	1474(291) 2		
Dra I	ttt/aaa		1	1(1587) 1	1588(177) 2		
Ecl136 II	gag/ctc		1	1(1343) 1	1344(421) 2		
EcoR V	gat/atc		1	1(75) 2	76(1689) 1		
Gdi II	yggccg	-5/-1	1	1(1185) 1	1186(579) 2		
Hga I	gacgc	5/10	1	1(466) 2	467(1298) 1		
HinC II	gty/rac		1	1(1272) 1	1273(492) 2		
Kpn I	ggtac/c		1	1(1577) 1	1578(187) 2		
Ksp I	ccgc/gg		1	1(68) 2	69(1696) 1		
Mfe I	c/aattg		1	1(532) 2	533(1232) 1		
Mme I	tccrac	20/18	1	1(221) 2	222(1543) 1		
Msc I	tgg/cca		1	1(389) 2	390(1375) 1		
Mun I	c/aattg		1	1(532) 2	533(1232) 1		
Nco I	c/catgg		1	1(577) 2	578(1187) 1		
Nde I	ca/tatg		1	1(999) 1	1000(765) 2		
Nsi I	atgca/t		1	1(594) 2	595(1170) 1		
Pci I	a/catgt		1	1(139) 2	140(1625) 1		
PflM I	ccannnn/ntgg		1	1(172) 2	173(1592) 1		
Ple I	gagtc	4/5	1	1(1131) 1	1132(633) 2		
Ppu10 I	a/tgcat		1	1(594) 2	595(1170) 1		
PpuM I	rg/gwccy		1	1(1468) 1	1469(296) 2		
Sac I	gagct/c		1	1(1343) 1	1344(421) 2		
Sac II	ccgc/gg		1	1(68) 2	69(1696) 1		
Sap I	gctcttc	1/4	1	1(164) 2	165(1600) 1		
Sca I	agt/act		1	1(773) 2	774(991) 1		
Ssp I	aat/att		1	1(1596) 1	1597(168) 2		
Tsp45 I	/gtsac		1	1(528) 2	529(1236) 1		
Xcm I	ccannnnn/nnmntgg		1	1(769) 2	770(995) 1		
Ban II	grgcy/c		2	1(1282) 1	1283(61) 3	1344(421) 2	
Bpm I	ctggag	16/14	2	1(365) 2	366(1298) 1	1664(101) 3	
BseR I	gaggag	10/8	2	1(982) 1	983(267) 3	1250(515) 2	
Dsa I	c/crygg		2	1(68) 3	69(509) 2	578(1187) 1	
Eae I	y/ggccr		2	1(389) 3	390(796) 1	1186(579) 2	
EcoN I	cctnn/nnnagg		2	1(318) 2	319(1179) 1	1498(267) 3	
EcoO109 I	rg/gnccy		2	1(115) 3	116(1353) 1	1469(296) 2	
Gsu I	ctggag	16/14	2	1(365) 2	366(1298) 1	1664(101) 3	
Hae I	wgg/ccw		2	1(389) 3	390(750) 1	1140(625) 2	
HinD III	a/agctt		2	1(372) 2	373(331) 3	704(1061) 1	
Pst I	ctgca/g		2	1(1048) 1	1049(696) 2	1745(20) 3	
Sty I	c/cwwgg		2	1(470) 2	471(107) 3	578(1187) 1	
Ava II	g/gwcc		3	1(32) 3	33(15) 4	48(1422) 1	
Bsa I	ggtctc	1/5	3	1470(295) 2	1(196) 4	197(789) 1	986(336) 3
Bsm I	gaatgc	1/-1	3	1322(443) 2	1(548) 2	549(48) 4	597(330) 3
BspH I	t/catga		3	927(838) 1	1(79) 4	80(562) 2	642(438) 3
Hph I	ggtga	8/7	3	1080(685) 1	1(53) 4	54(116) 3	170(494) 2
				664(1101) 1			
BsmA I	gtctc	1/5	4	1(136) 4	137(60) 5	197(789) 1	
BsrD I	gcaatg	2/0	4	986(337) 3	1323(442) 2		
Ear I	ctcttc	1/4	4	1(124) 5	125(554) 1	679(135) 4	
				814(416) 3	1230(535) 2		
Eco57 I	ctgaag	16/14	4	1(165) 4	166(589) 2	755(626) 1	
				1381(71) 5	1452(313) 3		
HgiA I	gwgw/c		4	1(723) 1	724(301) 4	1025(111) 5	
				1136(314) 3	1450(315) 2		
NspH I	rcatg/y		4	1(355) 3	356(69) 4	425(869) 1	
				1294(50) 5	1344(421) 2		
SfaN I	gcatc	5/9	4	1(139) 4	140(742) 1	882(150) 3	
				1032(134) 5	1166(599) 2		
				1(314) 3	315(170) 4	485(88) 5	
				573(325) 2	898(867) 1		

109 sites found

No Sites found for the following Restriction Endonucleases

Aat I	agg/cct	BsmB I	cgtctc	1/5	NgoM I	g/ccggc
Aat II	gacgt/c	Bsp120 I	g/ggccc		Nhe I	g/ctagc
Acc I	gt/mkac	BspE I	t/ccgga		Not I	gc/ggccgc
Acl I	aa/cggt	BspM I	acctgc	4/8	Nru I	tcg/cga
Afl II	c/ttaag	BspM II	t/ccgga		Pac I	ttaat/taa
Age I	a/ccggt	BsrB I	gagcgg	-3/-3	Paer7 I	c/tcgag
Ahd I	gacnnn/nngtc	BssH II	g/cgcg		PflF I	gacn/nngtc
AlwN I	cagnnn/ctg	Bst1107 I	gta/tac		Pme I	gttt/aaac
Aor51H I	agc/gct	BstB I	tt/cgaa		Pml I	cac/gtg
Apa I	gggcc/c	BstE II	g/gtnacc		PshA I	gacnn/nngtc
Asc I	gg/cgcgcc	BstX I	ccannnnn/ntgg		Psi I	tta/taa
Ase I	at/taat	BstY I	r/gatcy		Psp1406 I	aa/cggt
Asp700 I	gaann/nnttc	BstZ17 I	gta/tac		Pvu I	cgat/cg
AspE I	gacnnn/nngtc	Btr I	cac/gtc		Pvu II	cag/ctg
Asp I	gacn/nngtc	Bts I	gcagtg	2/0	Rsr II	cg/gwccg
Ava I	c/ycgrg	Cfr10 I	r/ccggy		Sal I	g/tcgac
Avi I	tgc/gca	Cla I	at/cgat		Sbf I	cctgca/gg
Avr II	c/ctagg	Dra III	cacnnn/gtg		Sfi I	ggccnnnn/nggcc
BamH I	g/gatcc	Drd I	gacnnnn/nngtc		SgrA I	cr/ccggyg
Ban III	at/cgat	Eag I	c/ggccg		Sma I	ccc/ggg
Bbe I	ggcgc/c	Eco47 III	agc/gct		SnaB I	tac/gta
BbrP I	cac/gtg	EcoR I	g/aattc		Spe I	a/ctagt
Bbu I	gcatg/c	Ehe I	ggc/gcc		Sph I	gcatg/c
BciV I	gtatcc	Esp3 I	cgtctc	1/5	Spl I	c/gtacg
Bfr I	c/ttaag	Esp I	gc/tnagc		Srf I	gccc/gggc
Bgl I	gccnnnn/nggc	Fse I	ggccgg/cc		Sse8387 I	cctgca/gg
Bgl II	a/gatct	Fsp I	tgc/gca		Stu I	agg/cct
Bln I	c/ctagg	Hae II	rgcgc/y		Swa I	attt/aaat
Blp I	gc/tnagc	HgiE II	accnnnnnnggt		Tth111 I	gacn/nngtc
Bpu1102 I	gc/tnagc	Hpa I	gtt/aac		Xba I	t/ctaga
BsaA I	yac/gtr	Kas I	g/gcgcc		Xca I	gta/tac
BsaB I	gatnn/nnatc	Mlu I	a/cgctg		Xho I	c/tcgag
Bsi I	ctcgtg	Nae I	gcc/ggc		Xma I	c/ccggg
BsiW I	c/gtacg	Nar I	gg/cgcc		Xmn I	gaann/nnttc