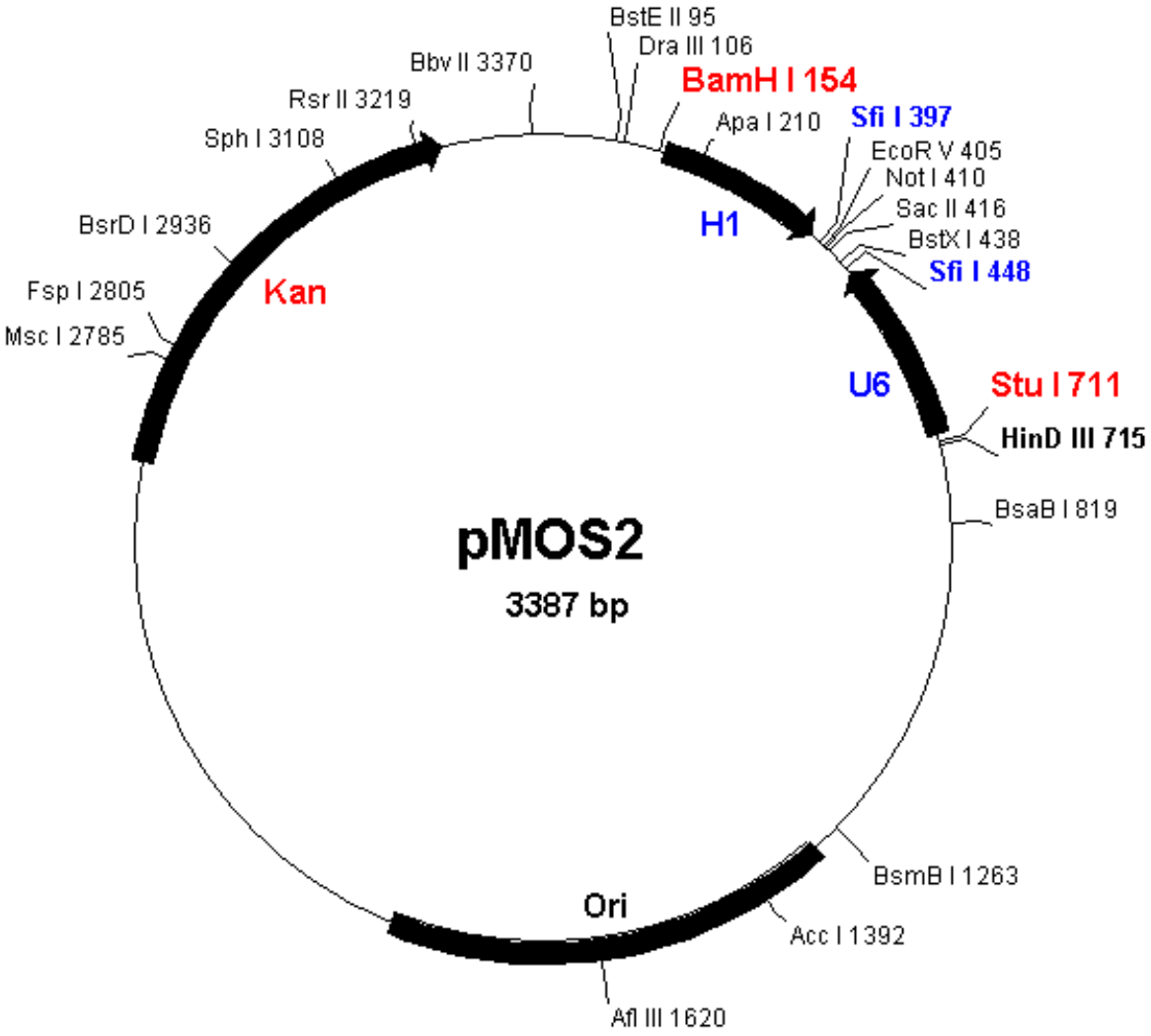
Vector: **pMOS2** (for stepwise cloning of pMPBOS knockdown vector)

Antibiotic Selection: Kan

Creator(s): **Chen Zhao, MD**, Molecular Oncology Lab of University of Chicago Medical Center

Date of Construction: March 2012



Sfi I Site Stuffer and siRNA Cassette Design:

```
                    EcoRV  Not I      M13Rev     BstX I
H1>>> ggccaaaacGGCCgatatcGCGGCCGCggaaacagctatgaCCAtgacgcTGGCCgttttggcc
      ccggttttgCCGGctatagcgccggcgcctttgtcgatactggtactgcgaccggcaaaaccgg <<<U6
```

Sfi I Digestion

5′-GGCCAAAA	A(n19-27nt)TTTT	TGGCC-3′
3′-CCGGT	TTTT(n19-27nt)A	AAAACCGG-5′

pMOS2 Full-Length Sequence

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTG
GAGCCATGGCTGGTGACCACGTCGTGGAATGCCTTCGaattAATTCAGCACCTGCACATGGGACGTCGAgGGATCCagctta
attcgaacgctgacgtcatcaacccgctccaaggaatcgcgggcccagtgtcactaggcgggaacacccagcgcgcgtgcgc
cctggcaggaagatggctgtgagggacaggggagtggcgccctgcaatatttgcatgtcgctatgtgttctgggaaatcacc
ataaacgtgaaatgtctttggatttgggaatcttataagttctgtatgagaccacagatcggccaaaacggccgatatcGCG
GCCGCggaaacagctatgaCCAtgacgcTggccgttttggcctcctttccacaagatatataaagccaagaaatcgaaatac
tttcaagttacggtaagcatatgatagtccattttaaaacataatttaaaactgcaaactacccaagaaattattactttc
tacgtcacgtattttgtactaatatctttgtgtttacagtcaaattaattctaattatctctctaacagccttgtatcgtat
atgcaaatatgaaggaatcatgggaaataggccctcttcctgcccgaccttAGGCCTAAGCTTGCCTAATCGGACGAAAAAA
TGACCATGATTACGCCAAGCTCCAATTCGCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTTACCCGGATCTGC
ATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCTACATCTGTATTAACGAAGCGCTGGCATTGACCCTGAGTGATTTTTC
TCTGGTCCCGCCGCATCCATACCGCCAGTTGTTTACCCTCACAACGTTCCAGTAACCGGGCATGTTCATCATCAGTAACCCG
TATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACCCCCATGAACAGAAATCCCCCTTACACGGAGGCATCAGTGACC
AAACAGGAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAACTCAACGAGCTGG
ACGCGGATGAACAGGCAGACATCTGTGAATCGCTTCACGACCACGCTGATGAGCTTTACCGCAGCTGCCTCGCGCGTTTCGG
TGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAA
GCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATA
CTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGG
AGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTAT
CAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA
AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGA
CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC
CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG
TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC
TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTA
GCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGG
TATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGC
GGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT
CTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT
AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAG
GCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCCATTCAAATATGTATCCGCTCATGAG
ACAATAACCCTGATAAATGCTTCAATAATATATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAG
AGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCC
CGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCAC
GACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTG
ATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGA
TCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGC
GAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACT
GTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATG
GGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTC
TTCTGAACCTTTCGTCTTCAAGaatt

Unique enzymes in pMOS2:

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	120
BamH I	G`GATC,C	154
Bsp120 I	G`GGCC,C	206
Apa I	G,GGCC`C	210
BssH II	G`CGCG,C	236
Ssp I	AAT|ATT	295
Bsa I	GGTCTC 7/11	371
EcoR V	GAT|ATC	405
Not I	GC`GGCC,GC	410
Sac II	CC,GC`GG	416
BstX I	CCAN,NNNN`NTGG	438
EcoO109 I	RG`GNC,CY	687
Bsu36 I	CC`TNA,GG	706
Stu I	AGG|CCT	711
HinD III	A`AGCT,T	715
BsaB I	GATNN|NNATC	819
Eco47 III	AGC|GCT	876
Psp1406 I	AA`CG,TT	947
BsmB I	CGTCTC 7/11	1263
Acc I	GT`MK,AC	1392
Bst1107 I	GTA|TAC	1393
Xca I	GTA|TAC	1393
Afl III	A`CRYG,T	1620
Msc I	TGG|CCA	2785
Fsp I	TGC|GCA	2805
BsrD I	GCAATG, 8	2936
Bsp1286 I	G,DGCH`C	3006
Sph I	G,CATG`C	3108
NgoM I	G`CCGG,C	3203
Nae I	GCC|GGC	3205
Rsr II	CG`GWC,CG	3219
Bbs I	GAAGAC 8/12	3369
Bbv II	GAAGAC 7/11	3370

Number of enzymes = 37

The following enzymes do not cut in pMOS2:

Acc65 I	Afl II	Age I	Apo I	Asc I
Asp718	Ava I	Avr II	Bcl I	Bgl II
Blp I	BseR I	BsiW I	BspM II	BsrG I
Cla I	Eco72 I	EcoN I	EcoR I	Esp I
Fse I	HinC II	Hind II	Hpa I	Kpn I
Mlu I	Mun I	Nhe I	Nru I	Nsi I
PaeR7 I	Pme I	Pml I	PpuM I	PspA I
Pst I	Pvu I	Sac I	Sal I	Sca I
Sma I	SnaB I	Spe I	Spl I	Srf I

pMOS2: sites sorted by name:

Aat II	(2)	149	181		
Acc I	(1)	1392			
Aci I	(46)	189	204	223	409
		413	415	911	914
		925	1081	1097	1152
		1208	1293	1332	1342
		1384	1409	1447	1460
		1486	1503	1546	1553
		1574	1665	1693	1820
		1839	1960	2070	2205
		2214	2533	2612	2675
		2769	2833	2934	2937
		3177	3217	3222	3272
		3288	3314		
Afl III	(1)	1620			
Aha II	(4)	146	178	284	2703
Ahd I	(2)	2513	3373		
Alu I	(19)	9	31	64	161
		424	717	758	1145
		1202	1213	1262	1281
		1562	1788	1878	1924
		2181	2809	3267	
Alw I	(11)	150	161	821	2182
		2268	2268	2365	2366
		2881	2948	3127	
AlwN I	(2)	134	2036		
Apa I	(1)	210			
ApaL I	(2)	1436	1934		
Ase I	(2)	123	620		
Ava II	(2)	907	3219		
BamH I	(1)	154			
Ban I	(4)	283	2461	2702	2737
Ban II	(2)	210	3068		
Bbe I	(2)	287	2706		
Bbs I	(1)	3369			
Bbv I	(9)	1222	1271	1368	2039
		2042	2248	2776	2818
		3339			
Bbv II	(1)	3370			
Bcn I	(7)	813	961	1267	1302
		2001	2708	2868	
Bfa I	(3)	219	2115	2368	
Bgl I	(2)	397	448		
Bpm I	(2)	102	1149		
Bsa I	(1)	371			
BsaA I	(3)	583	1374	3007	
BsaB I	(1)	819			
BsaH I	(4)	146	178	284	2703
BsaJ I	(7)	87	194	247	413
		1780	2866	3135	
BsaW I	(3)	1826	1973	2734	
Bsg I	(1)	120			
BsiC I	(2)	118	168		
BsiE I	(5)	401	413	1536	1960
		2612			
BsiHKA I	(4)	1440	1938	2816	3006
Bsm I	(1)	116			
BsmA I	(3)	372	1264	2536	
BsmB I	(1)	1263			
BsmF I	(4)	157	284	893	2854
BsoF I	(32)	410	413	833	914
		1211	1214	1260	1357
		1410	1526	1544	1547
		1665	1820	1963	2028
		2031	2237	2612	2664
		2675	2765	2770	2807
		2848	2935	2938	2941
		3177	3273	3314	3328
Bsp120 I	(1)	206			
Bsp1286 I	(1)	3006			
BspH I	(2)	2340	2537		
BspM I	(3)	142	2590	2971	
Bsr I	(11)	211	799	929	953
		1368	1399	2027	2040
		2154	2646	2847	
BsrB I	(4)	191	1553	2535	3316
BsrD I	(1)	2936			
BssH II	(1)	236			
BssS I	(2)	1793	3295		
Bst1107 I	(1)	1393			
BstB I	(2)	118	168		
BstE II	(1)	95			
BstN I	(5)	249	1648	1769	1782
		3090			
BstU I	(13)	204	238	240	409
		415	1152	1221	1223
		1326	1667	2248	2769
		3070			
BstX I	(1)	438			
BstY I	(8)	154	814	2261	2272
		2358	2370	2874	3120
Bsu36 I	(1)	706			
Cac8 I	(22)	206	238	242	440
		719	837	879	1097
		1551	1637	1674	2234
		2597	2783	3002	3068
		3074	3102	3106	3147
		3151	3205		
Cfr10 I	(2)	3022	3203		
Csp6 I	(4)	68	591	1427	3008
Dde I	(7)	706	713	890	1430
		1895	2304	2470	
Dpn I	(15)	156	387	816	2188
		2263	2274	2282	2360
		2372	2477	2876	2954
		3035	3044	3122	
DpnII	(15)	154	385	814	2186
		2261	2272	2280	2358
		2370	2475	2874	2952
		3033	3042	3120	
Dra I	(4)	528	541	2379	2398
Dra III	(1)	106			
Drd I	(3)	1315	1728	2730	
Dsa I	(3)	87	413	3135	
Eae I	(9)	389	398	410	440
		797	2609	2783	3174
		3201			
Eag I	(3)	398	410	2609	
Ear I	(4)	697	1504	3047	3257
Eco47 III	(1)	876			
Eco57 I	(3)	2167	2848	3280	
EcoO109 I	(1)	687			
EcoR II	(5)	247	1646	1767	1780
		3088			
EcoR V	(1)	405			
Ehe I	(2)	285	2704		
Fnu4H I	(32)	410	413	833	914
		1211	1214	1260	1357
		1410	1526	1544	1547
		1665	1820	1963	2028
		2031	2237	2612	2664
		2675	2765	2770	2807
		2848	2935	2938	2941
		3177	3273	3314	3328
Fok I	(8)	841	903	981	1167
		1308	2479	3027	3052
Fsp I	(1)	2805			
Gdi II	(11)	390	397	399	409
		411	439	796	2608
		2610	3173	3200	
Gsu I	(2)	101	1148		
Hae I	(6)	451	711	1635	1646
		2098	2785		
Hae II	(5)	287	878	1498	1868
		2706			
Hae III	(18)	208	391	400	412
		442	451	688	711
		799	1095	1635	1646
		1664	2098	2611	2785
		3176	3203		
Hga I	(5)	443	1157	1316	1730
		2308			
HgiA I	(4)	1440	1938	2816	3006
HgiE II	(2)	1438	2199		
Hha I	(21)	238	240	246	286
		877	1223	1326	1356
		1497	1530	1800	1867
		1967	2141	2250	2697
		2705	2769	2806	3072
		3332			
HinD III	(1)	715			
Hinf I	(11)	199	357	672	778
		1176	1520	1595	1991
		2508	3188	3322	
HinI I	(4)	146	178	284	2703
HinP I	(21)	236	238	244	284
		875	1221	1324	1354
		1495	1528	1798	1865
		1965	2139	2248	2695
		2703	2767	2804	3070
		3330			
Hpa II	(16)	812	959	1266	1300
		1827	1974	2000	2190
		2608	2685	2707	2735
		2866	2956	3023	3204
Hph I	(6)	106	318	1241	1250
		2357	2882		
Kas I	(2)	283	2702		
Mae I	(3)	219	2115	2368	
Mae II	(11)	102	146	178	334
		577	582	947	1373
		2323	2819	3006	
Mae III	(15)	95	214	499	578
		954	977	1061	1274
		1369	1976	2039	2155
		2438	2823	3129	
Mbo I	(15)	154	385	814	2186
		2261	2272	2280	2358
		2370	2475	2874	2952
		3033	3042	3120	
Mbo II	(9)	267	685	1492	2281
		2354	3063	3273	3355
		3370			
Mme I	(2)	1834	2018		
Mnl I	(20)	53	65	144	261
		461	699	949	1007
		1046	1226	1256	1518
		1728	1801	2052	2452
		2618	2754	3111	3303
Msc I	(1)	2785			
Mse I	(15)	39	123	163	527
		540	620	867	1087
		1119	1401	2326	2378
		2383	2397	2450	

Msl I	(2)	333	3140		
Msp I	(16)	812	959	1266	1300
		1827	1974	2000	2190
		2608	2685	2707	2735
		2866	2956	3023	3204
MspA1 I	(6)	415	1213	1332	1962
		2207	2809		
Nae I	(1)	3205			
Nar I	(2)	284	2703		
Nci I	(7)	812	960	1266	1301
		2000	2707	2867	
Nco I	(2)	87	3135		
Nde I	(2)	512	1443		
NgoM I	(1)	3203			
Nla III	(19)	20	91	143	304
		435	679	747	967
		1031	1094	1259	1364
		1624	2344	2541	2922
		3108	3139	3165	
Nla IV	(10)	85	156	208	285
		909	1652	1691	2463
		2704	2739		
Not I	(1)	410			
Nsp7524 I	(5)	300	963	1255	1620
		3104			
NspB II	(6)	415	1213	1332	1962
		2207	2809		
NspH I	(5)	304	967	1259	1624
		3108			
Pal I	(18)	208	391	400	412
		442	451	688	711
		799	1095	1635	1646
		1664	2098	2611	2785
		3176	3203		
PflM I	(1)	106			
Ple I	(2)	786	1999		
Psp1406 I	(1)	947			
Pvu II	(2)	1213	2809		
Rsa I	(4)	69	592	1428	3009
Rsr II	(1)	3219			
Sac II	(1)	416			
Sap I	(3)	1504	3047	3257	
Sau3A I	(15)	154	385	814	2186
		2261	2272	2280	2358
		2370	2475	2874	2952
		3033	3042	3120	
Sau96 I	(6)	206	207	687	907
		1094	3219		
ScrF I	(12)	249	812	960	1266
		1301	1648	1769	1782
		2000	2707	2867	3090
Sec I	(7)	87	194	247	413
		1780	2866	3135	
SfaN I	(16)	820	828	924	1002
		1064	1287	1420	1458
		1496	1716	2662	2917
		3001	3065	3133	3340
Sfc I	(3)	771	1885	2076	
Sfi I	(2)	397	448		
Sph I	(1)	3108			
Ssp I	(1)	295			
Stu I	(1)	711			
Sty I	(3)	87	194	3135	
Taq I	(11)	33	118	149	168
		485	1720	2816	2972
		2996	3032	3194	
Tfi I	(7)	199	357	672	1176
		1595	3188	3322	
Tsp45 I	(8)	95	214	578	1061
		1274	1369	2823	3129
Tth111 I	(3)	101	1367	2821	
Tth111 II	(5)	1082	2209	2218	2248
		3139			
Vsp I	(2)	123	620		
Xca I	(1)	1393			
Xho II	(8)	154	814	2261	2272
		2358	2370	2874	3120
Xma III	(3)	398	410	2609	
Xmn I	(3)	114	124	1180	

Site usage in pMOS2:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	-	Aci I	C`CG,C	46
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	1
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	4
Ahd I	GACNN,N`NNGTC	2	Alu I	AG|CT	19
Alw I	GGATC 8/9	11	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	-	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	-
Ava I	C`YCGR,G	-	Ava II	G`GWC,C	2
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	4	Ban II	G,RGCY`C	2
Bbe I	G,GCGC`C	2	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	7
Bfa I	C`TA,G	3	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
BsaA I	YAC|GTR	3	BsaB I	GATNN|NNATC	1
BsaH I	GR`CG,YC	4	BsaJ I	C`CNNG,G	7
BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	-
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	2
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	4
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1
BsmA I	GTCTC`/9	3	BsmB I	CGTCTC 7/11	1
BsmF I	GGGAC 15/19	4	BsoF I	GC`N,GC	32
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
BsrB I	GAG|CGG	4	BsrD I	GCAATG, 8	1
BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1
BssS I	C`TCGT,G	2	Bst1107 I	GTA|TAC	1
BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	5	BstU I	CG|CG	13
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	8
Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN|NGC	22
Cfr10 I	R`CCGG,Y	2	Cla I	AT`CG,AT	-
Csp6 I	G`TA,C	4	Dde I	C`TNA,G	7
Dpn I	GA|TC	15	DpnII	`GATC,	15
Dra I	TTT|AAA	4	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3
Eae I	Y`GGCC,R	9	Eag I	C`GGCC,G	3
Ear I	CTCTTC 7/10	4	Eco47 III	AGC|GCT	1
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC|GTG	-
EcoN I	CCTNN`N,NNAGG	-	EcoO109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	5
EcoR V	GAT|ATC	1	Ehe I	GGC|GCC	2
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	32
Fok I	GGATG 14/18	8	Fse I	GG,CCGG`CC	-
Fsp I	TGC|GCA	1	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	2	Hae I	WGG|CCW	6
Hae II	R,GCGC`Y	5	Hae III	GG|CC	18
Hga I	GACGC 9/14	5	HgiA I	G,WGCW`C	4
HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	21
HinC II	GTY|RAC	-	Hind II	GTY|RAC	-
HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	11
HinI I	GR`CG,YC	4	HinP I	G`CG,C	21
Hpa I	GTT|AAC	-	Hpa II	C`CG,G	16
Hph I	GGTGA 12/11	6	Kas I	G`GCGC,C	2
Kpn I	G,GTAC`C	-	Mae I	C`TA,G	3
Mae II	A`CG,T	11	Mae III	`GTNAC,	15
Mbo I	`GATC,	15	Mbo II	GAAGA 12/11	9
Mlu I	A`CGCG,T	-	Mme I	TCCRAC 25/23	2
Mnl I	CCTC 10/10	20	Msc I	TGG|CCA	1
Mse I	T`TA,A	15	Msl I	CAYNN|NNRTG	2
Msp I	C`CG,G	16	MspA1 I	CMG|CKG	6
Mun I	C`AATT,G	-	Nae I	GCC|GGC	1
Nar I	GG`CG,CC	2	Nci I	CC`S,GG	7
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	1	Nhe I	G`CTAG,C	-
Nla III	,CATG`	19	Nla IV	GGN|NCC	10
Not I	GC`GGCC,GC	1	Nru I	TCG|CGA	-
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	5
NspB II	CMG|CKG	6	NspH I	R,CATG`Y	5
PaeR7 I	C`TCGA,G	-	Pal I	GG|CC	18
PflM I	CCAN,NNN`NTGG	1	Ple I	GAGTC 9/10	2
Pme I	CTTT|AAAC	-	Pml I	CAC|GTG	-
PpuM I	RG`GWC,CY	-	Psp1406 I	AA`CG,TT	1
PspA I	C`CCGG,G	-	Pst I	C,TGCA`G	-
Pvu I	CG,AT`CG	-	Pvu II	CAG|CTG	2
Rsa I	GT|AC	4	Rsr II	CG`GWC,CG	1
Sac I	G,AGCT`C	-	Sac II	CC,GC`GG	1
Sal I	G`TCGA,C	-	Sap I	GCTCTTC 8/11	3
Sau3A I	`GATC,	15	Sau96 I	G`GNC,C	6
Sca I	AGT|ACT	-	ScrF I	CC`N,GG	12
Sec I	C`CNNG,G	7	SfaN I	GCATC 9/13	16
Sfc I	C`TRYA,G	3	Sfi I	GGCCN,NNN`NGGCC	2
Sma I	CCC|GGG	-	SnaB I	TAC|GTA	-
Spe I	A`CTAG,T	-	Sph I	G,CATG`C	1
Spl I	C`GTAC,G	-	Srf I	GCCC|GGGC	-
Ssp I	AAT|ATT	1	Stu I	AGG|CCT	1
Sty I	C`CWWG,G	3	Taq I	T`CG,A	11
Tfi I	G`AWT,C	7	Tsp45 I	`GTSAC,	8
Tth111 I	GACN`N,NGTC	3	Tth111 II	CAARCA 16/14	5
Vsp I	AT`TA,AT	2	Xba I	T`CTAG,A	-
Xca I	GTA|TAC	1	Xcm I	CCANNNN,N`NNNNTGG	-
Xho I	C`TCGA,G	-	Xho II	R`GATC,Y	8
Xma I	C`CCGG,G	-	Xma III	C`GGCC,G	3