Vector: pMOK

Antibiotic Selection: Kan

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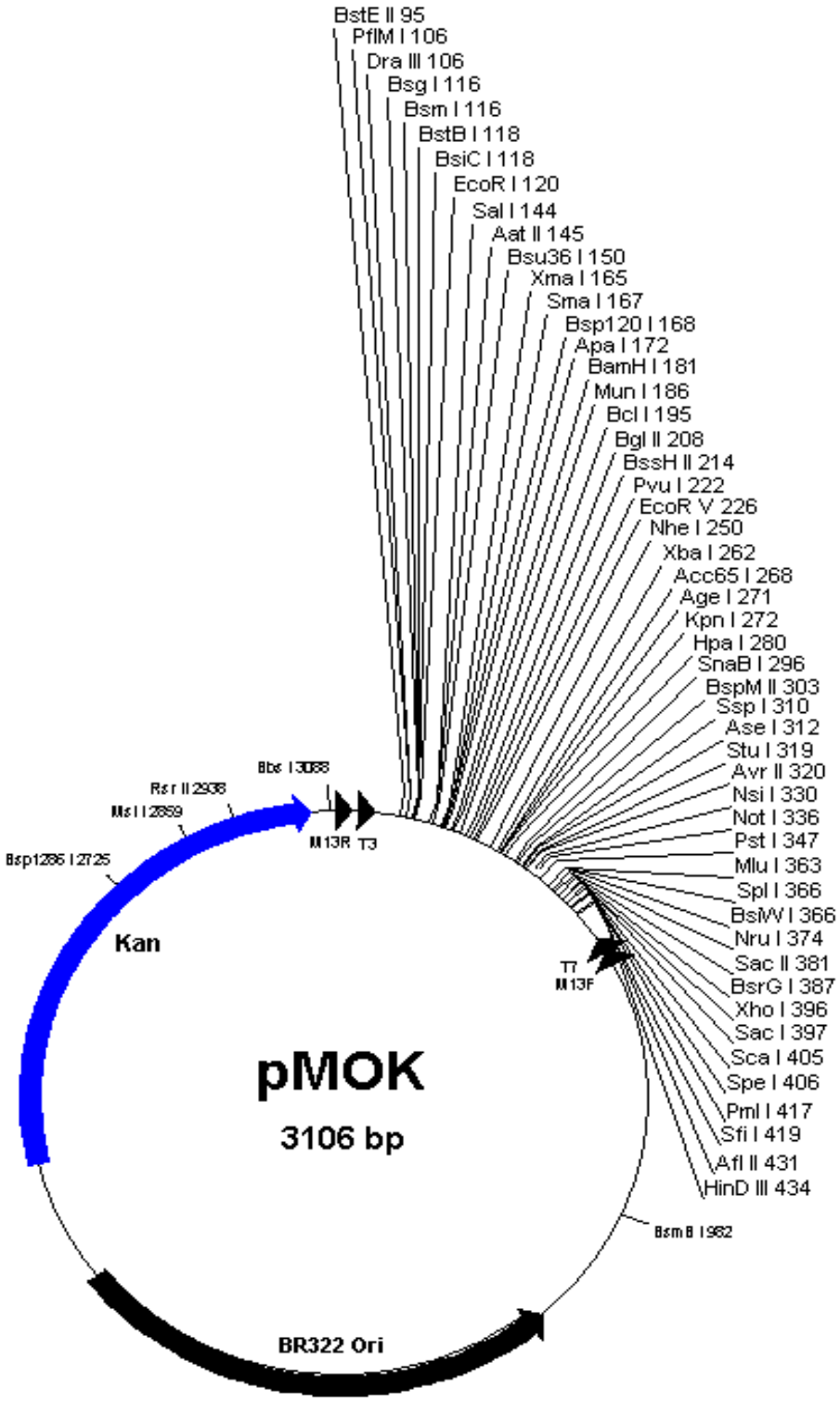
Date of Construction: June, 2006 (updated by Zongyue Zeng @ Nov 12, 2017)



pMOK Vector Full-Length Sequence

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTACCCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTGG
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ATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTG
GATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT
TGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTT
CTTGACGAGTTCTTCTGACCTTTCGTCTTCAAGaatt

Unique enzymes in pMOK:

BstE II	G`GTNAC,C	95
PflM I	CCAN,NNN`NTGG	106
Dra III	CAC,NNN`GTG	106
Bsm I	GAATG,C 7	116
Bsg I	GTGCAG 22/20	116
BsiC I	TT`CG,AA	118
BstB I	TT`CG,AA	118
EcoR I	G`AATT,C	120
Sal I	G`TCGA,C	144
Aat II	G,ACGT`C	145
Bsu36 I	CC`TNA,GG	150
PspA I	C`CCGG,G	165
Xma I	C`CCGG,G	165
Sma I	CCC|GGG	167
Bsp120 I	G`GGCC,C	168
EcoO109 I	RG`GNC,CY	169
Apa I	G,GGCC`C	172
BamH I	G`GATC,C	181
Mun I	C`AATT,G	186
Bcl I	T`GATC,A	195
Bgl II	A`GATC,T	208
BssH II	G`CGCG,C	214
Pvu I	CG,AT`CG	222
EcoR V	GAT|ATC	226
Nhe I	G`CTAG,C	250
Xba I	T`CTAG,A	262
Acc65 I	G`GTAC,C	268
Asp718	G`GTAC,C	268
Age I	A`CCGG,T	271
Kpn I	G,GTAC`C	272
Hpa I	GTT|AAC	280
SnaB I	TAC|GTA	296
BspM II	T`CCGG,A	303
Ssp I	AAT|ATT	310
Ase I	AT`TA,AT	312
Vsp I	AT`TA,AT	312
Stu I	AGG|CCT	319
Avr II	C`CTAG,G	320
Nsi I	A,TGCA`T	330
Not I	GC`GGCC,GC	336
Pst I	C,TGCA`G	347
Mlu I	A`CGCG,T	363
BsiW I	C`GTAC,G	366
Spl I	C`GTAC,G	366
Nru I	TCG|CGA	374
Sac II	CC,GC`GG	381
BsrG I	T`GTAC,A	387
PaeR7 I	C`TCGA,G	396
Xho I	C`TCGA,G	396
Sac I	G,AGCT`C	397
Sca I	AGT|ACT	405
Spe I	A`CTAG,T	406
Eco72 I	CAC|GTG	417
Pml I	CAC|GTG	417
Sfi I	GGCCN,NNN`NGGCC	419
Bgl I	GCCN,NNN`NGGC	419
Afl II	C`TTAA,G	431
HinD III	A`AGCT,T	434
BsmB I	CGTCTC 7/11	982
Bsp1286 I	G,DGCH`C	2725
Msl I	CAYNN|NNRTG	2859
Rsr II	CG`GWC,CG	2938

Bbs I	GAAGAC 8/12	3088			
Bbv II	GAAGAC 7/11	3089			

Number of enzymes = 64

The following enzymes do not cut in pMOK:

Asc I	Blp I	Bsa I	BseR I	BstX I
EcoN I	Esp I	Fse I	Pac I	Pme I

pMOK: sites sorted by name:

Aat II	(1)	145			
Acc I	(3)	145	298	1111	
Acc65 I	(1)	268			
Aci I	(44)	335	339	378	380
		630	633	644	800
		816	871	927	1012
		1051	1061	1103	1128
		1166	1179	1205	1222
		1265	1272	1293	1384
		1412	1539	1558	1679
		1789	1924	1933	2252
		2331	2394	2488	2552
		2653	2656	2896	2936
		2941	2991	3007	3033
Afl II	(1)	431			
Afl III	(3)	363	384	1339	
Age I	(1)	271			
Aha II	(3)	142	352	2422	
Ahd I	(2)	2232	3092		
Alu I	(20)	9	31	64	254
		348	395	436	477
		864	921	932	981
		1000	1281	1507	1597
		1643	1900	2528	2986
Alw I	(11)	177	188	540	1901
		1987	1987	2084	2085
		2600	2667	2846	
AlwN I	(2)	130	1755		
Apa I	(1)	172			
ApaL I	(3)	425	1155	1653	
Apo I	(2)	120	238		
Ase I	(1)	312			
Asp718	(1)	268			
Ava I	(2)	165	396		
Ava II	(2)	626	2938		
Avr II	(1)	320			
BamH I	(1)	181			
Ban I	(5)	268	351	2180	2421
		2456			
Ban II	(3)	172	397	2787	
Bbe I	(2)	355	2425		
Bbs I	(1)	3088			
Bbv I	(10)	357	941	990	1087
		1758	1761	1967	2495
		2537	3058		
Bbv II	(1)	3089			
Bcl I	(1)	195			
Bcn I	(9)	167	168	532	680
		986	1021	1720	2427
		2587			
Bfa I	(6)	251	263	321	407
		1834	2087		
Bgl I	(1)	419			
Bgl II	(1)	208			
Bpm I	(2)	102	868		
BsaA I	(4)	296	417	1093	2726
BsaB I	(2)	224	538		
BsaH I	(3)	142	352	2422	
BsaJ I	(7)	87	165	320	378
		1499	2585	2854	
BsaW I	(5)	271	303	1545	1692
		2453			
Bsg I	(1)	116			
BsiC I	(1)	118			
BsiE I	(6)	222	339	378	1255
		1679	2331		
BsiHKA I	(6)	397	429	1159	1657
		2535	2725		
BsiW I	(1)	366			
Bsm I	(1)	116			
BsmA I	(2)	983	2255		
BsmB I	(1)	982			
BsmF I	(3)	153	612	2573	
BsoF I	(33)	336	339	346	552
		633	930	933	979
		1076	1129	1245	1263
		1266	1384	1539	1682
		1747	1750	1956	2331
		2383	2394	2484	2489
		2526	2567	2654	2657
		2660	2896	2992	3033
		3047			
Bsp120 I	(1)	168			
Bsp1286 I	(1)	2725			
BspH I	(3)	201	2059	2256	
BspM I	(3)	138	2309	2690	
BspM II	(1)	303			
Bsr I	(10)	518	648	672	1087
		1118	1746	1759	1873
		2365	2566		
BsrB I	(3)	1272	2254	3035	
BsrD I	(2)	198	2655		
BsrG I	(1)	387			
BssH II	(1)	214			
BssS I	(2)	1512	3014		
Bst1107 I	(2)	299	1112		
BstB I	(1)	118			
BstE II	(1)	95			
BstN I	(4)	1367	1488	1501	2809
BstU I	(13)	216	218	365	374
		380	871	940	942
		1045	1386	1967	2488
		2789			
BstY I	(9)	181	208	533	1980
		1991	2077	2089	2593
		2839			
Bsu36 I	(1)	150			
Cac8 I	(24)	216	248	252	290
		343	350	438	556
		598	816	1270	1356
		1393	1953	2316	2502
		2721	2787	2793	2821
		2825	2866	2870	2924
Cfr10 I	(4)	271	288	2741	2922
Cla I	(2)	222	358		
Csp6 I	(7)	68	269	367	388
		404	1146	2727	
Dde I	(6)	150	609	1149	1614
		2023	2189		
Dpn I	(17)	183	197	210	221
		535	1907	1982	1993
		2001	2079	2091	2196
		2595	2673	2754	2763
		2841			
DpnII	(17)	181	195	208	219
		533	1905	1980	1991
		1999	2077	2089	2194
		2593	2671	2752	2761
		2839			
Dra I	(3)	237	2098	2117	
Dra III	(1)	106			
Drd I	(3)	1034	1447	2449	
Dsa I	(3)	87	378	2854	
Eae I	(7)	336	411	516	2328
		2502	2893	2920	
Eag I	(2)	336	2328		
Ear I	(3)	1223	2766	2976	
Eco47 III	(2)	232	595		
Eco57 I	(3)	1886	2567	2999	
Eco72 I	(1)	417			
EcoO109 I	(1)	169			
EcoR I	(1)	120			
EcoR II	(4)	1365	1486	1499	2807
EcoR V	(1)	226			
Ehe I	(2)	353	2423		
Fnu4H I	(33)	336	339	346	552
		633	930	933	979
		1076	1129	1245	1263
		1266	1384	1539	1682
		1747	1750	1956	2331
		2383	2394	2484	2489
		2526	2567	2654	2657
		2660	2896	2992	3033
		3047			
Fok I	(9)	337	560	622	700
		886	1027	2198	2746
		2771			
Fsp I	(2)	245	2524		
Gdi II	(7)	335	337	515	2327
		2329	2892	2919	
Gsu I	(2)	101	867		
Hae I	(6)	319	413	1354	1365
		1817	2504		
Hae II	(6)	234	355	597	1217
		1587	2425		
Hae III	(15)	170	319	338	413
		422	518	814	1354
		1365	1383	1817	2330
		2504	2895	2922	
Hga I	(4)	876	1035	1449	2027
HgiA I	(6)	397	429	1159	1657
		2535	2725		
HgiE II	(2)	1157	1918		
Hha I	(22)	216	218	233	246
		354	596	942	1045
		1075	1216	1249	1519
		1586	1686	1860	1969
		2416	2424	2488	2525
		2791	3051		
HinC II	(2)	146	280		
Hind II	(2)	146	280		
HinD III	(1)	434			
Hinf I	(8)	497	895	1239	1314
		1710	2227	2907	3041
HinI I	(3)	142	352	2422	
HinP I	(22)	214	216	231	244
		352	594	940	1043
		1073	1214	1247	1517
		1584	1684	1858	1967
		2414	2422	2486	2523
		2789	3049		
Hpa I	(1)	280			
Hpa II	(20)	166	272	289	304

		531	678	985	1019
		1546	1693	1719	1909
		2327	2404	2426	2454
		2585	2675	2742	2923
Hph I	(5)	106	960	969	2076
		2601			
Kas I	(2)	351	2421		
Kpn I	(1)	272			
Mae I	(6)	251	263	321	407
		1834	2087		
Mae II	(11)	102	142	282	295
		369	416	666	1092
		2042	2538	2725	
Mae III	(12)	95	673	696	780
		993	1088	1695	1758
		1874	2157	2542	2848
Mbo I	(17)	181	195	208	219
		533	1905	1980	1991
		1999	2077	2089	2194
		2593	2671	2752	2761
		2839			
Mbo II	(7)	1211	2000	2073	2782
		2992	3074	3089	
Mlu I	(1)	363			
Mme I	(2)	1553	1737		
Mnl I	(18)	53	65	145	259
		668	726	765	945
		975	1237	1447	1520
		1771	2171	2337	2473
		2830	3022		
Msc I	(2)	413	2504		
Mse I	(14)	39	236	279	312
		432	586	806	838
		1120	2045	2097	2102
		2116	2169		
Msl I	(1)	2859			
Msp I	(20)	166	272	289	304
		531	678	985	1019
		1546	1693	1719	1909
		2327	2404	2426	2454
		2585	2675	2742	2923
MspA1 I	(7)	348	380	932	1051
		1681	1926	2528	
Mun I	(1)	186			
Nae I	(2)	290	2924		
Nar I	(2)	352	2422		
Nci I	(9)	166	167	531	679
		985	1020	1719	2426
		2586			
Nco I	(2)	87	2854		
Nde I	(2)	330	1162		
NgoM I	(2)	288	2922		
Nhe I	(1)	250			
Nla III	(19)	20	91	139	205
		250	388	466	686
		750	813	978	1083
		1343	2063	2260	2641
		2827	2858	2884	
Nla IV	(11)	85	170	183	270
		353	628	1371	1410
		2182	2423	2458	
Not I	(1)	336			
Nru I	(1)	374			
Nsi I	(1)	330			
Nsp7524 I	(6)	246	384	682	974
		1339	2823		
NspB II	(7)	348	380	932	1051
		1681	1926	2528	
NspH I	(6)	250	388	686	978
		1343	2827		
PaeR7 I	(1)	396			
Pal I	(15)	170	319	338	413
		422	518	814	1354
		1365	1383	1817	2330
		2504	2895	2922	
PflM I	(1)	106			
Ple I	(2)	505	1718		
Pml I	(1)	417			
Psp1406 I	(2)	282	666		
PspA I	(1)	165			
Pst I	(1)	347			
Pvu I	(1)	222			
Pvu II	(3)	348	932	2528	
Rsa I	(7)	69	270	368	389
		405	1147	2728	
Rsr II	(1)	2938			
Sac I	(1)	397			
Sac II	(1)	381			
Sal I	(1)	144			
Sap I	(3)	1223	2766	2976	
Sau3A I	(17)	181	195	208	219
		533	1905	1980	1991
		1999	2077	2089	2194
		2593	2671	2752	2761
		2839			
Sau96 I	(6)	168	169	420	626
		813	2938		
Sca I	(1)	405			
ScrF I	(13)	166	167	531	679
		985	1020	1367	1488
		1501	1719	2426	2586
		2809			
Sec I	(7)	87	165	320	378
		1499	2585	2854	
SfaN I	(17)	316	539	547	643
		721	783	1006	1139
		1177	1215	1435	2381
		2636	2720	2784	2852
		3059			
Sfc I	(5)	255	343	490	1604
		1795			
Sfi I	(1)	419			
Sma I	(1)	167			
SnaB I	(1)	296			
Spe I	(1)	406			
Sph I	(2)	250	2827		
Spl I	(1)	366			
Ssp I	(1)	310			
Stu I	(1)	319			
Sty I	(3)	87	320	2854	
Taq I	(12)	33	118	145	222
		358	397	1439	2535
		2691	2715	2751	2913
Tfi I	(4)	895	1314	2907	3041
Tsp45 I	(6)	95	780	993	1088
		2542	2848		
Tth111 I	(3)	101	1086	2540	
Tth111 II	(5)	801	1928	1937	1967
		2858			
Vsp I	(1)	312			
Xba I	(1)	262			
Xca I	(2)	299	1112		
Xho I	(1)	396			
Xho II	(9)	181	208	533	1980
		1991	2077	2089	2593
		2839			
Xma I	(1)	165			
Xma III	(2)	336	2328		
Xmn I	(2)	114	899		

Site usage in pMOK:

Aat II	G,ACGT`C	1	Acc I	GT`MK,AC	3
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	44
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	3
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	3
Ahd I	GACNN,N`NNGTC	2	Alu I	AG|CT	20
Alw I	GGATC 8/9	11	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	2	Ava II	G`GWC,C	2
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	5	Ban II	G,RGCY`C	3
Bbe I	G,GCGC`C	2	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	9
Bfa I	C`TA,G	6	Bgl I	GCCN,NNN`NGGC	1
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	-
BsaA I	YAC|GTR	4	BsaB I	GATNN|NNATC	2
BsaH I	GR`CG,YC	3	BsaJ I	C`CNNG,G	7
BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	-
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	6	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	1
BsmA I	GTCTC`/9	2	BsmB I	CGTCTC 7/11	1
BsmF I	GGGAC 15/19	3	BsoF I	GC`N,GC	33
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	3
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	10
BsrB I	GAG|CGG	3	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	1
BssS I	C`TCGT,G	2	Bst1107 I	GTA|TAC	2
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	4	BstU I	CG|CG	13
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN|NGC	24
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	2
Csp6 I	G`TA,C	7	Dde I	C`TNA,G	6
Dpn I	GA|TC	17	DpnII	`GATC,	17
Dra I	TTT|AAA	3	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3
Eae I	Y`GGCC,R	7	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC|GCT	2
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC|GTG	1
EcoN I	CCTNN`N,NNAGG	-	Eco0109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	4
EcoR V	GAT|ATC	1	Ehe I	GGC|GCC	2
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	33
Fok I	GGATG 14/18	9	Fse I	GG,CCGG`CC	-
Fsp I	TGC|GCA	2	Gdi II	`YGGC,CG	7
Gsu I	CTGGAG 21/19	2	Hae I	WGG|CCW	6
Hae II	R,GCGC`Y	6	Hae III	GG|CC	15
Hga I	GACGC 9/14	4	HgiA I	G,WGCW`C	6
HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	22
HinC II	GTY|RAC	2	Hind II	GTY|RAC	2
HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	8
HinI I	GR`CG,YC	3	HinP I	G`CG,C	22
Hpa I	GTT|AAC	1	Hpa II	C`CG,G	20
Hph I	GGTGA 12/11	5	Kas I	G`GCGC,C	2
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	6
Mae II	A`CG,T	11	Mae III	`GTNAC,	12
Mbo I	`GATC,	17	Mbo II	GAAGA 12/11	7

Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	2	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	1
Mnl I	CCTC 10/10	18	Msc I	TGG|CCA	2	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Mse I	T`TA,A	14	Msl I	CAYNN|NNRTG	1	Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	17
Msp I	C`CG,G	20	MspA1 I	CMG|CKG	7	Sau96 I	G`GNC,C	6	Sca I	AGT|ACT	1
Mun I	C`AATT,G	1	Nae I	GCC|GGC	2	ScrF I	CC`N,GG	13	Sec I	C`CNNG,G	7
Nar I	GG`CG,CC	2	Nci I	CC`S,GG	9	SfaN I	GCATC 9/13	17	Sfc I	C`TRYA,G	5
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC|GGG	1
NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	1	SnaB I	TAC|GTA	1	Spe I	A`CTAG,T	1
Nla III	,CATG`	19	Nla IV	GGN|NCC	11	Sph I	G,CATG`C	2	Spl I	C`GTAC,G	1
Not I	GC`GGCC,GC	1	Nru I	TCG|CGA	1	Srf I	GCCC|GGGC	-	Ssp I	AAT|ATT	1
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	6	Stu I	AGG|CCT	1	Sty I	C`CWWG,G	3
NspB II	CMG|CKG	7	NspH I	R,CATG`Y	6	Taq I	T`CG,A	12	Tfi I	G`AWT,C	4
Pac I	TTA,AT`TAA	-	PaeR7 I	C`TCGA,G	1	Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	3
Pal I	GG|CC	15	PflM I	CCAN,NNN`NTGG	1	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
Ple I	GAGTC 9/10	2	Pme I	CTTT|AAAC	-	Xba I	T`CTAG,A	1	Xca I	GTA|TAC	2
Pml I	CAC|GTG	1	PpuM I	RG`GWC,CY	-	Xcm I	CCANNNN,N`NNNNTGG	-	Xho I	C`TCGA,G	1
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	1	Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	1
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1	Xma III	C`GGCC,G	2	Xmn I	GAANN|NNTTC	2
Pvu II	CAG|CTG	3	Rsa I	GT|AC	7						