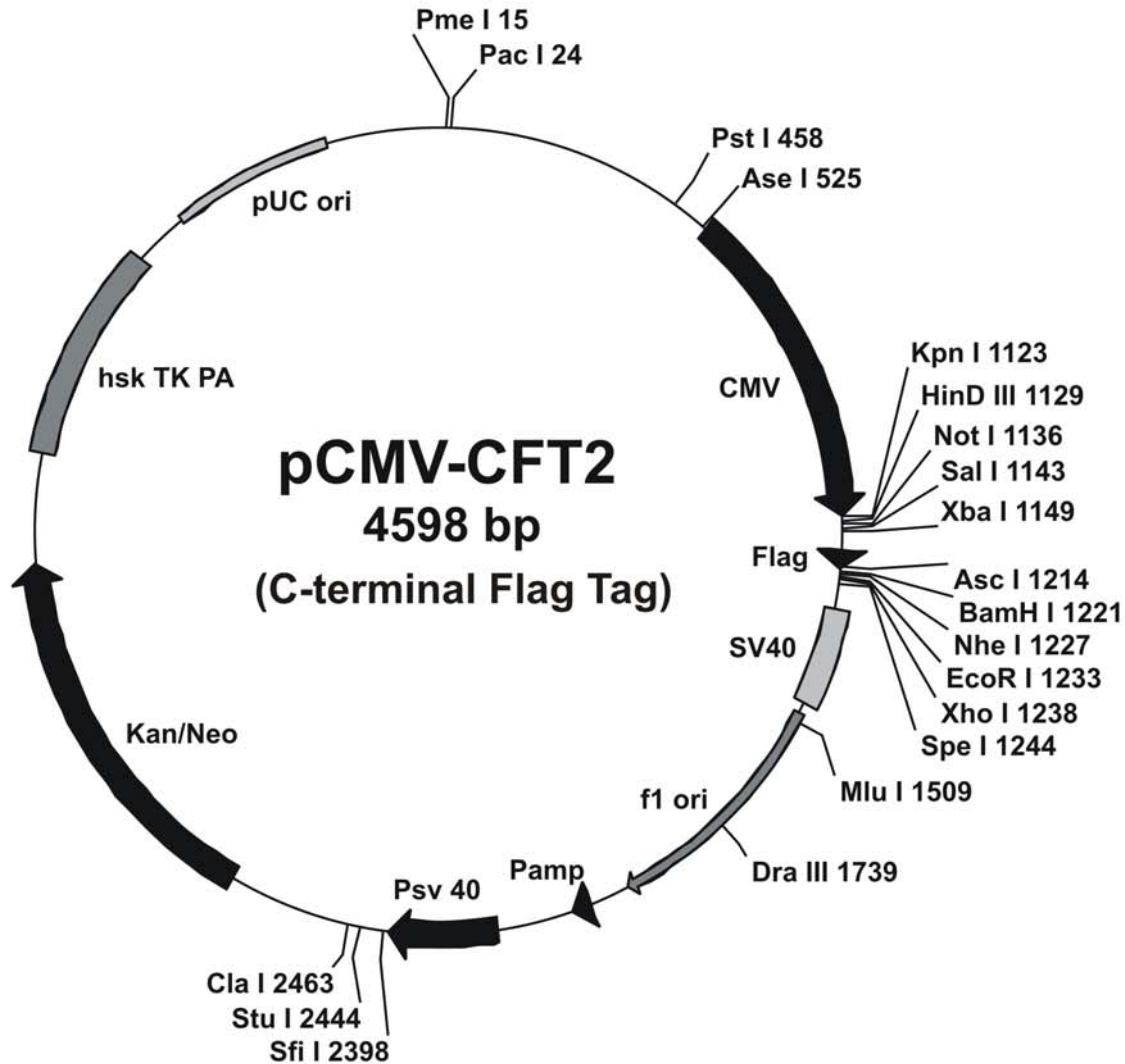


Name of Vector: pCMV-CFT2
 Antibiotic Selection: Kan
 Created by: Wei Jiang and Yien Li
 (He Lab @ The University of Chicago)
 Date of Creation: June 2004



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			
Flag Tag																			
GTC	GAG	GGA	GAT	TAC	AAG	GAT	GAC	GAC	GAT	AAG	ATA	TGA							
V	E	G	D	Y	K	D	D	D	D	K	I	-							

pCMV-CFT2 Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgagtgataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCAAAATGTCGTAACA 1020
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGCGGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGAGGGAGATTACAAGGATGACGACGATAA 1200
GATATGagatcGGCGCGCCGGATCCGCTAGCGAATTCTCGAGACTAGTGATCTatccgat 1260
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TTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATT 1440
TCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATG 1500
TATCTTAACCGGTAAATTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTTTGT 1560
TAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAA 1620
GAATAGACCGAGATAGGGTTGAGTGTGTCCAGTTTGGAAACAAGAGTCCACTATTAAG 1680
AACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGT 1740
GAACCATCACCTAATCAAGTTTTTTGGGGTGCAGGTGCCGTAAAGCACTAAATCGGAAC 1800
CCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAG 1860
GAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTG 1920
CGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACT 1980
TTTCGGGAAATGTGCGCGAAACCCCTATTTGTTATTTTTCTAAATACATTCAAATATG 2040
TATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT 2100
CCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAG 2160
GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTG 2220
GAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAG 2280
CAACCATAGTCCCGCCCCCTAACTCCGCCCATCCCGCCCCCTAACTCCGCCCAGTCCGCC 2340
ATTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGTCAGAGGCCGAGGCCGCTCGG 2400
CCTCTGAGCTATCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTTGCAAAG 2460
ATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCA 2520
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GACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCT 2820
GCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCT 2880
ACCTGCCATTTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCGGATGGAA 2940
GCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAA 3000
CTGTTCCGAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGC 3060
GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGT 3120
GGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCT 3180
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GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGG 3300
GGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCACCCG 3360
CCGCCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCC 3420
TCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAA 3480
CACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATA 3540
AAACGCACGGTGTGGGTCGTTTGTTCATAAACGCGGGGTTTCGGTCCCAGGGCTGGCACT 3600
CTGTTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTTCTTCTTTTCCC 3660
CACCCACCCCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAG 3720
GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTT 3780
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GTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 3900
ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCAGCTACCAGCGG 3960
TGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCA 4020
GAGCGCAGATAACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACCTCAAGA 4080
ACTCTGTAGCACCGCCTACATAACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCA 4140
GTGGCGATAAGTCTGTCTTACCAGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGC 4200
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AGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTC 4380
CAGGGGGAAACGCCCTGGTATCTTTATAGTCCCTGTTCGGGTTTTCGCCACCTCTGACTTGAGC 4440
GTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAACGCCAGCAACGCGG 4500
CCTTTTTACGGTTCCTGGCCTTTTGTCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTAT 4560
CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4598

Unique enzymes in CMVCF2.TXT:

	Fse I Sac I	Nru I Sac II	Pml I Sma I	PpuM I Spl I	PspA I Srf I
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	1214			
BssH II	G`CGCG,C	1214			
BamH I	G`GATC,C	1221			
Nhe I	G`CTAG,C	1227			
EcoR I	G`AATT,C	1233			
Ava I	C`YCGR,G	1238			
PaeR7 I	C`TCGA,G	1238			
Xho I	C`TCGA,G	1238			
Spe I	A`CTAG,T	1244			
PfI M	CCAN,NNN`NTGG	1268			
BstX I	CCAN,NNNN`NTGG	1269			
Bcl I	T`GATC,A	1280			
Mun I	C`AATT,G	1373			
Hpa I	GTT AAC	1386			
Mlu I	A`CGCG,T	1509			
Dra III	CAC,NNN`GTG	1739			
Sfi I	GGCCN,NNN`NGGCC	2398			
Stu I	AGG CCT	2444			
Cla I	AT`CG,AT	2463			
Kas I	G`GCGC,C	2622			
Nar I	GG`CG,CC	2623			
Ehe I	GGC GCC	2624			
Bbe I	G,GCGC`C	2626			
Msc I	TGG CCA	2705			
Tth111 I	GACN`N,NGTC	2741			
Rsr II	CG`GWC,CG	3139			
BsiC I	TT`CG,AA	3305			
BstB I	TT`CG,AA	3305			
Bsa I	GGTCTC 7/11	3612			
EcoO109 I	RG`GNC,CY	3721			
Number of enzymes = 49					

CMVCF2.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	1225
		1883	1910	1938	1941
		1955	1998	2045	2108
		2293	2305	2314	2326
		2336	2347	2393	2532
		2595	2689	2753	2854
		2857	3097	3137	3142
		3192	3208	3234	3290
		3359	3362	3428	3510
		3575	3642	3715	3949
		3958	4093	4203	4324
		4343	4470	4498	4589
Afl III	(2)	1509	4541		
Aha II	(8)	160	640	693	776
		962	2623	3325	3404
Alu I	(16)	347	410	510	1084
		1131	1402	1569	1826
		2121	2409	2729	3187
		3984	4241	4287	4377
Alw I	(18)	60	66	381	1099
		1217	1228	1254	2490
		2801	2868	3047	3412
		3439	3798	3799	3896
		3896	3982		
AlwN I	(2)	3724	4132		
Apal I	(2)	28	4227		
Apo I	(4)	1233	1437	1541	1552
Asc I	(1)	1214			
Ase I	(1)	525			
Asp718	(1)	1119			
Ava I	(1)	1238			
Ava II	(3)	336	3139	3584	
Avr I	(2)	2445	3460		
BamH I	(1)	1221			
Ban I	(5)	983	1119	1776	2622
		2657			
Ban II	(3)	1814	2988	3698	
Bbe I	(1)	2626			
Bbv I	(7)	468	1411	2696	2738
		3259	3712	4212	
Bcl I	(1)	1280			
Bcn I	(6)	165	516	2628	2788
		3401	4165		
Bfa I	(11)	507	1110	1150	1228
		1245	1472	1890	2446
		3461	3795	4048	
Bgl I	(4)	608	730	801	2398
Bpm I	(2)	3406	3463		

The following enzymes do not cut in CMVCF2.TXT:

Afl II	Age I	Ahd I	Apa I	Bbs I
Bbv II	Bgl II	Blp I	Bsg I	BsiW I
Bmb I	Bsp120 I	BspM II	BsrG I	Bst1107 I
BstE II	Eco47 III	Eco72 I	EcoR V	Esp I

Bsa I	(1)	3612				1136	1139	1160	1400		
BsaA I	(3)	858	1739	2927		1919	1941	1955	2393		
BsaB I	(2)	1285	2482			2532	2584	2595	2685		
BsaH I	(8)	160	640	693	776	2690	2727	2768	2855		
		962	2623	3325	3404	2858	2861	3097	3193		
BsaJ I	(16)	878	1123	2157	2229	3234	3248	3362	3701		
		2352	2387	2396	2445	3716	3927	4133	4136		
		2786	3055	3460	3587	4201	4344	4499			
		3588	3690	3691	4381	Fok I	(7)	261	1200	2296	2490
BsaW I	(6)	404	1264	2654	3498		2947	2972	3426		
		4188	4335			Fsp I	(2)	477	2725		
BseR I	(2)	1168	2441			Gdi II	(7)	308	1135	1137	2528
BsiC I	(1)	3305					2530	3093	3120		
BsiE I	(5)	182	331	1139	2532	Gsu I	(2)	3407	3462		
		4207				Hae I	(5)	2444	2705	4067	4519
BsiHKA I	(5)	32	117	2736	2926		4530				
		4231				Hae II	(4)	1890	1898	2626	4301
Bsm I	(2)	1374	1467			Hae III	(21)	309	602	795	1138
BsmA I	(6)	951	1236	2048	2466		1589	1731	2386	2392	
		3485	3613				2401	2444	2531	2705	
BsmF I	(10)	693	844	1012	2139		3096	3123	3632	3689	
		2211	2275	2774	3306		3722	4067	4501	4519	
		3415	3570				4530				
BsoF I	(35)	185	280	307	457	Hga I	(8)	167	1043	1131	1957
		1136	1139	1160	1400		3332	3411	3852	4430	
		1919	1941	1955	2393	HgiA I	(5)	32	117	2736	2926
		2532	2584	2595	2685		4231				
		2690	2727	2768	2855	HgiE II	(2)	1262	3952		
		2858	2861	3097	3193	Hha I	(24)	141	478	1216	1218
		3234	3248	3362	3701		1889	1897	1923	1945	
		3716	3927	4133	4136		1954	1967	1998	2617	
		4201	4344	4499			2625	2689	2726	2992	
Bspl286 I	(2)	117	2926				3252	3428	3514	3917	
BspH I	(2)	2049	3821				4026	4200	4300	4367	
BspM I	(3)	2510	2891	3341		HinC II	(3)	158	1145	1386	
Bsr I	(11)	54	226	493	814	Hind II	(3)	158	1145	1386	
		1653	2331	2566	2767	Hind III	(1)	1129			
		4013	4127	4140		Hinf I	(12)	928	1146	1666	1688
BsrB I	(4)	1883	2047	3236	3290		2098	3108	3242	3294	
BsrD I	(2)	466	2856				3352	3389	4171	4567	
BssH II	(1)	1214				HinI I	(8)	160	640	693	776
BssS I	(4)	31	3215	3341	4368		962	2623	3325	3404	
BstB I	(1)	3305				HinP I	(24)	139	476	1214	1216
BstN I	(11)	608	801	2159	2214		1887	1895	1921	1943	
		2231	3010	3589	3692		1952	1965	1996	2615	
		4382	4395	4516			2623	2687	2724	2990	
BstU I	(18)	141	578	1141	1216		3250	3426	3512	3915	
		1511	1547	1923	1943		4024	4198	4298	4365	
		1967	1998	2689	2990	Hpa I	(1)	1386			
		3428	3512	3575	3644	Hpa II	(21)	163	405	515	1219
		3917	4498				1265	1841	2528	2605	
BstX I	(1)	1269					2627	2655	2786	2876	
BstY I	(11)	53	70	1103	1221		2943	3124	3399	3407	
		2794	3040	3432	3791		3499	3973	4163	4189	
		3803	3889	3900			4336				
Bsu36 I	(2)	2103	3735			Hph I	(6)	215	893	1741	2802
Cac8 I	(31)	454	604	797	1133		3693	3809			
		1216	1229	1842	1885	Kas I	(1)	2622			
		1899	2172	2191	2244	Kpn I	(1)	1123			
		2263	2517	2703	2922	Mae I	(11)	507	1110	1150	1228
		2988	2994	3022	3026		1245	1472	1890	2446	
		3067	3071	3125	3408		3461	3795	4048		
		3595	3642	3698	3720	Mae II	(16)	98	471	640	652
		3931	4491	4528			693	776	857	962	
Cfr10 I	(4)	1840	2942	3123	3406		1683	1695	1738	1848	
Cla I	(1)	2463					2739	2926	3707	3840	
Csp6 I	(9)	218	736	761	816	Mae III	(16)	39	227	380	438
		849	900	1057	1120		579	666	1015	1411	
		2928					1912	1924	2743	3049	
Dde I	(7)	199	2103	2405	3286		3739	4005	4121	4184	
		3735	3858	4267		Mbo I	(28)	53	70	328	374
Dpn I	(28)	55	72	330	376		392	1103	1114	1208	
		394	1105	1116	1210		1221	1249	1258	1280	
		1223	1251	1260	1282		2460	2464	2483	2794	
		2462	2466	2485	2796		2872	2953	2962	3040	
		2874	2955	2964	3042		3416	3432	3791	3803	
		3418	3434	3793	3805		3881	3889	3900	3975	
		3883	3891	3902	3977	Mbo II	(10)	104	1878	2106	2983
DpnII	(28)	53	70	328	374		3193	3275	3442	3642	
		392	1103	1114	1208		3812	3885			
		1221	1249	1258	1280	Mlu I	(1)	1509			
		2460	2464	2483	2794	Mme I	(3)	1715	4149	4333	
		2872	2953	2962	3040	Mnl I	(29)	327	1059	1146	1149
		3416	3432	3791	3803		1158	1166	1302	1341	
		3881	3889	3900	3975		1350	1767	2098	2376	
Dra I	(5)	15	122	1325	3767		2382	2405	2411	2419	
		3786					2422	2434	2474	2538	
Dra III	(1)	1739					2674	3031	3223	3429	
Drd I	(3)	1694	2650	4439			3461	3743	4113	4364	
Dsa I	(4)	878	1123	2352	3055		4437				
Eae I	(6)	307	1136	2529	2703	Msc I	(1)	2705			
		3094	3121			Mse I	(20)	14	20	24	121
Eag I	(2)	1136	2529				486	525	1324	1385	
Ear I	(3)	2090	2967	3177			1506	1527	1538	1550	
Eco57 I	(3)	2768	3200	4000			1561	1578	1676	1947	
EcoN I	(1)	339					3766	3780	3785	3837	
EcoO109 I	(1)	3721				Msl I	(4)	288	883	1269	3060
EcoR I	(1)	1233				Msp I	(21)	163	405	515	1219
EcoR II	(11)	606	799	2157	2212		1265	1841	2528	2605	
		2229	3008	3587	3690		2627	2655	2786	2876	
		4380	4393	4514			2943	3124	3399	3407	
Ehe I	(1)	2624					3499	3973	4163	4189	
Fnu4H I	(35)	185	280	307	457		4336				

MspAl I	(5)	64	2121	2729	3958	Acc65 I	G`GTAC,C	1	AcI I	C`CG,C	64
Mun I	(1)	4203				Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	2
Nae I	(3)	1842	3125	3408		Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Nar I	(1)	2623				Ahd I	GCANN,N`NNGTC	-	Alu I	AG CT	16
Nci I	(6)	164	515	2627	2787	Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
Nco I	(4)	3400	4164			Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Nde I	(1)	878	1123	2352	3055	Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	1
Nde I	(1)	752				Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
NgoM I	(3)	1840	3123	3406		Ava I	C`YCGR,G	1	Ava II	G`GWC,C	3
Nhe I	(1)	1227				Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Nla III	(20)	257	293	371	381	Ban I	G`GYRC,C	5	Ban II	G,RCY`C	3
		822	882	1127	2053	Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	-
		2193	2265	2356	2497	Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
		2842	3028	3059	3085	Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	6
		3441	3825	4545	4596	Bfa I	C`TA,G	11	Bgl I	GCCN,NNN`NGGC	4
Nla IV	(17)	403	985	1121	1223	Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-
		1778	1799	1811	2002	Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
		2163	2235	2624	2659	BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
		3507	3586	3631	4474	BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	16
		4513				BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	2
Not I	(1)	1136				Bsg I	GTGCAG 22/20	-	BsIC I	TT`CG,AA	1
Nsi I	(3)	2195	2267	4598		BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
Nsp7524 I	(4)	2189	2261	3024	4541	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
NspB II	(5)	64	2121	2729	3958	BsmA I	GTCTC`9	6	BsmB I	CGTCTC 7/11	-
		4203				BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	35
NspH I	(4)	2193	2265	3028	4545	Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
Pac I	(1)	24				BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
Paer7 I	(1)	1238				BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
Pal I	(21)	309	602	795	1138	BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
		1589	1731	2386	2392	BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	1
		2401	2444	2531	2705	BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
		3096	3123	3632	3689	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
		3722	4067	4501	4519	BstN I	CC`W,GG	11	BstU I	CG CG	18
		4530				BstX I	CCAN,NNMN`NTGG	1	BstY I	R`GATC,Y	11
PflM I	(1)	1268				Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	31
Ple I	(2)	1674	2106			Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1
Pme I	(1)	15				Csp6 I	G`TA,C	9	Dde I	C`TNA,G	7
Psp1406 I	(2)	98	471			Dpn I	GA TC	28	DpnII	`GATC,	28
Pst I	(1)	458				Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Pvu I	(1)	331				Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Pvu II	(2)	2121	2729			Eae I	Y`GGCC,R	6	Eag I	C`GGCC,G	2
Rsa I	(9)	219	737	762	817	Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
		850	901	1058	1121	Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
		2929				EcoN I	CCTNN`N,NNAGG	1	EcoO109 I	RG`GNC,CY	1
		3139				EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	11
Rsr II	(1)	3139				EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Sal I	(1)	1143				Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	35
Sap I	(2)	2967	3177			Fok I	GGATG 14/18	7	Fse I	GG,CCGG`CC	-
Sau3A I	(28)	53	70	328	374	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
		392	1103	1114	1208	Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	5
		1221	1249	1258	1280	Hae II	R,GGCC`Y	4	Hae III	GG CC	21
		2460	2464	2483	2794	Hga I	GACCG 9/14	8	HgiA I	G,WGCW`C	5
		2872	2953	2962	3040	HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	24
		3416	3432	3791	3803	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
		3881	3889	3900	3975	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12
Sau96 I	(9)	336	601	794	1730	HinI I	GR`CG,YC	8	HinP I	G`CG,C	24
		3139	3584	3630	3688	Hpa I	GTT AAC	1	Hpa II	C`CG,G	21
		3721				Hph I	GGTGA 12/11	6	Kas I	G`GCGC,C	1
Sca I	(1)	219				Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11
ScrF I	(17)	164	515	608	801	Mae II	A`CG,T	16	Mae III	`GTNAC,	16
		2159	2214	2231	2627	Mbo I	`GATC,	28	Mbo II	GAAGA 12/11	10
		2787	3010	3400	3589	Mlu I	A`CCGG,T	1	Mme I	TCCRAC 25/23	3
		3692	4164	4382	4395	Mnl I	CCTC 10/10	29	Msc I	TGG CCA	1
		4516				Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
Sec I	(16)	878	1123	2157	2229	Msp I	C`CG,G	21	MspAl I	CMG CKG	5
		2352	2387	2396	2445	Mun I	C`AATT,G	1	Nae I	GCC GGC	3
		2786	3055	3460	3587	Nar I	GG`CG,CC	1	Nci I	CC`S,GG	6
		3588	3690	3691	4381	Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
SfaN I	(13)	247	440	876	1438	NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	1
		2201	2273	2582	2837	Nla III	,CATG`	20	Nla IV	GGN NCC	17
		2921	2985	3053	3260	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
		4445				Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
Sfc I	(4)	454	1958	4085	4276	NspB II	CMG CKG	5	NspH I	R,CATG`Y	4
Sfi I	(1)	2398				Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
SnaB I	(1)	858				Pal I	GG CC	21	PflM I	CCAN,NNN`NTGG	1
Spe I	(1)	1244				Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Sph I	(3)	2193	2265	3028		Pml I	CAC GTG	2	PpuM I	RG`GWC,CY	-
Ssp I	(2)	1531	2084			Psp1406 I	AA`CG,TT	-	PspA I	C`CCGG,G	-
Stu I	(1)	2444				Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Sty I	(6)	878	1123	2352	2445	Pvu II	CAG CTG	2	Rsa I	GT AC	9
		3055	3460			Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Taq I	(15)	46	1144	1171	1239	Sac II	CC,CC`GG	-	Sal I	G`TCGA,C	1
		1772	2463	2736	2892	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	28
		2916	2952	3114	3305	Sau96 I	G`GNC,C	9	Soa I	AGT ACT	1
		3350	3605	4443		ScrF I	CC`N,GG	17	Sec I	C`CNNG,G	16
Tfi I	(5)	3108	3242	3352	3389	SfaN I	GCATC 9/13	13	Sfc I	C`TRYA,G	4
		4567				Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Tsp45 I	(5)	227	438	1912	2743	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
		3049				Sph I	G,CATG`C	3	Spl I	C`GTAC,C	-
Tth111 I	(1)	2741				Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Tth111 II	(4)	3059	3919	3949	3958	Stu I	AGG CCT	1	Sty I	C`CWWG,G	6
Vsp I	(1)	525				Taq I	T`CG,A	15	Tfi I	G`AWT,C	5
Xba I	(1)	1149				Tsp45 I	`GTSAC,	5	Tth111 I	GACN`N,NGTC	1
Xho I	(1)	1238				Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	1
Xho II	(11)	53	70	1103	1221	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
		2794	3040	3432	3791	Xcm I	CCANNNN,N`NNNNTGG-		Xho I	C`TCGA,G	1
		3803	3889	3900		Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
Xma III	(2)	1136	2529			Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1
Xmn I	(1)	100									

Site usage in CMVCF2.TXT:

Aat II G,ACGT`C 4 Acc I GT`MK,AC 1