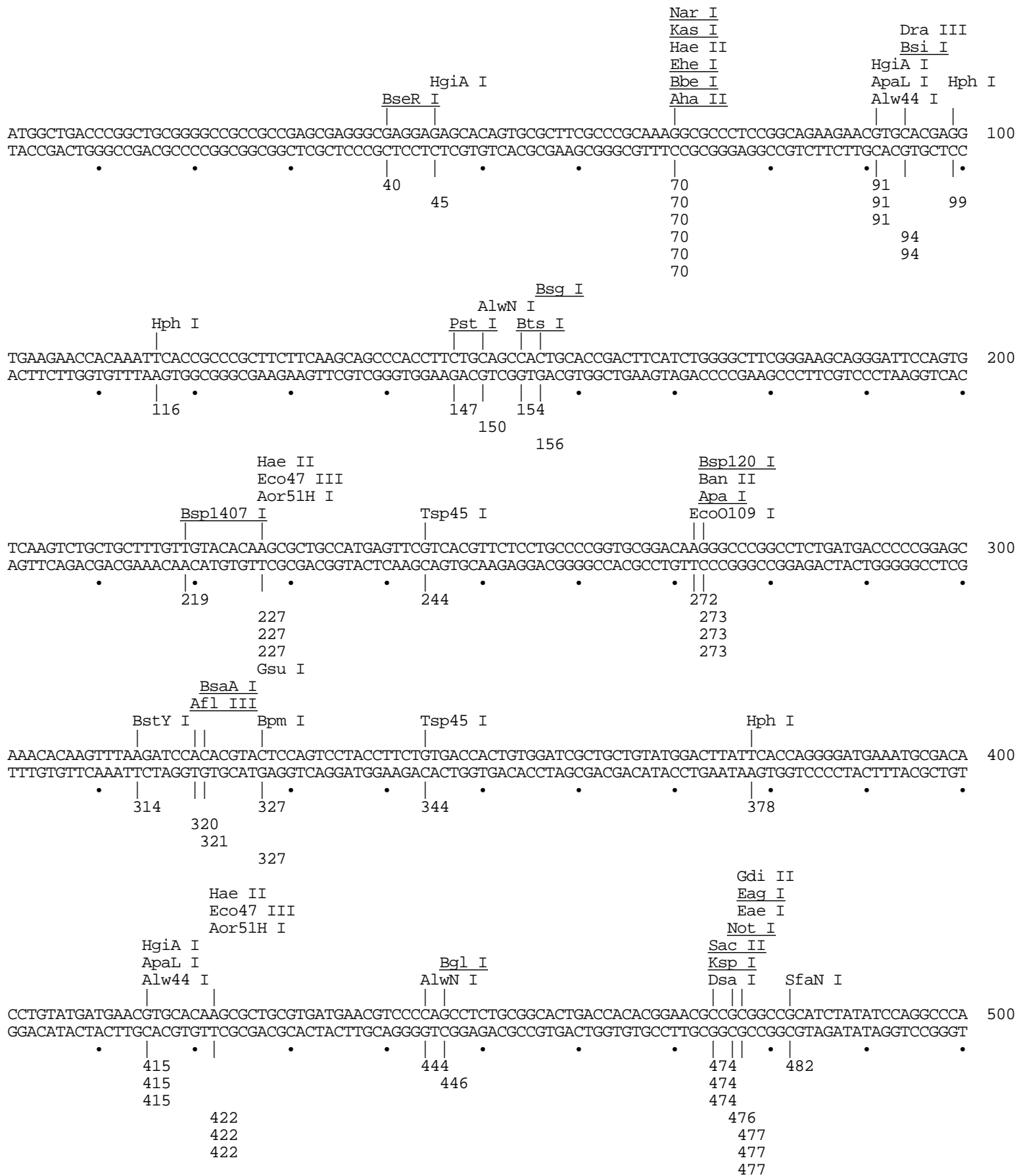
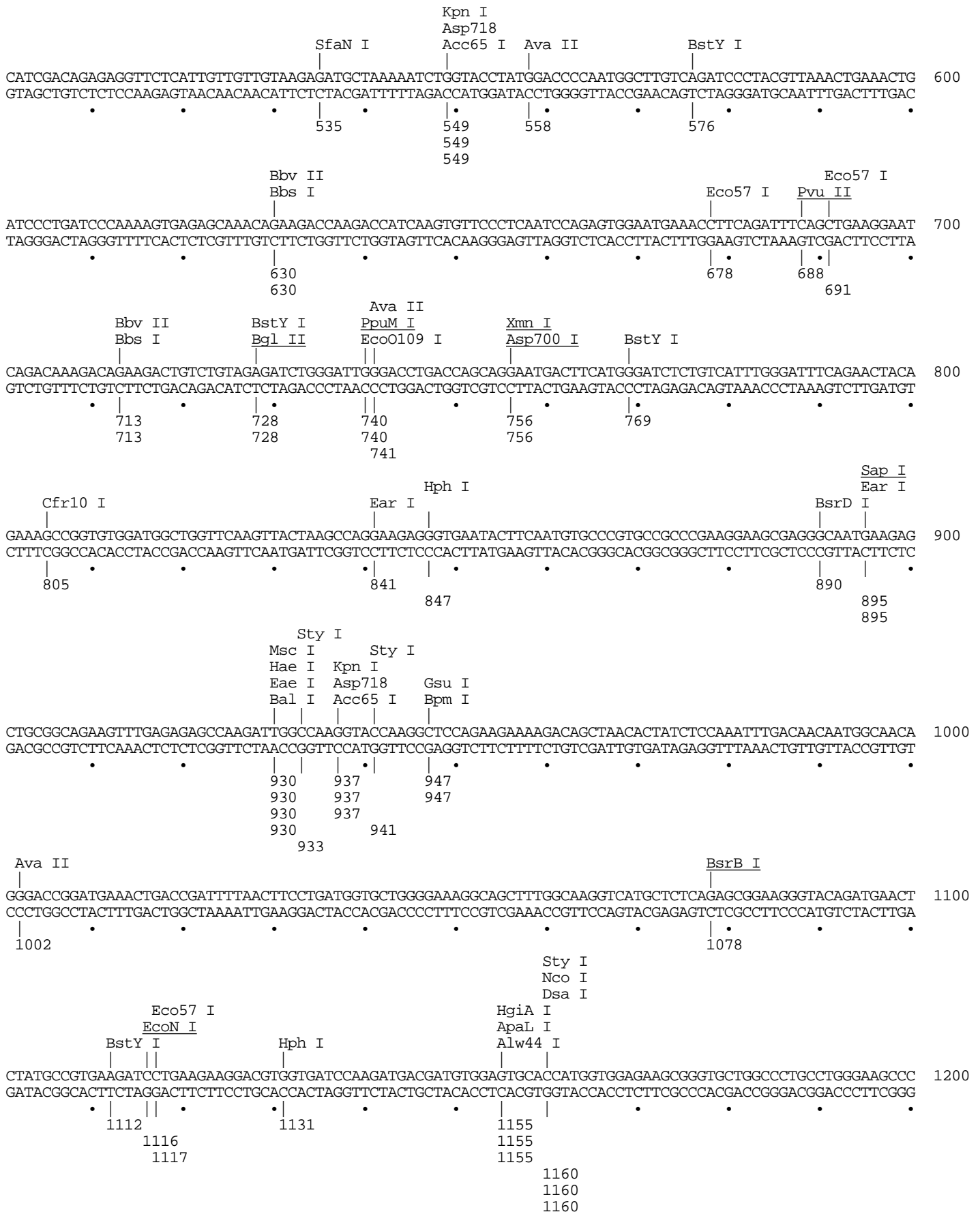


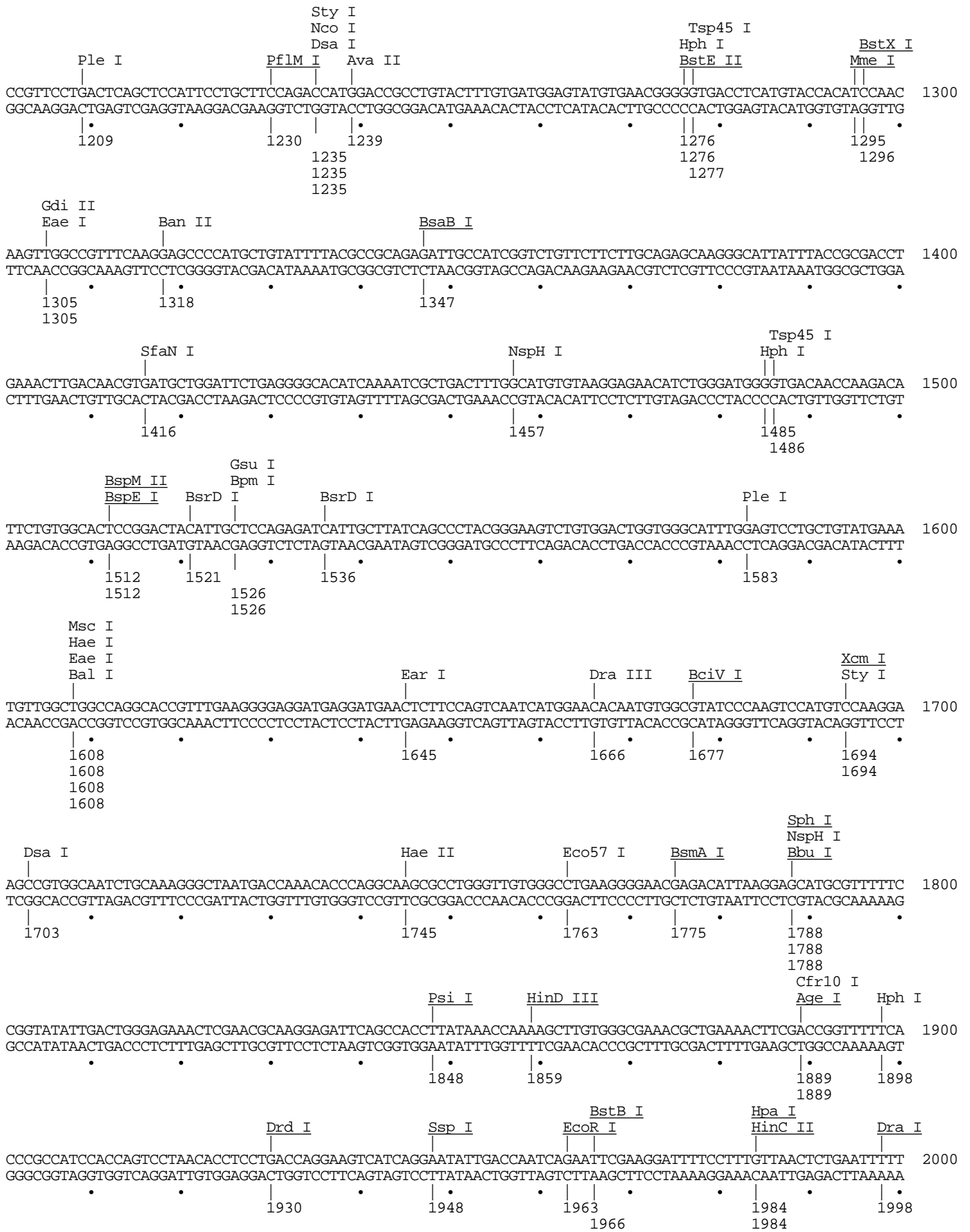
mPKCbeta2_ORF -> Full Restriction Map

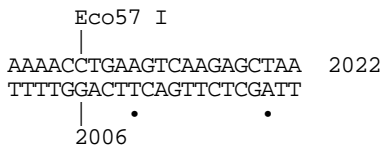
DNA sequence 2022 b.p. ATGGCTGACCCG ... GTCAAGAGCTAA linear

Positions of Restriction Endonucleases sites (unique sites underlined)









Restriction Endonucleases site usage

Aat I	-	Bbv II	2	BstY I	5	HinD III	1	Psp1406 I	-
Aat II	-	BciV I	1	BstZ17 I	-	Hpa I	1	Pst I	1
Acc65 I	2	Bcl I	-	Bsu36 I	-	Hph I	8	Pvu I	-
Acc I	-	Bfr I	-	Btr I	-	Kas I	1	Pvu II	1
Acl I	-	Bgl I	1	Bts I	1	Kpn I	2	Rsr II	-
Afl II	-	Bgl II	1	Cfr10 I	2	Ksp I	1	Sac I	-
Afl III	1	Bln I	-	Cla I	-	Mfe I	-	Sac II	1
Age I	1	Blp I	-	Dra I	1	Mlu I	-	Sal I	-
Aha II	1	Bpm I	3	Dra III	2	Mme I	1	Sap I	1
Ahd I	-	Bpull102 I	-	Drd I	1	Msc I	2	Sbf I	-
Alw44 I	3	Bsa I	-	Dsa I	4	Mun I	-	Sca I	-
AlwN I	2	BsaA I	1	Eae I	4	Nae I	-	SfaN I	3
Aor51H I	2	BsaB I	1	Eag I	1	Nar I	1	Sfi I	-
Apa I	1	BseR I	1	Ear I	3	Nco I	2	SgrA I	-
ApaL I	3	Bsg I	1	Ecl1136 II	-	Nde I	-	Sma I	-
Asc I	-	Bsi I	1	Eco47 III	2	NgoM I	-	SnaB I	-
Ase I	-	BsiW I	-	Eco57 I	5	Nhe I	-	Spe I	-
Asp700 I	1	Bsm I	-	EcoN I	1	Not I	1	Sph I	1
Asp718	2	BsmA I	1	EcoO109 I	2	Nru I	-	Spl I	-
AspE I	-	BsmB I	-	EcoR I	1	Nsi I	-	Srf I	-
Asp I	-	Bsp120 I	1	EcoR V	-	NspH I	2	Sse8387 I	-
Ava I	-	Bsp1407 I	1	Ehe I	1	Pac I	-	Ssp I	1
Ava II	4	BspE I	1	Esp3 I	-	Paer7 I	-	Stu I	-
Avi I	-	BspH I	-	Esp I	-	Pci I	-	Sty I	5
Avr II	-	BspM I	-	Fse I	-	PflF I	-	Swa I	-
Axy I	-	BspM II	1	Fsp I	-	PflM I	1	Tsp45 I	4
Bal I	2	BspLU11 I	-	Gdi II	2	Ple I	2	Tth111 I	-
BamH I	-	BsrB I	1	Gsu I	3	Pme I	-	Xba I	-
Ban II	2	BsrD I	3	Hae I	2	Pml I	-	Xca I	-
Ban III	-	BsrH II	-	Hae II	4	Ppu10 I	-	Xho I	-
Bbe I	1	Bst1107 I	-	Hga I	-	PpuM I	1	Xcm I	1
BbrP I	-	BstB I	1	HgiA I	4	PshA I	-	Xma I	-
Bbs I	2	BstE II	1	HgiE II	-	Psi I	1	Xmn I	1
Bbu I	1	BstX I	1	HinC II	1				

Enzyme Site Use Site position (Fragment length) Fragment order

Afl III	a/crygt	1	1(319) 2	320(1703) 1
Age I	a/ccggt	1	1(1888) 1	1889(134) 2
Aha II	gr/cgyc	1	1(69) 2	70(1953) 1
Apa I	gggcc/c	1	1(272) 2	273(1750) 1
Asp700 I	gaann/nmttc	1	1(755) 2	756(1267) 1
Bbe I	ggcgc/c	1	1(69) 2	70(1953) 1
Bbu I	gcatg/c	1	1(1787) 1	1788(235) 2
BciV I	gtatcc	6/5	1(1676) 1	1677(346) 2
Bgl I	gccnnm/nggc	1	1(445) 2	446(1577) 1
Bgl II	a/gatct	1	1(727) 2	728(1295) 1
BsaA I	yac/gtr	1	1(320) 2	321(1702) 1
BsaB I	gatnn/nnatc	1	1(1346) 1	1347(676) 2
BseR I	gaggag	10/8	1(39) 2	40(1983) 1
Bsg I	gtgcag	16/14	1(155) 2	156(1867) 1
Bsi I	ctcgtg	-5/-1	1(93) 2	94(1929) 1
BsmA I	gtctc	1/5	1(1774) 1	1775(248) 2
Bsp120 I	g/ggccc	1	1(272) 2	273(1750) 1
Bsp1407 I	t/gtaca	1	1(218) 2	219(1804) 1
BspE I	t/ccgga	1	1(1511) 1	1512(511) 2
BspM II	t/ccgga	1	1(1511) 1	1512(511) 2
BsrB I	gagcgg	-3/-3	1(1077) 1	1078(945) 2
BstB I	tt/cgaa	1	1(1965) 1	1966(57) 2
BstE II	g/gtnacc	1	1(1275) 1	1276(747) 2
BstX I	ccannmnn/ntgg	1	1(1295) 1	1296(727) 2
Bts I	gcagtg	2/0	1(153) 2	154(1869) 1
Dra I	ttt/aaa	1	1(1997) 1	1998(25) 2

Drd I	gacnnnn/nngtc	1	1(1929)	1	1930(93)	2		
Eag I	c/ggccg	1	1(476)	2	477(1546)	1		
EcoN I	cctnn/nnnagg	1	1(1115)	1	1116(907)	2		
EcoR I	g/aattc	1	1(1962)	1	1963(60)	2		
Ehe I	ggc/gcc	1	1(69)	2	70(1953)	1		
HinC II	gty/rac	1	1(1983)	1	1984(39)	2		
HinD III	a/agctt	1	1(1858)	1	1859(164)	2		
Hpa I	gtt/aac	1	1(1983)	1	1984(39)	2		
Kas I	g/gcgcc	1	1(69)	2	70(1953)	1		
Ksp I	ccgc/gg	1	1(473)	2	474(1549)	1		
Mme I	tccrac	20/18	1(1294)	1	1295(728)	2		
Nar I	gg/cgcc	1	1(69)	2	70(1953)	1		
Not I	gc/ggccc	1	1(475)	2	476(1547)	1		
PflM I	ccannnn/ntgg	1	1(1229)	1	1230(793)	2		
PpuM I	rg/gwccy	1	1(739)	2	740(1283)	1		
Psi I	tta/taa	1	1(1847)	1	1848(175)	2		
Pst I	ctgca/g	1	1(146)	2	147(1876)	1		
Pvu II	cag/ctg	1	1(687)	2	688(1335)	1		
Sac II	ccgc/gg	1	1(473)	2	474(1549)	1		
Sap I	gctcttc	1/4	1(894)	2	895(1128)	1		
Sph I	gcatg/c	1	1(1787)	1	1788(235)	2		
Ssp I	aat/att	1	1(1947)	1	1948(75)	2		
Xcm I	ccannnnn/nnntgg	1	1(1693)	1	1694(329)	2		
Xmn I	gaann/nnttc	1	1(755)	2	756(1267)	1		
Acc65 I	g/gtacc	2	1(548)	2	549(388)	3	937(1086)	1
AlwN I	cagnnn/ctg	2	1(149)	3	150(294)	2	444(1579)	1
Aor51H I	agc/gct	2	1(226)	2	227(195)	3	422(1601)	1
Asp718	g/gtacc	2	1(548)	2	549(388)	3	937(1086)	1
Bal I	tgg/cca	2	1(929)	1	930(678)	2	1608(415)	3
Ban II	grgcy/c	2	1(272)	3	273(1045)	1	1318(705)	2
Bbs I	gaagac	2/6	1(629)	2	630(83)	3	713(1310)	1
Bbv II	gaagac	2/6	1(629)	2	630(83)	3	713(1310)	1
Cfr10 I	r/ccggy	2	1(804)	2	805(1084)	1	1889(134)	3
Dra III	cacnnn/gtg	2	1(93)	3	94(1572)	1	1666(357)	2
Eco47 III	agc/gct	2	1(226)	2	227(195)	3	422(1601)	1
EcoO109 I	rg/gnccy	2	1(271)	3	272(468)	2	740(1283)	1
Gdi II	yggccg	-5/-1	1(476)	3	477(828)	1	1305(718)	2
Hae I	wgg/ccw	2	1(929)	1	930(678)	2	1608(415)	3
Kpn I	ggtac/c	2	1(548)	2	549(388)	3	937(1086)	1
Msc I	tgg/cca	2	1(929)	1	930(678)	2	1608(415)	3
Nco I	c/catgg	2	1(1159)	1	1160(75)	3	1235(788)	2
NspH I	rcatg/y	2	1(1456)	1	1457(331)	2	1788(235)	3
Ple I	gagtc	4/5	1(1208)	1	1209(374)	3	1583(440)	2
Alw44 I	g/tgcac	3	1(90)	4	91(324)	3	415(740)	2
			1155(868)	1				
ApaL I	g/tgcac	3	1(90)	4	91(324)	3	415(740)	2
			1155(868)	1				
Bpm I	ctggag	16/14	1(326)	4	327(620)	1	947(579)	2
			1526(497)	3				
BsrD I	gcaatg	2/0	1(889)	1	890(631)	2	1521(15)	4
			1536(487)	3				
Ear I	ctcttc	1/4	1(840)	1	841(54)	4	895(750)	2
			1645(378)	3				
Gsu I	ctggag	16/14	1(326)	4	327(620)	1	947(579)	2
			1526(497)	3				
SfaN I	gcatc	5/9	1(481)	3	482(53)	4	535(881)	1
			1416(607)	2				
Ava II	g/gwcc	4	1(557)	2	558(183)	5	741(261)	3
			1002(237)	4	1239(784)	1		
Dsa I	c/crygg	4	1(473)	2	474(686)	1	1160(75)	5
			1235(468)	3	1703(320)	4		
Eae I	y/ggccr	4	1(476)	1	477(453)	2	930(375)	4
			1305(303)	5	1608(415)	3		
Hae II	rgcgc/y	4	1(69)	5	70(157)	4	227(195)	3
			422(1323)	1	1745(278)	2		
HgiA I	gwgcw/c	4	1(44)	5	45(46)	4	91(324)	3
			415(740)	2	1155(868)	1		
Tsp45 I	/gtsac	4	1(243)	3	244(100)	5	344(933)	1
			1277(209)	4	1486(537)	2		
BstY I	r/gatcy	5	1(313)	3	314(262)	4	576(152)	5
			728(41)	6	769(343)	2	1112(911)	1
Eco57 I	ctgaag	16/14	1(677)	1	678(13)	6	691(426)	3
			1117(646)	2	1763(243)	4	2006(17)	5
Sty I	c/cwggg	5	1(932)	1	933(8)	6	941(219)	4

				1160(75) 5	1235(459) 2	1694(329) 3
Hph I	ggtga	8/7	8	1(98) 8	99(17) 9	116(262) 4
				378(469) 1	847(284) 3	1131(145) 6
				1276(209) 5	1485(413) 2	1898(125) 7

156 sites found

No Sites found for the following Restriction Endonucleases

Aat I	agg/cct	BspLU11 I	a/catgt	PflF I	gacn/nngtc
Aat II	gacgt/c	BssH II	g/cgctc	Pme I	gttt/aaac
Acc I	gt/mkac	Bst1107 I	gta/tac	Pml I	cac/gtg
Acl I	aa/cggt	BstZ17 I	gta/tac	Ppu10 I	a/tgcat
Afl II	c/ttaag	Bsu36 I	cc/tnagg	PshA I	gacnn/nngtc
Ahd I	gacnnn/nngtc	Btr I	cac/gtc	Psp1406 I	aa/cggt
Asc I	gg/cgctc	Cla I	at/cgat	Pvu I	cgat/cg
Ase I	at/taat	Ecl136 II	gag/ctc	Rsr II	cg/gwccg
AspE I	gacnnn/nngtc	EcoR V	gat/atc	Sac I	gagct/c
Asp I	gacn/nngtc	Esp3 I	cgtctc 1/5	Sal I	g/tcgac
Ava I	c/ycgrg	Esp I	gc/tnagc	Sbf I	cctgca/gg
Avi I	tgc/gca	Fse I	ggccgg/cc	Sca I	agt/act
Avr II	c/ctagg	Fsp I	tgc/gca	Sfi I	ggccnnnn/nggcc
Axy I	cc/tnagg	Hga I	gacgc 5/10	SgrA I	cr/ccggyg
BamH I	g/gatcc	HgiE II	accnnnnnnggt	Sma I	ccc/ggg
Ban III	at/cgat	Mfe I	c/aattg	SnaB I	tac/gta
BbrP I	cac/gtg	Mlu I	a/cgctg	Spe I	a/ctagt
Bcl I	t/gatca	Mun I	c/aattg	Spl I	c/gtacg
Bfr I	c/ttaag	Nae I	gcc/ggc	Srf I	gccc/gggc
Bln I	c/ctagg	Nde I	ca/tatg	Sse8387 I	cctgca/gg
Blp I	gc/tnagc	NgoM I	g/ccggc	Stu I	agg/cct
Bpu1102 I	gc/tnagc	Nhe I	g/ctagc	Swa I	attt/aaat
Bsa I	ggtctc 1/5	Nru I	tcg/cga	Tth111 I	gacn/nngtc
BsiW I	c/gtacg	Nsi I	atgca/t	Xba I	t/ctaga
Bsm I	gaatgc 1/-1	Pac I	ttaat/taa	Xca I	gta/tac
BsmB I	cgtctc 1/5	Paer7 I	c/tcgag	Xho I	c/tcgag
BspH I	t/catga	Pci I	a/catgt	Xma I	c/ccggg
BspM I	acctgc 4/8				