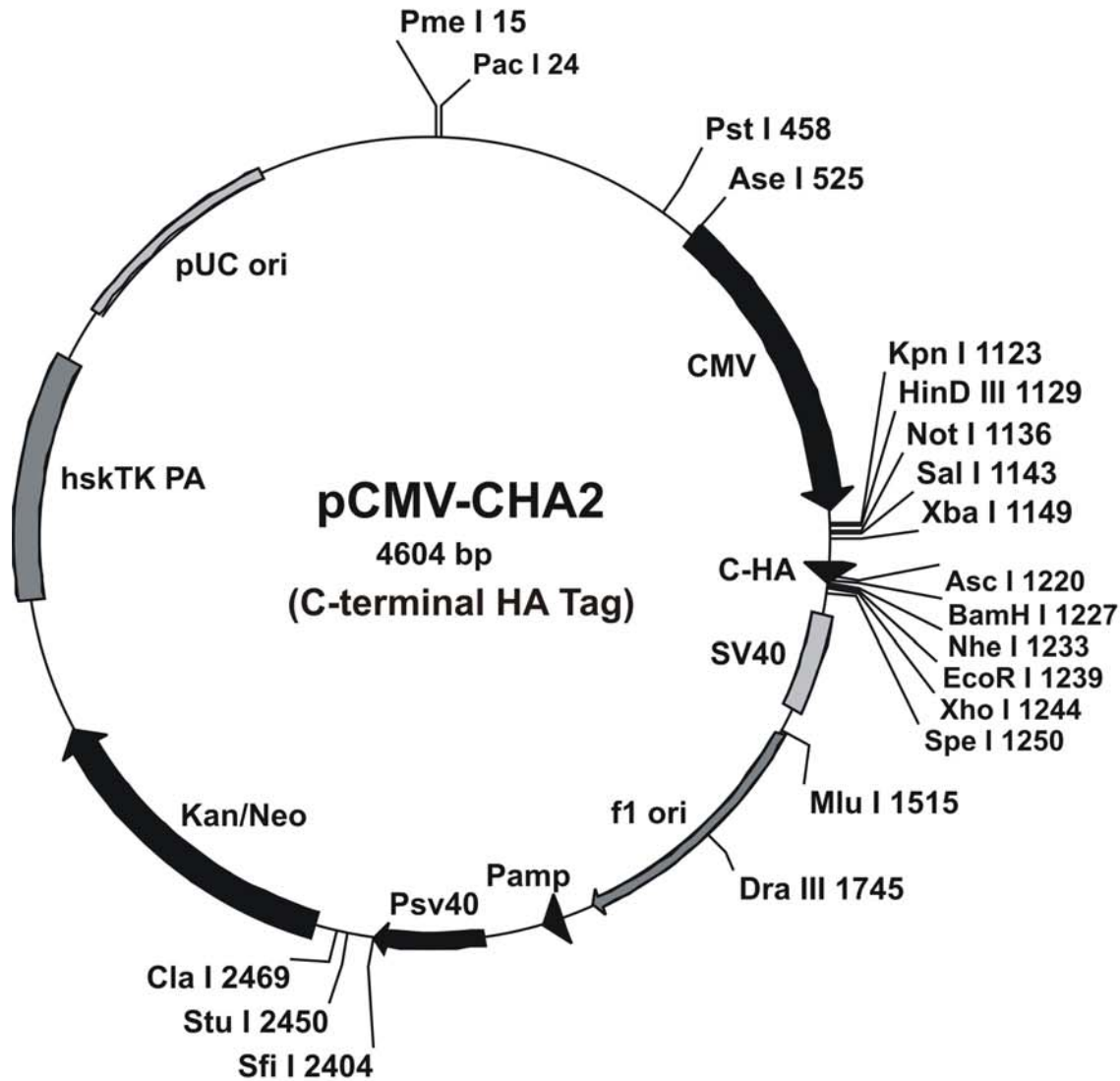
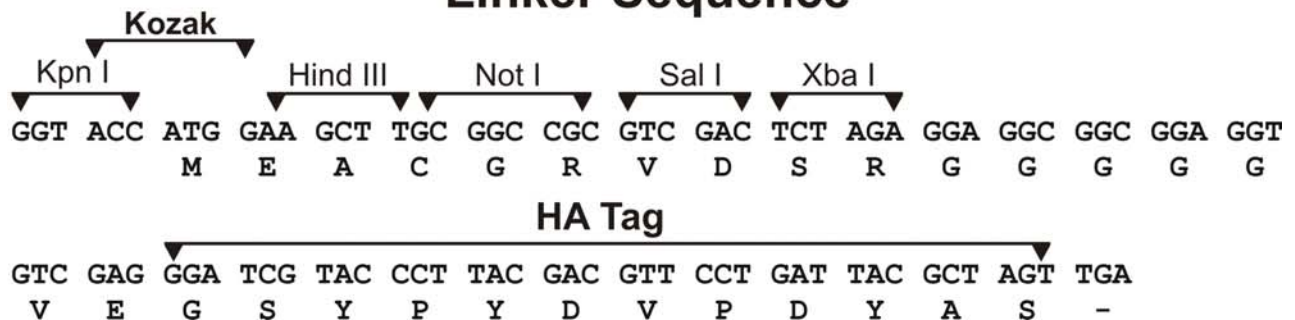


Name of Vector: pCMV-CHA2  
 Antibiotic Selection: Kan  
 Created by: Wei Jiang and Yien Li  
 (He Lab @ The University of Chicago)  
 Date of Creation: June 2004



### Linker Sequence



## pCMV-CHA2 Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60  
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120  
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180  
tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240  
tcttacggatggcatgacagtaagagaattatgcagtgtgcccataacatgagtataaa 300  
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360  
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420  
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480  
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540  
CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600  
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTGACGTCAATAATGACGTATGTTT 660  
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720  
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780  
ATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCCTA 840  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900  
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960  
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020  
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080  
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGCGGCCG 1140  
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGAGGGATCGTACCCTTACGACGTTCTCTGA 1200  
TTACGCTAGTTGagatcGGCGCGCCGGATCCGCTAGCGAATTCTCGAGACTAGTGATCta 1260  
tccgatccaccggannnnnnTAACTGATCATAATCAGCCATAACCACATTTGTAGAGGTTT 1320  
TACTTGCTTTAAAAAACCTCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAA 1380  
TTGTTGTTGTTAACTTGTATTATGCGCTTATAATGGTTACAAATAAAGCAATAGCATCA 1440  
CAAATTTACAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCA 1500  
TCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTTGTAAAATTCGCGTTAAAT 1560  
TTTTGTAAAATCAGCTCATTTTTTTAACCAATAGGCCGAAATCGGCAAATCCCTTATAAA 1620  
TCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTA 1680  
TTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAACCGTCTATCAGGGCGATGGCCCA 1740  
CTACGTGAACCATCACCTAATCAAGTTTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAAT 1800  
CGGAACCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCG 1860  
AGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTC 1920  
ACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGGTCAGGT 1980  
GGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCA 2040  
AATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAGG 2100  
AAGAGTCTGAGGCGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAGT 2160  
CCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCA 2220  
GGTGTGGAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATT 2280  
AGTCAGCAACCATAGTCCCGCCCTAACTCCGCCATCCCGCCCTAACTCCGCCAGTT 2340  
CCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCG 2400  
CCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTT 2460  
GCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTG 2520  
CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGCTATGACTGGGCACAACAG 2580  
ACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTGAGCGCAGGGGCGCCCGTTCTT 2640  
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GGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTT 2820  
GCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGAT 2880  
CCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGG 2940  
ATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCA 3000  
GCCGAACTGTTCCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACC 3060  
CATGGCGATGCCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGTTTTTCTGGATTTCATC 3120  
GACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGAT 3180  
ATTGCTGAAGAGCTTGGCGGCAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCC 3240

GCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGA 3300  
 CTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATT 3360  
 CCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGA 3420  
 TGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAA 3480  
 CTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGAC 3540  
 AGAATAAAACGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCT 3600  
 GGCACCTCTGTGATAACCCACCGAGACCCCATTTGGGGCAATACGCCCGGTTTTCTTCT 3660  
 TTTCCCCACCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGG 3720  
 CGGCAGGCCCTGCCATAGCCTCAGTTACTCATATATACTTTAGATTGATTTAAAACCTTC 3780  
 ATTTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAATCC 3840  
 CTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTT 3900  
 CTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCACCGCTAC 3960  
 CAGCGGTGGTTTTGTTTGC CGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGCT 4020  
 TCAGCAGAGCGCAGATAACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACT 4080  
 TCAAGAACTCTGTAGCACCGCCTACATACTCGTCTGCTAATCCTGTTACCAGTGGCTG 4140  
 CTGCCAGTGGCGATAAGTCTGTGCTTACC GGGTTGGACTCAAGACGATAGTTACC GGATA 4200  
 AGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTGGAGCGAACGA 4260  
 CCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAG 4320  
 GGAGAAAAGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGG 4380  
 AGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTCCGGTTTTCCGCCACCTCTGAC 4440  
 TTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCA 4500  
 ACGCGCCCTTTTTACGGTTCCTGTCCTTTTTGCTGTCCTTTTTGCTCACATGTTCTTTCCTG 4560  
 CGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4604

Unique enzymes in CMVCHA2.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 1220  
 BssH II G`CGCG,C 1220  
 BamH I G`GATC,C 1227  
 Nhe I G`CTAG,C 1233  
 EcoR I G`AATT,C 1239  
 Ava I C`YCGR,G 1244  
 PaeR7 I C`TCGA,G 1244  
 Xho I C`TCGA,G 1244  
 Spe I A`CTAG,T 1250  
 PflM I CCAN,NNN`NTGG 1274  
 BstX I CCAN,NNNN`NTGG 1275  
 Bcl I T`GATC,A 1286  
 Mun I C`AATT,G 1379  
 Hpa I GTT|AAC 1392  
 Mlu I A`CGCG,T 1515  
 Dra III CAC,NNN`GTG 1745  
 Sfi I GGCCN,NNN`NGGCC 2404  
 Stu I AGG|CCT 2450  
 Cla I AT`CG,AT 2469  
 Kas I G`GCGC,C 2628  
 Nar I GG`CG,CC 2629  
 Ehe I GGC|GCC 2630

Bbe I G,GCGC`C 2632  
 Msc I TGG|CCA 2711  
 Tth111 I GACN`N,NGTC 2747  
 Rsr II CG`GWC,CG 3145  
 BsiC I TT`CG,AA 3311  
 BstB I TT`CG,AA 3311  
 Bsa I GGTCTC 7/11 3618  
 EcoO109 I RG`GNC,CY 3727  
 Number of enzymes = 49

The following enzymes do not cut in CMVCHA2.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

CMVCHA2.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	1231
		1889	1916	1944	1947
		1961	2004	2051	2114
		2299	2311	2320	2332
		2342	2353	2399	2538
		2601	2695	2759	2860
		2863	3103	3143	3148
		3198	3214	3240	3296
		3365	3368	3434	3516
		3581	3648	3721	3955
		3964	4099	4209	4330
		4349	4476	4504	4595
Afl III	(2)	1515	4547		
Aha II	(8)	160	640	693	776
		962	2629	3331	3410
Alu I	(16)	347	410	510	1084
		1131	1408	1575	1832
		2127	2415	2735	3193
		3990	4247	4293	4383
Alw I	(19)	60	66	381	1099
		1183	1223	1234	1260
		2496	2807	2874	3053

		3418	3445	3804	3805			3811	3889	3897	3908
		3902	3902	3988				3983			
AlwN I	(2)	3730	4138			DpnII	(29)	53	70	328	374
Apal I	(2)	28	4233					392	1103	1114	1176
Apo I	(4)	1239	1443	1547	1558			1214	1227	1255	1264
Asc I	(1)	1220						1286	2466	2470	2489
Ase I	(1)	525						2800	2878	2959	2968
Asp718	(1)	1119						3046	3422	3438	3797
Ava I	(1)	1244						3809	3887	3895	3906
Ava II	(3)	336	3145	3590				3981			
Avr II	(2)	2451	3466			Dra I	(5)	15	122	1331	3773
BamH I	(1)	1227						3792			
Ban I	(5)	983	1119	1782	2628	Dra III	(1)	1745			
		2663				Drd I	(3)	1700	2656	4445	
Ban II	(3)	1820	2994	3704		Dsa I	(4)	878	1123	2358	3061
Bbe I	(1)	2632				Eae I	(6)	307	1136	2535	2709
Bbv I	(7)	468	1417	2702	2744			3100	3127		
		3265	3718	4218		Eag I	(2)	1136	2535		
Bcl I	(1)	1286				Ear I	(3)	2096	2973	3183	
Bcn I	(6)	165	516	2634	2794	Eco57 I	(3)	2774	3206	4006	
		3407	4171			EcoN I	(1)	339			
Bfa I	(12)	507	1110	1150	1207	EcoO109 I	(1)	3727			
		1234	1251	1478	1896	EcoR I	(1)	1239			
		2452	3467	3801	4054	EcoR II	(11)	606	799	2163	2218
Bgl I	(4)	608	730	801	2404			2235	3014	3593	3696
Bpm I	(2)	3412	3469					4386	4399	4520	
Bsa I	(1)	3618				Ehe I	(1)	2630			
BsaA I	(3)	858	1745	2933		Fnu4H I	(35)	185	280	307	457
BsaB I	(2)	1291	2488					1136	1139	1160	1406
BsaH I	(8)	160	640	693	776			1925	1947	1961	2399
		962	2629	3331	3410			2538	2590	2601	2691
BsaJ I	(16)	878	1123	2163	2235			2696	2733	2774	2861
		2358	2393	2402	2451			2864	2867	3103	3199
		2792	3061	3466	3593			3240	3254	3368	3707
		3594	3696	3697	4387			3722	3933	4139	4142
BsaW I	(6)	404	1270	2660	3504			4207	4350	4505	
		4194	4341			Fok I	(6)	261	2302	2496	2953
BseR I	(2)	1168	2447					2978	3432		
BsiC I	(1)	3311				Fsp I	(2)	477	2731		
BsiE I	(5)	182	331	1139	2538	Gdi II	(7)	308	1135	1137	2534
		4213						2536	3099	3126	
BsiHKA I	(5)	32	117	2742	2932	Gsu I	(2)	3413	3468		
		4237				Hae I	(5)	2450	2711	4073	4525
Bsm I	(2)	1380	1473					4536			
BsmA I	(6)	951	1242	2054	2472	Hae II	(4)	1896	1904	2632	4307
		3491	3619			Hae III	(21)	309	602	795	1138
BsmF I	(10)	693	844	1012	2145			1595	1737	2392	2398
		2217	2281	2780	3312			2407	2450	2537	2711
		3421	3576					3102	3129	3638	3695
BsoF I	(35)	185	280	307	457			3728	4073	4507	4525
		1136	1139	1160	1406			4536			
		1925	1947	1961	2399	Hga I	(8)	167	1043	1131	1963
		2538	2590	2601	2691			3338	3417	3858	4436
		2696	2733	2774	2861	HgiA I	(5)	32	117	2742	2932
		2864	2867	3103	3199			4237			
		3240	3254	3368	3707	HgiE II	(2)	1268	3958		
		3722	3933	4139	4142	Hha I	(24)	141	478	1222	1224
		4207	4350	4505				1895	1903	1929	1951
Bspl286 I	(2)	117	2932					1960	1973	2004	2623
BspH I	(2)	2055	3827					2631	2695	2732	2998
BspM I	(3)	2516	2897	3347				3258	3434	3520	3923
Bsr I	(11)	54	226	493	814			4032	4206	4306	4373
		1659	2337	2572	2773	HinC II	(3)	158	1145	1392	
		4019	4133	4146		Hind II	(3)	158	1145	1392	
BsrB I	(4)	1889	2053	3242	3296	Hind III	(1)	1129			
BsrD I	(2)	466	2862			Hinf I	(12)	928	1146	1672	1694
BssH II	(1)	1220						2104	3114	3248	3300
BssS I	(4)	31	3221	3347	4374			3358	3395	4177	4573
BstB I	(1)	3311				HinI I	(8)	160	640	693	776
BstN I	(11)	608	801	2165	2220			962	2629	3331	3410
		2237	3016	3595	3698	HinP I	(24)	139	476	1220	1222
		4388	4401	4522				1893	1901	1927	1949
BstU I	(18)	141	578	1141	1222			1958	1971	2002	2621
		1517	1553	1929	1949			2629	2693	2730	2996
		1973	2004	2695	2996			3256	3432	3518	3921
		3434	3518	3581	3650			4030	4204	4304	4371
		3923	4504			Hpa I	(1)	1392			
BstX I	(1)	1275				Hpa II	(21)	163	405	515	1225
BstY I	(11)	53	70	1103	1227			1271	1847	2534	2611
		2800	3046	3438	3797			2633	2661	2792	2882
		3809	3895	3906				2949	3130	3405	3413
Bsu36 I	(2)	2109	3741					3505	3979	4169	4195
Cac8 I	(31)	454	604	797	1133			4342			
		1222	1235	1848	1891	Hph I	(6)	215	893	1747	2808
		1905	2178	2197	2250			3699	3815		
		2269	2523	2709	2928	Kas I	(1)	2628			
		2994	3000	3028	3032	Kpn I	(1)	1123			
		3073	3077	3131	3414	Mae I	(12)	507	1110	1150	1207
		3601	3648	3704	3726			1234	1251	1478	1896
		3937	4497	4534				2452	3467	3801	4054
Cfr10 I	(4)	1846	2948	3129	3412	Mae II	(17)	98	471	640	652
Cla I	(1)	2469						693	776	857	962
Csp6 I	(10)	218	736	761	816			1192	1689	1701	1744
		849	900	1057	1120			1854	2745	2932	3713
		1181	2934					3846			
Dde I	(7)	199	2109	2411	3292	Mae III	(16)	39	227	380	438
		3741	3864	4273				579	666	1015	1417
Dpn I	(29)	55	72	330	376			1918	1930	2749	3055
		394	1105	1116	1178			3745	4011	4127	4190
		1216	1229	1257	1266	Mbo I	(29)	53	70	328	374
		1288	2468	2472	2491			392	1103	1114	1176
		2802	2880	2961	2970			1214	1227	1255	1264
		3048	3424	3440	3799			1286	2466	2470	2489

		2800	2878	2959	2968
		3046	3422	3438	3797
		3809	3887	3895	3906
		3981			
Mbo II	(10)	104	1884	2112	2989
		3199	3281	3448	3648
		3818	3891		
Mlu I	(1)	1515			
Mme I	(3)	1721	4155	4339	
Mnl I	(29)	327	1059	1146	1149
		1158	1166	1308	1347
		1356	1773	2104	2382
		2388	2411	2417	2425
		2428	2440	2480	2544
		2680	3037	3229	3435
		3467	3749	4119	4370
		4443			
Msc I	(1)	2711			
Mse I	(20)	14	20	24	121
		486	525	1330	1391
		1512	1533	1544	1556
		1567	1584	1682	1953
		3772	3786	3791	3843
Msl I	(4)	288	883	1275	3066
Msp I	(21)	163	405	515	1225
		1271	1847	2534	2611
		2633	2661	2792	2882
		2949	3130	3405	3413
		3505	3979	4169	4195
		4342			
MspAl I	(5)	64	2127	2735	3964
		4209			
Mun I	(1)	1379			
Nae I	(3)	1848	3131	3414	
Nar I	(1)	2629			
Nci I	(6)	164	515	2633	2793
		3406	4170		
Nco I	(4)	878	1123	2358	3061
Nde I	(1)	752			
NgoM I	(3)	1846	3129	3412	
Nhe I	(1)	1233			
Nla III	(20)	257	293	371	381
		822	882	1127	2059
		2199	2271	2362	2503
		2848	3034	3065	3091
		3447	3831	4551	4602
Nla IV	(17)	403	985	1121	1229
		1784	1805	1817	2008
		2169	2241	2630	2665
		3513	3592	3637	4480
		4519			
Not I	(1)	1136			
Nsi I	(3)	2201	2273	4604	
Nsp7524 I	(4)	2195	2267	3030	4547
NspB II	(5)	64	2127	2735	3964
		4209			
NspH I	(4)	2199	2271	3034	4551
Pac I	(1)	24			
Paer7 I	(1)	1244			
Pal I	(21)	309	602	795	1138
		1595	1737	2392	2398
		2407	2450	2537	2711
		3102	3129	3638	3695
		3728	4073	4507	4525
		4536			
PflM I	(1)	1274			
Ple I	(2)	1680	2112		
Pme I	(1)	15			
Psp1406 I	(2)	98	471		
Pst I	(1)	458			
Pvu I	(1)	331			
Pvu II	(2)	2127	2735		
Rsa I	(10)	219	737	762	817
		850	901	1058	1121
		1182	2935		
Rsr II	(1)	3145			
Sal I	(1)	1143			
Sap I	(2)	2973	3183		
Sau3A I	(29)	53	70	328	374
		392	1103	1114	1176
		1214	1227	1255	1264
		1286	2466	2470	2489
		2800	2878	2959	2968
		3046	3422	3438	3797
		3809	3887	3895	3906
		3981			
Sau96 I	(9)	336	601	794	1736
		3145	3590	3636	3694
		3727			
Sca I	(1)	219			
ScrF I	(17)	164	515	608	801
		2165	2220	2237	2633
		2793	3016	3406	3595
		3698	4170	4388	4401
		4522			
Sec I	(16)	878	1123	2163	2235
		2358	2393	2402	2451
		2792	3061	3466	3593
		3594	3696	3697	4387
SfaN I	(13)	247	440	876	1444
		2207	2279	2588	2843
		2927	2991	3059	3266
		4451			

Sfc I	(4)	454	1964	4091	4282
Sfi I	(1)	2404			
SnaB I	(1)	858			
Spe I	(1)	1250			
Sph I	(3)	2199	2271	3034	
Ssp I	(2)	1537	2090		
Stu I	(1)	2450			
Sty I	(6)	878	1123	2358	2451
		3061	3466		
Taq I	(15)	46	1144	1171	1245
		1778	2469	2742	2898
		2922	2958	3120	3311
		3356	3611	4449	
Tfi I	(5)	3114	3248	3358	3395
		4573			
Tsp45 I	(5)	227	438	1918	2749
		3055			
Tth111 I	(1)	2747			
Tth111 II	(4)	3065	3925	3955	3964
Vsp I	(1)	525			
Xba I	(1)	1149			
Xho I	(1)	1244			
Xho II	(11)	53	70	1103	1227
		2800	3046	3438	3797
		3809	3895	3906	
Xma III	(2)	1136	2535		
Xmn I	(1)	100			

Site usage in CMVCHA2.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 I 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,RCY`C	3
Bbe I	G,CGCC`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	12	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	ACCTGC 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	4	Bssh II	G`CGCG,C	1
BssS I	C`TCGT,G	-	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	11
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	10	Dde I	C`TNA,G	7
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	3	Eco47 III	AGC GTG	-
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTC	-
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,CGCC`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	12
Mae II	A`CG,T	17	Mae III	`GTNAC,	16
Mbo I	`GATC,	29	Mbo II	GAAGA 12/11	10
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
Mnl I	CCTC 10/10	29	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`CGCG,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	TCG 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	-
Psp1406 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	10
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	11	Xma I	C`CCGG,G	-
Xma III	C`GCC,G	2	Xmn I	GAANN NNTTC	1