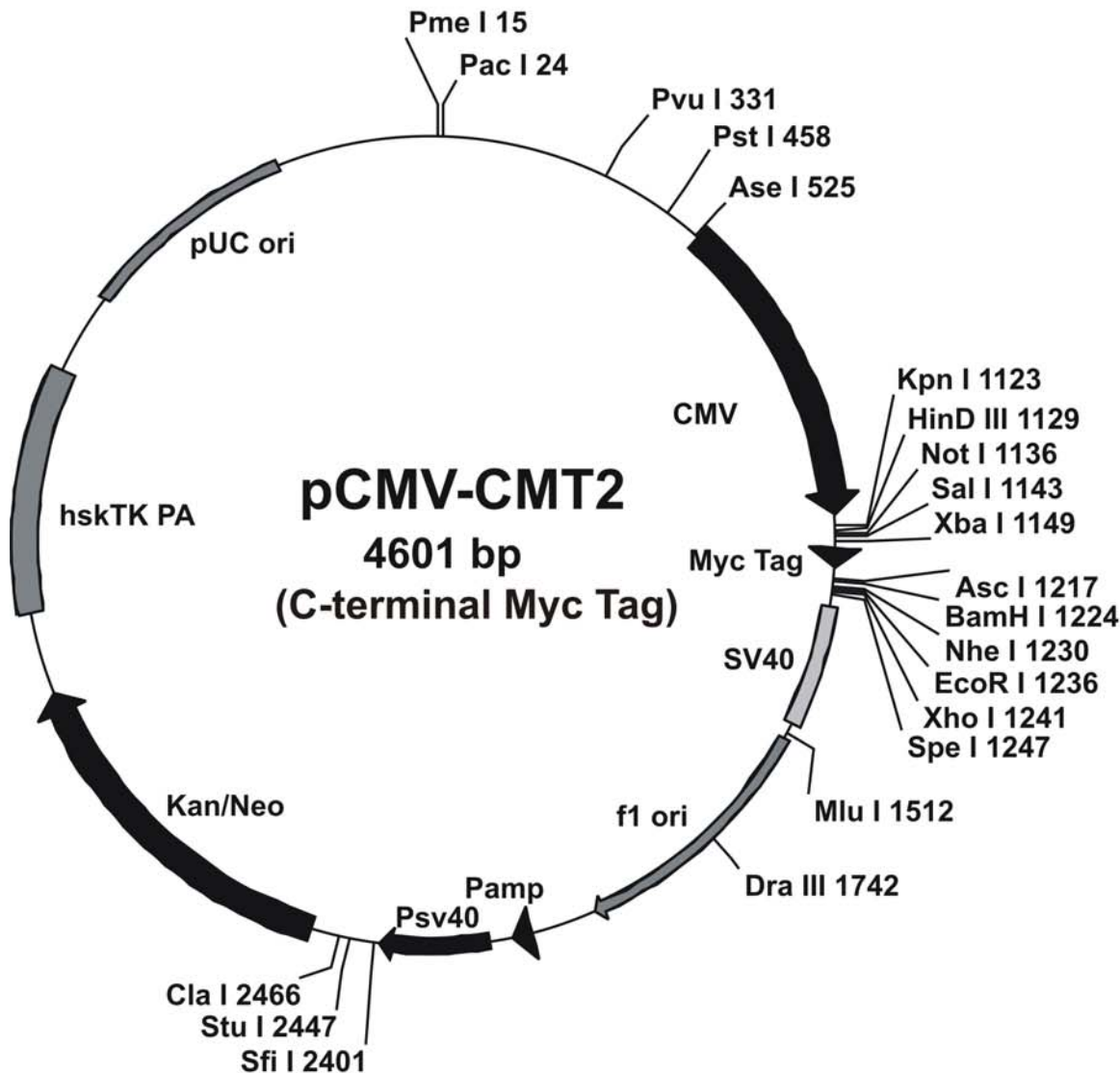


Name of Vector: pCMV-CMT2
 Antibiotic Selection: Kan
 Created by: Wei Jiang and Yien Li
 (He Lab @ The University of Chicago)
 Date of Creation: June 2004



Linker Sequence

Kozak																
Kpn I											Hind III	Not I		Sal I		Xba I
GGT	ACC	ATG	GAA	GCT	TGC	GGC	CGC	GTC	GAC	TCT	AGA	GGA	GGC	GGC	GGA	GGT
		M	E	A	C	G	R	V	D	S	R	G	G	G	G	G
Myc Tag																
GTC	GAG	GGA	GAA	CAA	AAA	CTC	ATC	TCA	GAA	GAG	GAT	CTG	TGA			
V	E	G	E	Q	K	L	I	S	E	E	D	L	-			

pCMV-CMT2 Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgcgccgaagaacgttttccaatgatgagcacttt 120
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tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgagtataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCCTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900
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Unique enzymes in CMVCMT2.TXT:

Pme I	CTTT AAAC	15
Pac I	TTA,AT`TAA	24
Xmn I	GAANN NNTTC	100
Sca I	AGT ACT	219
Pvu I	CG,AT`CG	331
EcoN I	CCTNN`N,NNAGG	339
Pst I	C,TGCA`G	458
Ase I	AT`TA,AT	525
Vsp I	AT`TA,AT	525
Nde I	CA`TA,TG	752
SnaB I	TAC GTA	858
Acc65 I	G`GTAC,C	1119
Asp718	G`GTAC,C	1119
Kpn I	G,GTAC`C	1123
HinD III	A`AGCT,T	1129
Not I	GC`GGCC,GC	1136
Sal I	G`TCGA,C	1143
Acc I	GT`MK,AC	1144
Xba I	T`CTAG,A	1149
Asc I	GG`CGCG,CC	1217
BssH II	G`CGCG,C	1217
BamH I	G`GATC,C	1224
Nhe I	G`CTAG,C	1230
EcoR I	G`AATT,C	1236
Ava I	C`YCGR,G	1241
PaeR7 I	C`TCGA,G	1241
Xho I	C`TCGA,G	1241
Spe I	A`CTAG,T	1247
PflM I	CCAN,NNN`NTGG	1271
BstX I	CCAN,NNNN`NTGG	1272
Bcl I	T`GATC,A	1283
Mun I	C`AATT,G	1376
Hpa I	GTT AAC	1389
Mlu I	A`CGCG,T	1512
Dra III	CAC,NNN`GTG	1742
Sfi I	GGCCN,NNN`NGGCC	2401
Stu I	AGG CCT	2447
Cla I	AT`CG,AT	2466
Kas I	G`GCGC,C	2625
Nar I	GG`CG,CC	2626
Ehe I	GGC GCC	2627

Bbe I	G,GCGC`C	2629
Msc I	TGG CCA	2708
Tth111 I	GACN`N,NGTC	2744
Rsr II	CG`GWC,CG	3142
BsiC I	TT`CG,AA	3308
BstB I	TT`CG,AA	3308
Bsa I	GGTCTC 7/11	3615
EcoO109 I	RG`GNC,CY	3724
Number of enzymes = 49		

The following enzymes do not cut in CMVCMT2.TXT:

Afl II	Age I	Ahd I	Apa I	Bbs I
Bbv II	Bgl II	Blp I	Bsg I	BsiW I
BsmB I	Bsp120 I	BspM II	BsrG I	Bst1107 I
BstE II	Eco47 III	Eco72 I	EcoR V	Esp I
Fse I	Nru I	Pml I	PpuM I	PspA I
Sac I	Sac II	Sma I	Spl I	Srf I

CMVCMT2.TXT: sites sorted by name:

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
Aci I	(64)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1228
		1886	1913	1941	1944
		1958	2001	2048	2111
		2296	2308	2317	2329
		2339	2350	2396	2535
		2598	2692	2756	2857
		2860	3100	3140	3145
		3195	3211	3237	3293
		3362	3365	3431	3513
		3578	3645	3718	3952
		3961	4096	4206	4327
		4346	4473	4501	4592
Afl III	(2)	1512	4544		
Aha II	(8)	160	640	693	776
		962	2626	3328	3407
Alu I	(16)	347	410	510	1084
		1131	1405	1572	1829
		2124	2412	2732	3190
		3987	4244	4290	4380
Alw I	(19)	60	66	381	1099
		1209	1220	1231	1257
		2493	2804	2871	3050
		3415	3442	3801	3802

AlwN I	(2)	3899	3899	3985							
ApaL I	(2)	3727	4135			DpnII	(29)	53	70	328	374
Apo I	(4)	28	4230					392	1103	1114	1202
Asc I	(1)	1236	1440	1544	1555			1211	1224	1252	1261
Ase I	(1)	1217						1283	2463	2467	2486
Asp718	(1)	525						2797	2875	2956	2965
Ava I	(1)	1119						3043	3419	3435	3794
Ava II	(3)	1241						3806	3884	3892	3903
Avr II	(3)	336	3142	3587				3978			
BamH I	(2)	2448	3463			Dra I	(5)	15	122	1328	3770
Ban I	(1)	1224						3789			
Ban II	(5)	983	1119	1779	2625	Dra III	(1)	1742			
Bbe I	(3)	2660				Drd I	(3)	1697	2653	4442	
Bbv I	(1)	1817	2991	3701		Dsa I	(4)	878	1123	2355	3058
Bcl I	(7)	2629				Eae I	(6)	307	1136	2532	2706
Bcn I	(1)	468	1414	2699	2741			3097	3124		
Bfa I	(2)	3262	3715	4215		Eag I	(2)	1136	2532		
Bgl I	(1)	1283				Ear I	(4)	1192	2093	2970	3180
Bhm I	(6)	165	516	2631	2791	Eco57 I	(3)	2771	3203	4003	
Bhs I	(1)	3404	4168			EcoN I	(1)	339			
Bla I	(11)	507	1110	1150	1231	EcoO109 I	(1)	3724			
Bla II	(2)	1248	1475	1893	2449	EcoR I	(1)	1236			
Bla III	(3)	3464	3798	4051		EcoR II	(11)	606	799	2160	2215
Bla IV	(4)	608	730	801	2401			2232	3011	3590	3693
Bla V	(2)	3409	3466			Ehe I	(1)	2627	4383	4396	
Bla VI	(1)	3615				Fnu4H I	(35)	185	280	307	457
Bla VII	(3)	858	1742	2930				1136	1139	1160	1403
Bla VIII	(2)	1288	2485					1922	1944	1958	2396
Bla IX	(8)	160	640	693	776			2535	2587	2598	2688
Bla X	(16)	962	2626	3328	3407			2693	2730	2771	2858
Bla XI	(16)	878	1123	2160	2232			2861	2864	3100	3196
Bla XII	(16)	2355	2390	2399	2448			3237	3251	3365	3704
Bla XIII	(16)	2789	3058	3463	3590			3719	3930	4136	4139
Bla XIV	(16)	3591	3693	3694	4384			4204	4347	4502	
Bla XV	(6)	404	1267	2657	3501	Fok I	(6)	261	2299	2493	2950
Bla XVI	(6)	4191	4338					2975	3429		
Bla XVII	(2)	1168	2444			Fsp I	(2)	477	2728		
Bla XVIII	(1)	3308				Gdi II	(7)	308	1135	1137	2531
Bla XIX	(5)	182	331	1139	2535			2533	3096	3123	
Bla XX	(5)	32	117	2739	2929	Gsu I	(2)	3410	3465		
Bla XXI	(5)	4234				Hae I	(5)	2447	2708	4070	4522
Bla XXII	(2)	1377	1470					4533			
Bla XXIII	(6)	951	1239	2051	2469	Hae II	(4)	1893	1901	2629	4304
Bla XXIV	(6)	3488	3616			Hae III	(21)	309	602	795	1138
Bla XXV	(10)	693	844	1012	2142			1592	1734	2389	2395
Bla XXVI	(10)	2214	2278	2777	3309			2404	2447	2534	2708
Bla XXVII	(10)	3418	3573					3099	3126	3635	3692
Bla XXVIII	(35)	185	280	307	457			3725	4070	4504	4522
Bla XXIX	(35)	1136	1139	1160	1403			4533			
Bla XXX	(35)	1922	1944	1958	2396	Hga I	(8)	167	1043	1131	1960
Bla XXXI	(35)	2535	2587	2598	2688			3335	3414	3855	4433
Bla XXXII	(35)	2693	2730	2771	2858	HgiA I	(5)	32	117	2739	2929
Bla XXXIII	(35)	2861	2864	3100	3196			4234			
Bla XXXIV	(35)	3237	3251	3365	3704	HgiE II	(2)	1265	3955		
Bla XXXV	(35)	3719	3930	4136	4139	Hha I	(24)	141	478	1219	1221
Bla XXXVI	(35)	4204	4347	4502				1892	1900	1926	1948
Bla XXXVII	(2)	117	2929					1957	1970	2001	2620
Bla XXXVIII	(2)	2052	3824					2628	2692	2729	2995
Bla XXXIX	(3)	2513	2894	3344				3255	3431	3517	3920
Bla XL	(11)	54	226	493	814			4029	4203	4303	4370
Bla XLI	(11)	1656	2334	2569	2770	HinC II	(3)	158	1145	1389	
Bla XLII	(11)	4016	4130	4143		Hind II	(3)	158	1145	1389	
Bla XLIII	(4)	1886	2050	3239	3293	Hind III	(1)	1129			
Bla XLIV	(4)	466	2859			Hinf I	(12)	928	1146	1669	1691
Bla XLV	(1)	1217						2101	3111	3245	3297
Bla XLVI	(4)	31	3218	3344	4371			3355	3392	4174	4570
Bla XLVII	(1)	3308				HinI I	(8)	160	640	693	776
Bla XLVIII	(11)	608	801	2162	2217			962	2626	3328	3407
Bla XLIX	(11)	2234	3013	3592	3695	HinP I	(24)	139	476	1217	1219
Bla L	(11)	4385	4398	4519				1890	1898	1924	1946
Bla LI	(18)	141	578	1141	1219			1955	1968	1999	2618
Bla LII	(18)	1514	1550	1926	1946			2626	2690	2727	2993
Bla LIII	(18)	1970	2001	2692	2993			3253	3429	3515	3918
Bla LIV	(18)	3431	3515	3578	3647			4027	4201	4301	4368
Bla LV	(18)	3920	4501			Hpa I	(1)	1389			
Bla LVI	(1)	1272				Hpa II	(21)	163	405	515	1222
Bla LVII	(12)	53	70	1103	1202			1268	1844	2531	2608
Bla LVIII	(12)	1224	2797	3043	3435			2630	2658	2789	2879
Bla LIX	(12)	3794	3806	3892	3903			2946	3127	3402	3410
Bla LX	(2)	2106	3738					3502	3976	4166	4192
Bla LXI	(31)	454	604	797	1133			4339			
Bla LXII	(31)	1219	1232	1845	1888	Hph I	(6)	215	893	1744	2805
Bla LXIII	(31)	1902	2175	2194	2247			3696	3812		
Bla LXIV	(31)	2266	2520	2706	2925	Kas I	(1)	2625			
Bla LXV	(31)	2991	2997	3025	3029	Kpn I	(1)	1123			
Bla LXVI	(31)	3070	3074	3128	3411	Mae I	(11)	507	1110	1150	1231
Bla LXVII	(31)	3598	3645	3701	3723			1248	1475	1893	2449
Bla LXVIII	(31)	3934	4494	4531				3464	3798	4051	
Bla LXIX	(4)	1843	2945	3126	3409	Mae II	(16)	98	471	640	652
Bla LXX	(4)	2466						693	776	857	962
Bla LXXI	(1)	218	736	761	816			1686	1698	1741	1851
Bla LXXII	(9)	849	900	1057	1120			2742	2929	3710	3843
Bla LXXIII	(9)	2931				Mae III	(16)	39	227	380	438
Bla LXXIV	(8)	199	1193	2106	2408			579	666	1015	1414
Bla LXXV	(8)	3289	3738	3861	4270			1915	1927	2746	3052
Bla LXXVI	(29)	55	72	330	376	Mbo I	(29)	3742	4008	4124	4187
Bla LXXVII	(29)	394	1105	1116	1204			53	70	328	374
Bla LXXVIII	(29)	1213	1226	1254	1263			392	1103	1114	1202
Bla LXXIX	(29)	1285	2465	2469	2488			1211	1224	1252	1261
Bla LXXX	(29)	2799	2877	2958	2967			1283	2463	2467	2486
Bla LXXXI	(29)	3045	3421	3437	3796			2797	2875	2956	2965
Bla LXXXII	(29)	3808	3886	3894	3905			3043	3419	3435	3794

		3806	3884	3892	3903
		3978			
Mbo II	(11)	104	1208	1881	2109
		2986	3196	3278	3445
		3645	3815	3888	
Mlu I	(1)	1512			
Mme I	(3)	1718	4152	4336	
Mnl I	(30)	327	1059	1146	1149
		1158	1166	1193	1305
		1344	1353	1770	2101
		2379	2385	2408	2414
		2422	2425	2437	2477
		2541	2677	3034	3226
		3432	3464	3746	4116
		4367	4440		
Msc I	(1)	2708			
Mse I	(20)	14	20	24	121
		486	525	1327	1388
		1509	1530	1541	1553
		1564	1581	1679	1950
		3769	3783	3788	3840
Msl I	(4)	288	883	1272	3063
Msp I	(21)	163	405	515	1222
		1268	1844	2531	2608
		2630	2658	2789	2879
		2946	3127	3402	3410
		3502	3976	4166	4192
		4339			
MspAl I	(5)	64	2124	2732	3961
		4206			
Mun I	(1)	1376			
Nae I	(3)	1845	3128	3411	
Nar I	(1)	2626			
Nci I	(6)	164	515	2630	2790
		3403	4167		
Nco I	(4)	878	1123	2355	3058
Nde I	(1)	752			
NgoM I	(3)	1843	3126	3409	
Nhe I	(1)	1230			
Nla III	(20)	257	293	371	381
		822	882	1127	2056
		2196	2268	2359	2500
		2845	3031	3062	3088
		3444	3828	4548	4599
Nla IV	(17)	403	985	1121	1226
		1781	1802	1814	2005
		2166	2238	2627	2662
		3510	3589	3634	4477
		4516			
Not I	(1)	1136			
Nsi I	(3)	2198	2270	4601	
Nsp7524 I	(4)	2192	2264	3027	4544
NspB II	(5)	64	2124	2732	3961
		4206			
NspH I	(4)	2196	2268	3031	4548
Pac I	(1)	24			
Paer7 I	(1)	1241			
Pal I	(21)	309	602	795	1138
		1592	1734	2389	2395
		2404	2447	2534	2708
		3099	3126	3635	3692
		3725	4070	4504	4522
		4533			
Pf1M I	(1)	1271			
Ple I	(2)	1677	2109		
Pme I	(1)	15			
Psp1406 I	(2)	98	471		
Pst I	(1)	458			
Pvu I	(1)	331			
Pvu II	(2)	2124	2732		
Rsa I	(9)	219	737	762	817
		850	901	1058	1121
		2932			
Rsr II	(1)	3142			
Sal I	(1)	1143			
Sap I	(2)	2970	3180		
Sau3A I	(29)	53	70	328	374
		392	1103	1114	1202
		1211	1224	1252	1261
		1283	2463	2467	2486
		2797	2875	2956	2965
		3043	3419	3435	3794
		3806	3884	3892	3903
		3978			
Sau96 I	(9)	336	601	794	1733
		3142	3587	3633	3691
		3724			
Sca I	(1)	219			
ScrF I	(17)	164	515	608	801
		2162	2217	2234	2630
		2790	3013	3403	3592
		3695	4167	4385	4398
		4519			
Sec I	(16)	878	1123	2160	2232
		2355	2390	2399	2448
		2789	3058	3463	3590
		3591	3693	3694	4384
SfaN I	(13)	247	440	876	1441
		2204	2276	2585	2840
		2924	2988	3056	3263
		4448			
Sfc I	(4)	454	1961	4088	4279
Sfi I	(1)	2401			

SnaB I	(1)	858			
Spe I	(1)	1247			
Sph I	(3)	2196	2268	3031	
Ssp I	(2)	1534	2087		
Stu I	(1)	2447			
Sty I	(6)	878	1123	2355	2448
		3058	3463		
Taq I	(15)	46	1144	1171	1242
		1775	2466	2739	2895
		2919	2955	3117	3308
		3353	3608	4446	
Tfi I	(5)	3111	3245	3355	3392
		4570			
Tsp45 I	(5)	227	438	1915	2746
		3052			
Tth111 I	(1)	2744			
Tth111 II	(4)	3062	3922	3952	3961
Vsp I	(1)	525			
Xba I	(1)	1149			
Xho I	(1)	1241			
Xho II	(12)	53	70	1103	1202
		1224	2797	3043	3435
		3794	3806	3892	3903
Xma III	(2)	1136	2532		
Xmn I	(1)	100			

Site usage in CMVCMT2.TXT:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	64
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	-	Alu I	AG CT	16
Alw I	GGATC 8/9	19	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	Apal I	G`TGCA,C	2
Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	1	Ava II	G`GWC,C	3
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	5	Ban II	G,RCGY`C	3
Bbe I	G,GGCC`C	1	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	6
Bfa I	C`TA,G	11	Bgl I	GCCN,NNN`NGGC	4
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	2
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	16
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	2
Bsg I	GTGCAG 22/20	-	Bsic I	TT`CG,AA	1
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
BsmA I	GTCTC`/9	6	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	35
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	2	BspM I	ACCTCG 10/14	3
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	11	BstU I	CG CG	18
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	12
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	31
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	8
Dpn I	GA TC	29	DpnII	`GATC,	29
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	6	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	11
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	35
Fok I	GGATG 14/18	6	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	5
Hae II	R,GGCC`Y	4	Hae III	GG CC	21
Hga I	GACGC 9/14	8	HgiA I	G,WGCW`C	5
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	24
Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12
HinI I	GR`CG,YC	8	HinP I	G`CG,C	24
Hpa I	GTT AAC	1	Hpa II	C`CG,G	21
Hph I	GGTGA 12/11	6	Kas I	G`GCGC,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11
Mae II	A`CG,T	16	Mae III	`GTNAC,	16
Mbo I	`GATC,	29	Mbo II	GAAGA 12/11	11
Mlu I	A`CCGG,T	1	Mme I	TCCRAC 25/23	3
Mnl I	CCTC 10/10	30	Msc I	TGG CCA	1
Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	21	MspAl I	CMG CKG	5
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	6
Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	1
Nla III	,CATG`	20	Nla IV	GNN NCC	17
Not I	GC`GGCC,GC	1	Nru I	TGC CGA	-
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
NspB II	CMG CKG	5	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1

Pal I	GG CC	21	PflM I	CCAN,NNN`NTGG	1
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
Pep1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Pvu II	CAG CTG	2	Rsa I	GT AC	9
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	29
Sau96 I	G`GNC,C	9	Sca I	AGT ACT	1
ScrF I	CC`N,GG	17	Sec I	C`CNNG,G	16
SfaN I	GCATC 9/13	13	Sfc I	C`TRYA,G	4
Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`CWWG,G	6
Taq I	T`CG,A	15	Tfi I	G`AWT,C	5
Tsp45 I	`GTSAC,	5	Tth111 I	GACN`N,NGTC	1
Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	1
Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	-
Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1