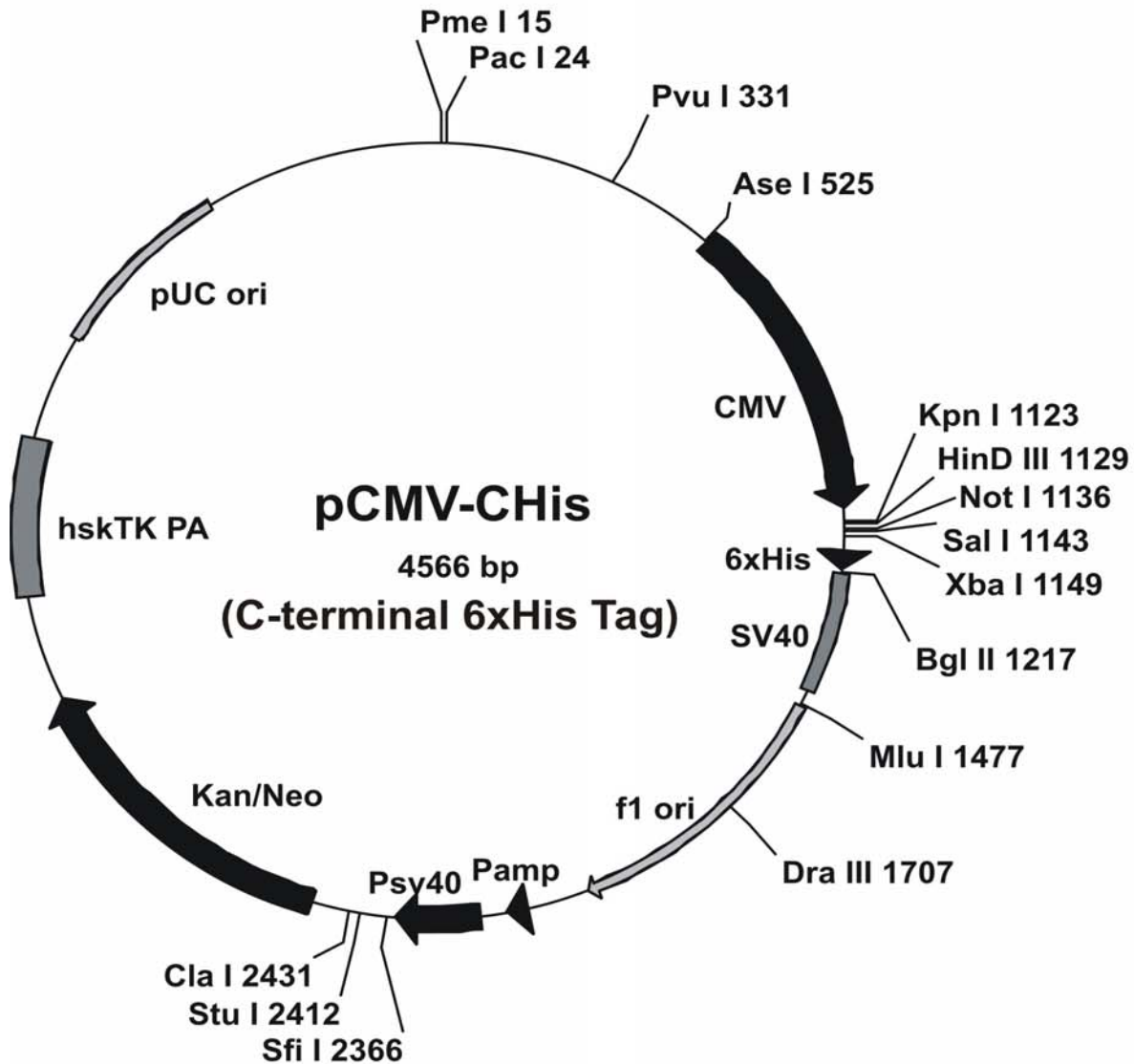
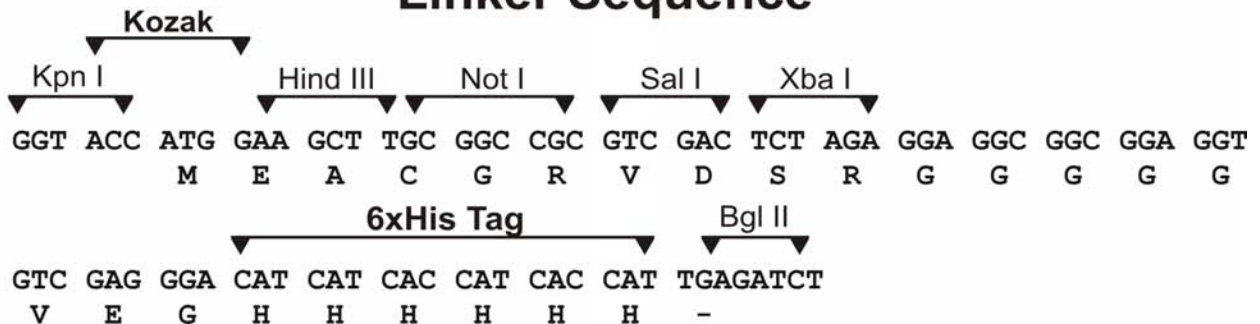


Name of Vector: pCMV-CHis
 Antibiotic Selection: Kan
 Created by: Wei Jiang and Qing Luo
 (He Lab @ The University of Chicago)
 Date of Creation: February 2004



Linker Sequence



pCMV-CHis Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgcgccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgtgcccataacatgagtgataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020
ACTCCGCCCATGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGCGGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGAGGGACATCATCACCATCACCATTGaga 1200
tctatccgatccaccggannnnnnTAAGTATCATAATCAGCCATACCACATTTGTAGAG 1260
GTTTTACTTGCTTTAAAAAACCTCCACACCTCCCCCTGAACCTGAAACATAAAATGAAT 1320
GCAATTGTTGTTGTTAACTTGTATTATGACGCTTATAATGGTTACAAATAAAGCAATAGC 1380
ATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAA 1440
CTCATCAATGTATCTTAACCGCTAAATTGTAAGCGTTAATATTTTTGTTAAAAATTCGCGTT 1500
AAATTTTTGTTAAATCAGCTCATTTTTTTAAACCAATAGGCCGAAATCGGCAAAATCCCTTA 1560
TAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCC 1620
ACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGG 1680
CCCCTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACT 1740
AAATCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGCGCAACGT 1800
GGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGC 1860
GGTCACGCTGCGCGTAACCACCACACCCGCGCGCTTAATGCGCCGCTACAGGGCGCGTC 1920
AGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACA 1980
TTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTGAAA 2040
AAGGAAGAGTCTTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGA 2100
AAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCA 2160
ACCAGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTC 2220
AATTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCATCCCGCCCTAACTCCGCC 2280
AGTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAG 2340
GCCGCTCGGCCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGC 2400
TTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGG 2460
ATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACA 2520
ACAGACAATCGGCTGCTCTGATGCCGCCGTGTCCGGCTGTCAGCGCAGGGGCGCCCGGT 2580
TCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCG 2640
GCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGA 2700
AGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCA 2760
CCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCT 2820
TGATCCGGCTACCTGCCATTGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAC 2880
TCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGC 2940
GCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGT 3000
GACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATT 3060
CATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG 3120
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTAT 3180
CGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGC 3240

GGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTC 3300
 GATTCACCCGCCGCCTTCTATGAAAGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGC 3360
 TGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGG 3420
 CTAAC TGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAA 3480
 AGACAGAATAAAACGCACGGTGTGGGTTCGTTTTCATAAACGCGGGGTTTCGGTCCCAG 3540
 GGCTGGCACTCTGTGATACCCCCACCGAGACCCCATTTGGGGCCAATACGCCCGCGTTTCT 3600
 TCCTTTTTCCCCACCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTC 3660
 GGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAA 3720
 CTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAA 3780
 ATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGA 3840
 TCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCCG 3900
 CTACCAGCGGTGGTTTTGTTTCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAC 3960
 GGCTTCAGCAGAGCGCAGATAACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCAC 4020
 CACTTCAAGAACTCTGTAGCACCCGCCTACATACTCGCTCTGCTAATCCTGTTACCAGTG 4080
 GCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACC 4140
 GATAAGGCGCAGCGGTTCGGGCTGAACGGGGGTTCTGTGCACACAGCCCAGCTTGGAGCGA 4200
 ACGACCTACACCGAACTGAGATACTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCC 4260
 GAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACG 4320
 AGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTCGGGTTTCGCCACCTC 4380
 TGACTTGAGCGTCGATTTTTTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCC 4440
 AGCAACGCGGCCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTT 4500
 CCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4548

Unique enzymes in CMVCHIS

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
Bgl II	A`GATC,T	1199
PfI M I	CCAN,NNN`NTGG	1218
BstX I	CCAN,NNNN`NTGG	1219
Bcl I	T`GATC,A	1230
Mun I	C`AATT,G	1323
Hpa I	GTT AAC	1336
Mlu I	A`CGCG,T	1459
Dra III	CAC,NNN`GTG	1689
Sfi I	GGCCN,NNN`NGGCC	2348
Stu I	AGG CCT	2394
Cla I	AT`CG,AT	2413
Kas I	G`GCGC,C	2572
Nar I	GG`CG,CC	2573
Ehe I	GGC GCC	2574
Bbe I	G,GCGC`C	2576
Msc I	TGG CCA	2655
Tth111 I	GACN`N,NGTC	2691
Rsr II	CG`GWC,CG	3089
BsiC I	TT`CG,AA	3255
BstB I	TT`CG,AA	3255
Bsa I	GGTCTC 7/11	3562
EcoO109 I	RG`GNC,CY	3671

Number of enzymes = 41

CMVCHIS: sites sorted by name:

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
Aci I	(63)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1833
		1860	1888	1891	1905
		1948	1995	2058	2243
		2255	2264	2276	2286
		2297	2343	2482	2545
		2639	2703	2804	2807
		3047	3087	3092	3142
		3158	3184	3240	3309
		3312	3378	3460	3525
		3592	3665	3899	3908
		4043	4153	4274	4293
		4420	4448	4539	
Afl III	(2)	1459	4491		
Aha II	(8)	160	640	693	776
		962	2573	3275	3354
Alu I	(16)	347	410	510	1084
		1131	1352	1519	1776
		2071	2359	2679	3137
		3934	4191	4237	4327
Alw I	(16)	60	66	381	1099
		1204	2440	2751	2818
		2997	3362	3389	3748
		3749	3846	3846	3932
AlwN I	(2)	3674	4082		
ApaL I	(2)	28	4177		
Apo I	(3)	1387	1491	1502	
Ase I	(1)	525			
Asp718	(1)	1119			
Ava II	(3)	336	3089	3534	
Avr II	(2)	2395	3410		
Ban I	(5)	983	1119	1726	2572
		2607			
Ban II	(3)	1764	2938	3648	
Bbe I	(1)	2576			
Bbv I	(7)	468	1361	2646	2688
		3209	3662	4162	
Bcl I	(1)	1230			
Bcn I	(6)	165	516	2578	2738
		3351	4115		
Bfa I	(9)	507	1110	1150	1422
		1840	2396	3411	3745
		3998			
Bgl I	(4)	608	730	801	2348
Bgl II	(1)	1199			
Bpm I	(2)	3356	3413		
Bsa I	(1)	3562			
BsaA I	(3)	858	1689	2877	
BsaB I	(2)	1235	2432		
BsaH I	(8)	160	640	693	776

The following enzymes do not cut in CMVCHIS

Afl II	Age I	Ahd I	Apa I	Asc I
Ava I	BamH I	Bbs I	Bbv II	Blp I
Bsg I	BsiW I	BsmB I	Bsp120 I	BspM II
BsrG I	BssH II	Bst1107 I	BstE II	Eco47 III
Eco72 I	EcoR I	EcoR V	Esp I	Fse I
Nhe I	Nru I	PaeR7 I	Pml I	PpuM I
PspA I	Sac I	Sac II	Sma I	Spe I
Spl I	Srf I	Xca I	Xcm I	Xho I

BsaJ I	(16)	962	2573	3275	3354				3666	3877	4083	4086
		878	1123	2107	2179				4151	4294	4449	
		2302	2337	2346	2395	Fok I	(6)	261	2246	2440	2897	
		2736	3005	3410	3537				2922	3376		
		3538	3640	3641	4331	Fsp I	(2)	477	2675			
BsaW I	(6)	404	1214	2604	3448	Gdi II	(7)	308	1135	1137	2478	
		4138	4285						2480	3043	3070	
BseR I	(2)	1168	2391			Gsu I	(2)	3357	3412			
BsiC I	(1)	3255				Hae I	(5)	2394	2655	4017	4469	
BsiE I	(5)	182	331	1139	2482				4480			
		4157				Hae II	(4)	1840	1848	2576	4251	
BsiHKA I	(5)	32	117	2686	2876	Hae III	(21)	309	602	795	1138	
		4181							1539	1681	2336	2342
Bsm I	(2)	1324	1417						2351	2394	2481	2655
BsmA I	(5)	951	1998	2416	3435				3046	3073	3582	3639
		3563							3672	4017	4451	4469
BsmF I	(11)	693	844	1012	1189				4480			
		2089	2161	2225	2724	Hga I	(8)	167	1043	1131	1907	
		3256	3365	3520					3282	3361	3802	4380
BsoF I	(35)	185	280	307	457	HgiA I	(5)	32	117	2686	2876	
		1136	1139	1160	1350				4181			
		1869	1891	1905	2343	HgiE II	(2)	1212	3902			
		2482	2534	2545	2635	Hha I	(22)	141	478	1839	1847	
		2640	2677	2718	2805				1873	1895	1904	1917
		2808	2811	3047	3143				1948	2567	2575	2639
		3184	3198	3312	3651				2676	2942	3202	3378
		3666	3877	4083	4086				3464	3867	3976	4150
		4151	4294	4449					4250	4317		
Bspl286 I	(2)	117	2876			HinC II	(3)	158	1145	1336		
BspH I	(2)	1999	3771			Hind II	(3)	158	1145	1336		
BspM I	(3)	2460	2841	3291		HinD III	(1)	1129				
Bsr I	(11)	54	226	493	814	Hinf I	(12)	928	1146	1616	1638	
		1603	2281	2516	2717				2048	3058	3192	3244
		3963	4077	4090					3302	3339	4121	4517
BsrB I	(4)	1833	1997	3186	3240	HinI I	(8)	160	640	693	776	
BsrD I	(2)	466	2806						962	2573	3275	3354
BssS I	(4)	31	3165	3291	4318	HinP I	(22)	139	476	1837	1845	
BstB I	(1)	3255							1871	1893	1902	1915
BstN I	(11)	608	801	2109	2164				1946	2565	2573	2637
		2181	2960	3539	3642				2674	2940	3200	3376
		4332	4345	4466					3462	3865	3974	4148
BstU I	(17)	141	578	1141	1461				4248	4315		
		1497	1873	1893	1917	Hpa I	(1)	1336				
		1948	2639	2940	3378	Hpa II	(20)	163	405	515	1215	
		3462	3525	3594	3867				1791	2478	2555	2577
		4448							2605	2736	2826	2893
BstX I	(1)	1219							3074	3349	3357	3449
BstY I	(11)	53	70	1103	1199				3923	4113	4139	4286
		2744	2990	3382	3741	Hph I	(8)	215	893	1177	1183	
		3753	3839	3850					1691	2752	3643	3759
Bsu36 I	(2)	2053	3685			Kas I	(1)	2572				
Cac8 I	(29)	454	604	797	1133	Kpn I	(1)	1123				
		1792	1835	1849	2122	Mae I	(9)	507	1110	1150	1422	
		2141	2194	2213	2467				1840	2396	3411	3745
		2653	2872	2938	2944				3998			
		2972	2976	3017	3021	Mae II	(16)	98	471	640	652	
		3075	3358	3545	3592				693	776	857	962
		3648	3670	3881	4441				1633	1645	1688	1798
		4478							2689	2876	3657	3790
Cfr10 I	(4)	1790	2892	3073	3356	Mae III	(16)	39	227	380	438	
Cla I	(1)	2413							579	666	1015	1361
Csp6 I	(9)	218	736	761	816				1862	1874	2693	2999
		849	900	1057	1120				3689	3955	4071	4134
		2878				Mbo I	(26)	53	70	328	374	
Dde I	(7)	199	2053	2355	3236				392	1103	1114	1199
		3685	3808	4217					1208	1230	2410	2414
Dpn I	(26)	55	72	330	376				2433	2744	2822	2903
		394	1105	1116	1201				2912	2990	3366	3382
		1210	1232	2412	2416				3741	3753	3831	3839
		2435	2746	2824	2905				3850	3925		
		2914	2992	3368	3384	Mbo II	(10)	104	1828	2056	2933	
		3743	3755	3833	3841				3143	3225	3392	3592
		3852	3927						3762	3835		
DpnII	(26)	53	70	328	374	Mlu I	(1)	1459				
		392	1103	1114	1199	Mme I	(3)	1665	4099	4283		
		1208	1230	2410	2414	Mnl I	(29)	327	1059	1146	1149	
		2433	2744	2822	2903				1158	1166	1252	1291
		2912	2990	3366	3382				1300	1717	2048	2326
		3741	3753	3831	3839				2332	2355	2361	2369
		3850	3925						2372	2384	2424	2488
Dra I	(5)	15	122	1275	3717				2624	2981	3173	3379
		3736							3411	3693	4063	4314
Dra III	(1)	1689							4387			
Drd I	(3)	1644	2600	4389		Msc I	(1)	2655				
Dsa I	(4)	878	1123	2302	3005	Mse I	(20)	14	20	24	121	
Eae I	(6)	307	1136	2479	2653				486	525	1274	1335
		3044	3071						1456	1477	1488	1500
Eag I	(2)	1136	2479						1511	1528	1626	1897
Ear I	(3)	2040	2917	3127					3716	3730	3735	3787
Eco57 I	(3)	2718	3150	3950		Msl I	(4)	288	883	1219	3010	
EcoN I	(1)	339				Msp I	(20)	163	405	515	1215	
EcoO109 I	(1)	3671							1791	2478	2555	2577
EcoR II	(11)	606	799	2107	2162				2605	2736	2826	2893
		2179	2958	3537	3640				3074	3349	3357	3449
		4330	4343	4464					3923	4113	4139	4286
Ehe I	(1)	2574				MspA1 I	(5)	64	2071	2679	3908	
Fnu4H I	(35)	185	280	307	457				4153			
		1136	1139	1160	1350	Mun I	(1)	1323				
		1869	1891	1905	2343	NaE I	(3)	1792	3075	3358		
		2482	2534	2545	2635	Nar I	(1)	2573				
		2640	2677	2718	2805	Nci I	(6)	164	515	2577	2737	
		2808	2811	3047	3143				3350	4114		
		3184	3198	3312	3651	Nco I	(4)	878	1123	2302	3005	

Nde I	(1)	752				Bbe I	G,CGGC`C	1	Bbs I	GAAGAC 8/12	-
NgoM I	(3)	1790	3073	3356		Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
Nla III	(20)	257	293	371	381	Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	6
		822	882	1127	2003	Bfa I	C`TA,G	9	Bgl I	GCCN,NNN`NGGC	4
		2143	2215	2306	2447	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
		2792	2978	3009	3035	Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
		3391	3775	4495	4546	BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
Nla IV	(16)	403	985	1121	1728	BsaH I	GR`CG,YC	8	BsaJ I	C`CANN,G	16
		1749	1761	1952	2113	BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	2
		2185	2574	2609	3457	Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	1
		3536	3581	4424	4463	BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
Not I	(1)	1136				BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
Nsi I	(3)	2145	2217	4548		Bsma I	GTCTC`/9	5	BsmB I	CGTCTC 7/11	-
Nsp7524 I	(4)	2139	2211	2974	4491	BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	35
NspB II	(5)	64	2071	2679	3908	Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
		4153				BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
NspH I	(4)	2143	2215	2978	4495	BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
Pac I	(1)	24				BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
Pal I	(21)	309	602	795	1138	BsrG I	T`GTAC,A	-	Bssh II	G`CCGG,C	-
		1539	1681	2336	2342	BssS I	C`TCTG,G	4	Bst1107 I	GTA TAC	-
		2351	2394	2481	2655	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
		3046	3073	3582	3639	BstN I	CC`W,GG	11	BstU I	CG CG	17
		3672	4017	4451	4469	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	11
Pf1M I	(1)	1218				Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	29
Ple I	(2)	1624	2056			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	26	DpnII	`GATC,	26
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)	2071	2679			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	-
		2879				EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
Rsr II	(1)	3089				EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	11
Sal I	(1)	1143				EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Sap I	(2)	2917	3127			Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	35
Sau3A I	(26)	53	70	328	374	Fok I	GGATG 14/18	6	Fse I	GG,CCGG`CC	-
		392	1103	1114	1199	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
		1208	1230	2410	2414	Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	5
		2433	2744	2822	2903	Hae II	R,CGC`Y	4	Hae III	GG CC	21
		2912	2990	3366	3382	Hga I	GACGC 9/14	8	HgiA I	G,WGCW`C	5
		3741	3753	3831	3839	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	22
Sau96 I	(9)	336	601	794	1680	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
		3089	3534	3580	3638	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12
		3671				HinI I	GR`CG,YC	8	HinP I	G`CG,C	22
Sca I	(1)	219				Hpa I	GTT AAC	1	Hpa II	C`CG,C	20
ScrF I	(17)	164	515	608	801	Hph I	GGTGA 12/11	8	Kas I	G`CGGC,C	1
		2109	2164	2181	2577	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	9
		2737	2960	3350	3539	Mae II	A`CG,T	16	Mae III	`GTNAC,	16
		3642	4114	4332	4345	Mbo I	`GATC,	26	Mbo II	GAAGA 12/11	10
Sec I	(16)	878	1123	2107	2179	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
		2302	2337	2346	2395	Mnl I	CCTC 10/10	29	Msc I	TGG CCA	1
		2736	3005	3410	3537	Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
		3538	3640	3641	4331	Msp I	C`CG,G	20	MspAl I	CMG CKG	5
SfaN I	(13)	247	440	876	1388	Mun I	C`AATT,G	1	Nae I	GCC GGC	3
		2151	2223	2532	2787	Nar I	GG`CG,CC	1	Nci I	CC`S,GG	6
		2871	2935	3003	3210	Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
Sfc I	(4)	454	1908	4035	4226	NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
Sfi I	(1)	2348				Nla III	,CATG`	20	Nla IV	GGN NCC	16
SnaB I	(1)	858				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Sph I	(3)	2143	2215	2978		Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
Ssp I	(2)	1481	2034			NspB II	CMG CKG	5	NspH I	R,CATG`Y	4
Stu I	(1)	2394				Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
Sty I	(6)	878	1123	2302	2395	Pal I	GG CC	21	Pf1M I	CCAN,NNN`NTGG	1
Taq I	(14)	46	1144	1171	1722	Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
		2413	2686	2842	2866	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
		2902	3064	3255	3300	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
		3555	4393			Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Tfi I	(5)	3058	3192	3302	3339	Pvu II	CAG CTG	2	Rsa I	GT AC	9
		4517				Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Tsp45 I	(5)	227	438	1862	2693	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
		2999				Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	26
Tth111 I	(1)	2691				Sau96 I	G`GNC,C	9	Sca I	AGT ACT	1
Tth111 II	(4)	3009	3869	3899	3908	ScrF I	CC`N,GG	17	Sec I	C`CNNG,G	16
Vsp I	(1)	525				SfaN I	GCATC 9/13	13	Sfc I	C`TRYA,G	4
Xba I	(1)	1149				Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Xho II	(11)	53	70	1103	1199	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	-
		2744	2990	3382	3741	Sph I	G,CATG`C	3	Spl I	C`GTAG,C	-
Xma III	(2)	1136	2479			Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Xmn I	(1)	100				Stu I	AGG CCT	1	Sty I	C`CWVG,G	6
						Taq I	T`CG,A	14	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	-
						Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
						Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1

Site usage in CMVCHIS

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	63
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	16	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	3	Asc I	GG`CGCC,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	-	Ava II	G`GWC,C	3
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	-
Ban I	G`GYRC,C	5	Ban II	G,RCGY`C	3