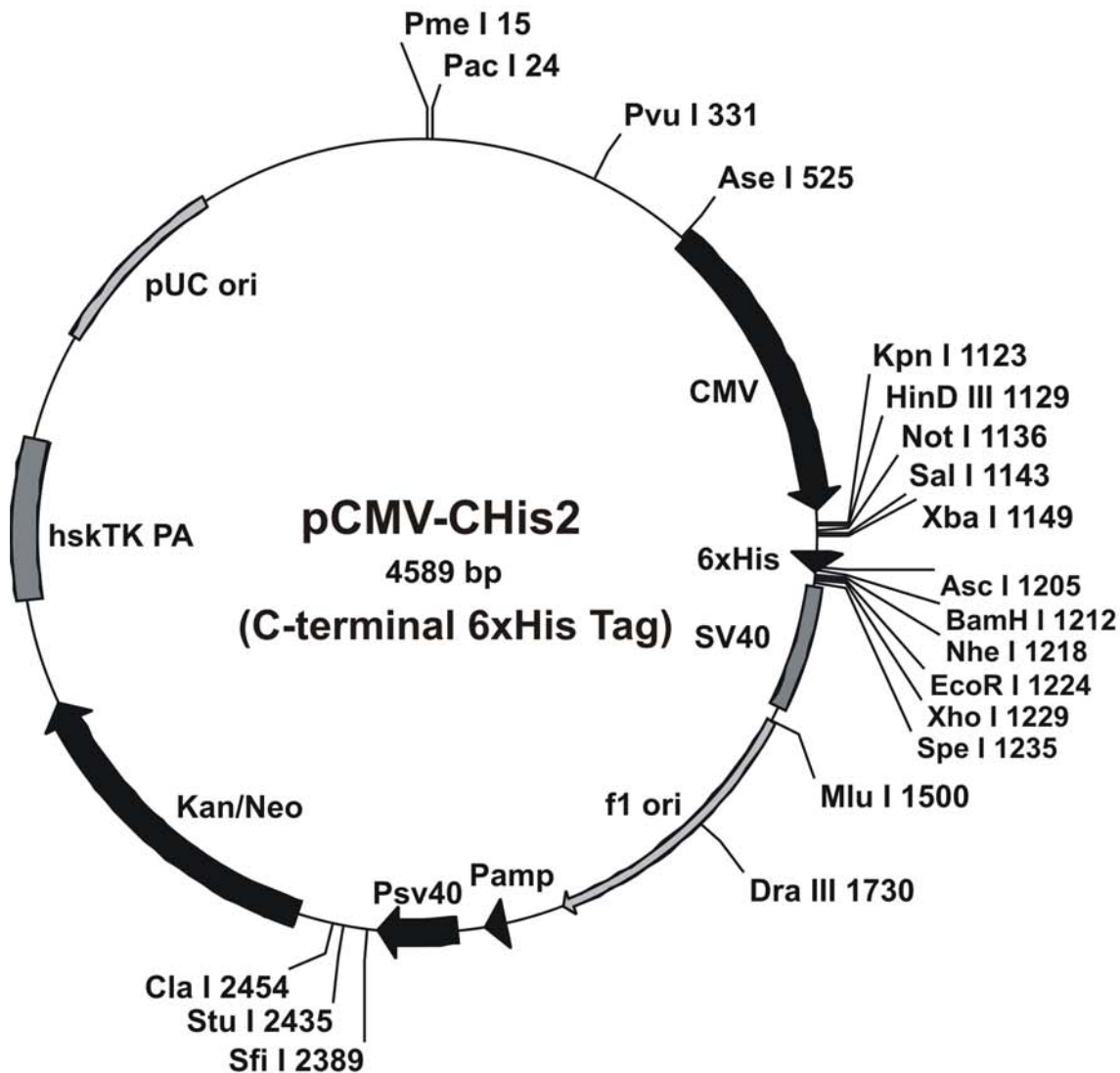
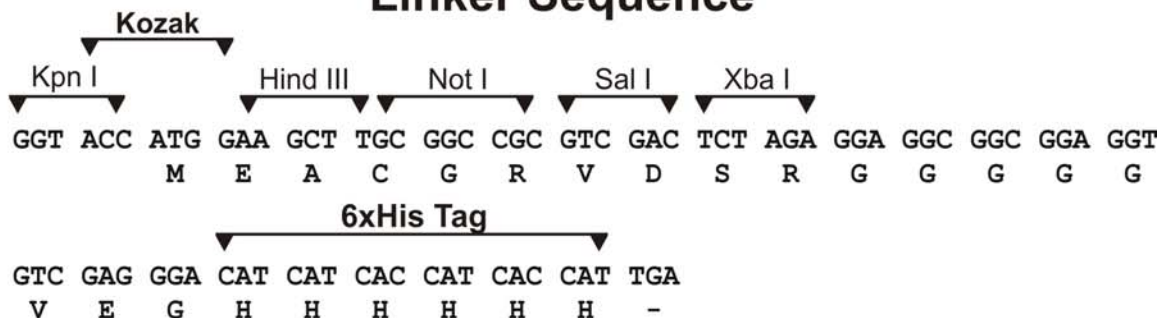


Name of Vector: pCMV-CHis2
 Antibiotic Selection: Kan
 Created by: Wei Jiang and Yien Li
 (He Lab @ The University of Chicago)
 Date of Creation: June 2004



Linker Sequence



pCMV-CHis2 Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgtgccataacatgagtgataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTTCTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGCGGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGAGGGACATCATCACCATCACCATTGaga 1200
tcGGCGCGCCGGATCCGCTAGCGAATTCTCGAGACTAGTGATCtatccgatccaccggan 1260
nnnnnTAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAA 1320
ACCTCCACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACT 1380
TGTTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATA 1440
AAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAC 1500
GCGTAAATTGTAAGCGTTAATATTTTTGTTAAAAATTCGCGTTAAATTTTTGTTAAATCAGC 1560
TCATTTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACC 1620
GAGATAGGGTTGAGTGTGTTCCAGTTTTGGAACAAGAGTCCACTATTAAGAACGTGGAC 1680
TCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCACTACGTGAACCATCA 1740
CCCTAATCAAGTTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGG 1800
AGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAG 1860
AAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACC 1920
ACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGA 1980
AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTC 2040
ATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGCG 2100
GAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGTTGTGAAAAGTCCCCAGGCTCCCCAG 2160
CAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCC 2220
CAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAG 2280
TCCCGCCCCCTAACTCCGCCCATCCGCCCCCTAACTCCGCCCAGTTCGCCCCATTCTCCGC 2340
CCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGC 2400
TATTCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAA 2460
GAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCG 2520
GCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCT 2580
GATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGAC 2640
CTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACG 2700
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GTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCA 2880
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GTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACGTGTTCCGC 3000
AGGCTCAAGGCGAGCATGCCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGC 3060
TTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTG 3120
GGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTT 3180
GGCGGCAATGGGCTGACCGCTTCCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCCGAG 3240

CGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAA 3300
 TGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCT 3360
 ATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCG 3420
 GGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGG 3480
 AGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAACGCACG 3540
 GTGTTGGGTTCGTTTGTTCATAAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTCGATA 3600
 CCCCACCGAGACCCCAATTGGGGCCAATACGCCCGCCTTCTTCCTTTTTCCACCCACC 3660
 CCCCAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCA 3720
 TAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAA 3780
 GGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTT 3840
 CGTTCCTACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTT 3900
 TTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCCGCTACCAGCGGTGGTTTTGTT 3960
 TGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGA 4020
 TACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACCTTCAAGAACTCTGTAG 4080
 CACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATA 4140
 AGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCG 4200
 GCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGA 4260
 GATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACA 4320
 GGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAA 4380
 ACGCCTGGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTT 4440
 TGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAACGCCAGCAACGCGGCCTTTTTTAC 4500
 GGTTCCTGGCCTTTTGTCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGATT 4560
 CTGTGGATAACCGTATTACCGCCATGCAT 4589

Unique enzymes in CMVCHIS2.TXT:

Pme I	CTTT AAAC	15	BstE II	Eco47 III	Eco72 I	EcoR V	Esp I	
Pac I	TTA,AT`TAA	24	Fse I	Nru I	Pml I	PpuM I	PspA I	
Xmn I	GAANN NNTTC	100	Sac I	Sac II	Sma I	Spl I	Srf I	
Sca I	AGT ACT	219	CMVCHIS2.TXT: sites sorted by name:					
Pvu I	CG,AT`CG	331	Aat II	(4)	643	696	779	965
EcoN I	CCTNN`N,NNAGG	339	Acc I	(1)	1144			
Pst I	C,TGCA`G	458	Acc65 I	(1)	1119			
Ase I	AT`TA,AT	525	Aci I	(64)	64	141	185	306
Vsp I	AT`TA,AT	525				352	576	604
Nde I	CA`TA,TG	752				630	797	888
SnaB I	TAC GTA	858				1025	1046	1107
Acc65 I	G`GTAC,C	1119				1139	1159	1162
Asp718	G`GTAC,C	1119				1874	1901	1929
Kpn I	G,GTAC`C	1123				1946	1989	2036
Hind III	A`AGCT,T	1129				2284	2296	2305
Not I	GC`GGCC,GC	1136				2327	2338	2384
Sal I	G`TCGA,C	1143				2586	2680	2744
Acc I	GT`MK,AC	1144				2848	3088	3128
Xba I	T`CTAG,A	1149				3183	3199	3225
Asc I	GG`CGCG,CC	1205				3350	3353	3419
BssH II	G`CGCG,C	1205				3566	3633	3706
BamH I	G`GATC,C	1212				3949	4084	4194
Nhe I	G`CTAG,C	1218				4334	4461	4489
EcoR I	G`AATT,C	1224	Afl III	(2)	1500	4532		
Ava I	C`YCGR,G	1229	Aha II	(8)	160	640	693	776
PaeR7 I	C`TCGA,G	1229				962	2614	3316
Xho I	C`TCGA,G	1229	Alu I	(16)	347	410	510	1084
Spe I	A`CTAG,T	1235				1131	1393	1560
PflM I	CCAN,NNN`NTGG	1259				2112	2400	2720
BstX I	CCAN,NNNN`NTGG	1260				3975	4232	4278
Bcl I	T`GATC,A	1271	Alw I	(18)	60	66	381	1099
Mun I	C`AATT,G	1364				1208	1219	1245
Hpa I	GTT AAC	1377				2792	2859	3038
Mlu I	A`CGCG,T	1500				3430	3789	3790
Dra III	CAC,NNN`GTG	1730				3887	3973	
Sfi I	GGCCN,NNN`NGGCC	2389	AlwN I	(2)	3715	4123		
Stu I	AGG CCT	2435	ApaL I	(2)	28	4218		
Cla I	AT`CG,AT	2454	Apo I	(4)	1224	1428	1532	1543
Kas I	G`GCGC,C	2613	Asc I	(1)	1205			
Nar I	GG`CG,CC	2614	Ase I	(1)	525			
Ehe I	GGC GCC	2615	Asp718	(1)	1119			
Bbe I	G,GCGC`C	2617	Ava I	(1)	1229			
Mec I	TGG CCA	2696	Ava II	(3)	336	3130	3575	
Tth111 I	GACN`N,NGTC	2732	Avr II	(2)	2436	3451		
Rsr II	CG`GWC,CG	3130	BamH I	(1)	1212			
BsiC I	TT`CG,AA	3296	Ban I	(5)	983	1119	1767	2613
BstB I	TT`CG,AA	3296				2648		
Bsa I	GGTCTC 7/11	3603	Ban II	(3)	1805	2979	3689	
EcoO109 I	RG`GNC,CY	3712	Bbe I	(1)	2617			
Number of enzymes = 49			Bbv I	(7)	468	1402	2687	2729
						3250	3703	4203
			Bcl I	(1)	1271			
			Bcn I	(6)	165	516	2619	2779
						3392	4156	
			Bfa I	(11)	507	1110	1150	1219
						1236	1463	1881
								2437

The following enzymes do not cut in CMVCHIS2.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

Bgl I	(4)	3452	3786	4039				4371	4384	4505	
Bpm I	(2)	608	730	801	2389	Ehe I	(1)	2615			
Bsa I	(1)	3397	3454			Fnu4H I	(35)	185	280	307	457
BsaA I	(3)	3603						1136	1139	1160	1391
BsaB I	(2)	858	1730	2918				1910	1932	1946	2384
BsaH I	(8)	1276	2473					2523	2575	2586	2676
		160	640	693	776			2681	2718	2759	2846
		962	2614	3316	3395			2849	2852	3088	3184
BsaJ I	(16)	878	1123	2148	2220			3225	3239	3353	3692
		2343	2378	2387	2436			3707	3918	4124	4127
		2777	3046	3451	3578			4192	4335	4490	
		3579	3681	3682	4372	Fok I	(6)	261	2287	2481	2938
BsaW I	(6)	404	1255	2645	3489			2963	3417		
		4179	4326			Fsp I	(2)	477	2716		
BseR I	(2)	1168	2432			Gdi II	(7)	308	1135	1137	2519
BsiC I	(1)	3296						2521	3084	3111	
BsiE I	(5)	182	331	1139	2523	Gsu I	(2)	3398	3453		
		4198				Hae I	(5)	2435	2696	4058	4510
BsiHKA I	(5)	32	117	2727	2917			4521			
		4222				Hae II	(4)	1881	1889	2617	4292
Bsm I	(2)	1365	1458			Hae III	(21)	309	602	795	1138
BsmA I	(6)	951	1227	2039	2457			1580	1722	2377	2383
		3476	3604					2392	2435	2522	2696
BsmF I	(11)	693	844	1012	1189			3087	3114	3623	3680
		2130	2202	2266	2765			3713	4058	4492	4510
		3297	3406	3561				4521			
BsoF I	(35)	185	280	307	457	Hga I	(8)	167	1043	1131	1948
		1136	1139	1160	1391			3323	3402	3843	4421
		1910	1932	1946	2384	HgiA I	(5)	32	117	2727	2917
		2523	2575	2586	2676			4222			
		2681	2718	2759	2846	HgiE II	(2)	1253	3943		
		2849	2852	3088	3184	Hha I	(24)	141	478	1207	1209
		3225	3239	3353	3692			1880	1888	1914	1936
		3707	3918	4124	4127			1945	1958	1989	2608
		4192	4335	4490				2616	2680	2717	2983
Bspl286 I	(2)	117	2917					3243	3419	3505	3908
BspH I	(2)	2040	3812			HinC II	(3)	158	1145	1377	
BspM I	(3)	2501	2882	3332		Hind II	(3)	158	1145	1377	
Bsr I	(11)	54	226	493	814	HinD III	(1)	1129			
		1644	2322	2557	2758	Hinf I	(12)	928	1146	1657	1679
		4004	4118	4131				2089	3099	3233	3285
BsrB I	(4)	1874	2038	3227	3281			3343	3380	4162	4558
BsrD I	(2)	466	2847			HinI I	(8)	160	640	693	776
BssH II	(1)	1205						962	2614	3316	3395
BssS I	(4)	31	3206	3332	4359	HinP I	(24)	139	476	1205	1207
BstB I	(1)	3296						1878	1886	1912	1934
BstN I	(11)	608	801	2150	2205			1943	1956	1987	2606
		2222	3001	3580	3683			2614	2678	2715	2981
		4373	4386	4507				3241	3417	3503	3906
BstU I	(18)	141	578	1141	1207	Hpa I	(1)	1377			
		1502	1538	1914	1934	Hpa II	(21)	163	405	515	1210
		1958	1989	2680	2981			1256	1832	2519	2596
		3419	3503	3566	3635			2618	2646	2777	2867
		3908	4489					2934	3115	3390	3398
BstX I	(1)	1260						3490	3964	4154	4180
BstY I	(11)	53	70	1103	1212			4327			
		2785	3031	3423	3782	Hph I	(8)	215	893	1177	1183
		3794	3880	3891				1732	2793	3684	3800
Bsu36 I	(2)	2094	3726			Kas I	(1)	2613			
Cac8 I	(31)	454	604	797	1133	Kpn I	(1)	1123			
		1207	1220	1833	1876	Mae I	(11)	507	1110	1150	1219
		1890	2163	2182	2235			1236	1463	1881	2437
		2254	2508	2694	2913			3452	3786	4039	
		2979	2985	3013	3017	Mae II	(16)	98	471	640	652
		3058	3062	3116	3399			693	776	857	962
		3586	3633	3689	3711			1674	1686	1729	1839
		3922	4482	4519				2730	2917	3698	3831
Cfr10 I	(4)	1831	2933	3114	3397	Mae III	(16)	39	227	380	438
Cla I	(1)	2454						579	666	1015	1402
Csp6 I	(9)	218	736	761	816			1903	1915	2734	3040
		849	900	1057	1120			3730	3996	4112	4175
		2919				Mbo I	(28)	53	70	328	374
Dde I	(7)	199	2094	2396	3277			392	1103	1114	1199
		3726	3849	4258				1212	1240	1249	1271
Dpn I	(28)	55	72	330	376			2451	2455	2474	2785
		394	1105	1116	1201			2863	2944	2953	3031
		1214	1242	1251	1273			3407	3423	3782	3794
		2453	2457	2476	2787			3872	3880	3891	3966
		2865	2946	2955	3033	Mbo II	(10)	104	1869	2097	2974
		3409	3425	3784	3796			3184	3266	3433	3633
		3874	3882	3893	3968			3803	3876		
DpnII	(28)	53	70	328	374	Mlu I	(1)	1500			
		392	1103	1114	1199	Mme I	(3)	1706	4140	4324	
		1212	1240	1249	1271	Mnl I	(29)	327	1059	1146	1149
		2451	2455	2474	2785			1158	1166	1293	1332
		2863	2944	2953	3031			1341	1758	2089	2367
		3407	3423	3782	3794			2373	2396	2402	2410
Dra I	(5)	3872	3880	3891	3966			2413	2425	2465	2529
		3777	122	1316	3758			2665	3022	3214	3420
Dra III	(1)	1730						3452	3734	4104	4355
Drd I	(3)	1685	2641	4430		Msc I	(1)	2696			
Dsa I	(4)	878	1123	2343	3046	Mse I	(20)	14	20	24	121
Eae I	(6)	307	1136	2520	2694			486	525	1315	1376
		3085	3112					1497	1518	1529	1541
Eag I	(2)	1136	2520					1552	1569	1667	1938
Ear I	(3)	2081	2958	3168				3757	3771	3776	3828
Eco57 I	(3)	2759	3191	3991				288	883	1260	3051
EcoN I	(1)	339				Msl I	(4)	288	883	1260	3051
EcoO109 I	(1)	3712				Msp I	(21)	163	405	515	1210
EcoR I	(1)	1224						1256	1832	2519	2596
EcoR II	(11)	606	799	2148	2203			2618	2646	2777	2867
		2220	2999	3578	3681						

		2934	3115	3390	3398
		3490	3964	4154	4180
		4327			
MspA1 I	(5)	64	2112	2720	3949
		4194			
Mun I	(1)	1364			
Nae I	(3)	1833	3116	3399	
Nar I	(1)	2614			
Nci I	(6)	164	515	2618	2778
		3391	4155		
Nco I	(4)	878	1123	2343	3046
Nde I	(1)	752			
NgoM I	(3)	1831	3114	3397	
Nhe I	(1)	1218			
Nla III	(20)	257	293	371	381
		822	882	1127	2044
		2184	2256	2347	2488
		2833	3019	3050	3076
		3432	3816	4536	4587
Nla IV	(17)	403	985	1121	1214
		1769	1790	1802	1993
		2154	2226	2615	2650
		3498	3577	3622	4465
		4504			
Not I	(1)	1136			
Nsi I	(3)	2186	2258	4589	
Nsp7524 I	(4)	2180	2252	3015	4532
NspB II	(5)	64	2112	2720	3949
		4194			
NspH I	(4)	2184	2256	3019	4536
Pac I	(1)	24			
Paer7 I	(1)	1229			
Pal I	(21)	309	602	795	1138
		1580	1722	2377	2383
		2392	2435	2522	2696
		3087	3114	3623	3680
		3713	4058	4492	4510
		4521			
Pf1M I	(1)	1259			
Ple I	(2)	1665	2097		
Pme I	(1)	15			
Psp1406 I	(2)	98	471		
Pst I	(1)	458			
Pvu I	(1)	331			
Pvu II	(2)	2112	2720		
Rsa I	(9)	219	737	762	817
		850	901	1058	1121
		2920			
Rsr II	(1)	3130			
Sal I	(1)	1143			
Sap I	(2)	2958	3168		
Sau3A I	(28)	53	70	328	374
		392	1103	1114	1199
		1212	1240	1249	1271
		2451	2455	2474	2785
		2863	2944	2953	3031
		3407	3423	3782	3794
		3872	3880	3891	3966
Sau96 I	(9)	336	601	794	1721
		3130	3575	3621	3679
		3712			
Sca I	(1)	219			
ScrF I	(17)	164	515	608	801
		2150	2205	2222	2618
		2778	3001	3391	3580
		3683	4155	4373	4386
		4507			
Sec I	(16)	878	1123	2148	2220
		2343	2378	2387	2436
		2777	3046	3451	3578
		3579	3681	3682	4372
SfaN I	(13)	247	440	876	1429
		2192	2264	2573	2828
		2912	2976	3044	3251
		4436			
Sfc I	(4)	454	1949	4076	4267
Sfi I	(1)	2389			
SnaB I	(1)	858			
Spe I	(1)	1235			
Sph I	(3)	2184	2256	3019	
Ssp I	(2)	1522	2075		
Stu I	(1)	2435			
Sty I	(6)	878	1123	2343	2436
		3046	3451		
Taq I	(15)	46	1144	1171	1230
		1763	2454	2727	2883
		2907	2943	3105	3296
		3341	3596	4434	
		3099	3233	3343	3380
		4558			
Tsp45 I	(5)	227	438	1903	2734
		3040			
Tth111 I	(1)	2732			
Tth111 II	(4)	3050	3910	3940	3949
Vsp I	(1)	525			
Xba I	(1)	1149			
Xho I	(1)	1229			
Xho II	(11)	53	70	1103	1212
		2785	3031	3423	3782
		3794	3880	3891	
Xma III	(2)	1136	2520		
Xmn I	(1)	100			

Site usage in CMVCHIS2.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	18	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	11	Bgl I	CCCN,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	11	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	-	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	11
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	31
Cfr10 I	R`CCGG,Y	4	Clal I	AT`CG,AT	1
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	7
Dpn I	GA TC	28	DpnII	`GATC,	28
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,C	2
Ear I	CTCTTC 7/10	3	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,CGCC`Y	4	Hae III	GG CC	21
Hga I	GACCG 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,C	21
Hph I	GGTGA 12/11	8	Kas I	G`GGCG,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,	28	Mbo II	GAAGA 12/11	10
Mlu I	A`CCGG,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	MspA1 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	GGN 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	Pf1M 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	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	GCTCTC 8/11	2	Sau3A I	`GATC,	28
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	GGCC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`CWVG,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`NNNNNTGG-	1	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
Xma III	C`GGCC,G	2	Xmn I	GAANN NNYTC	1