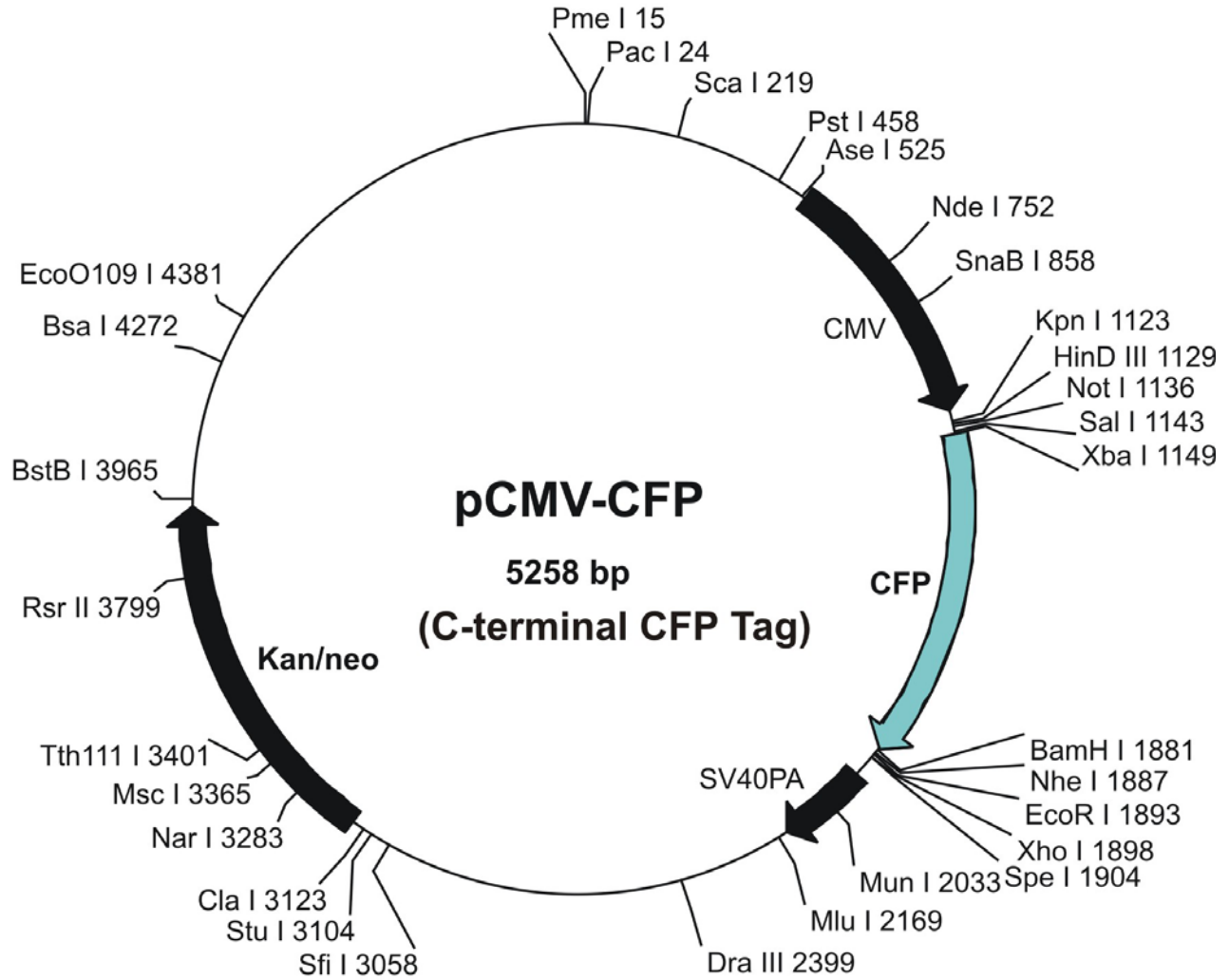
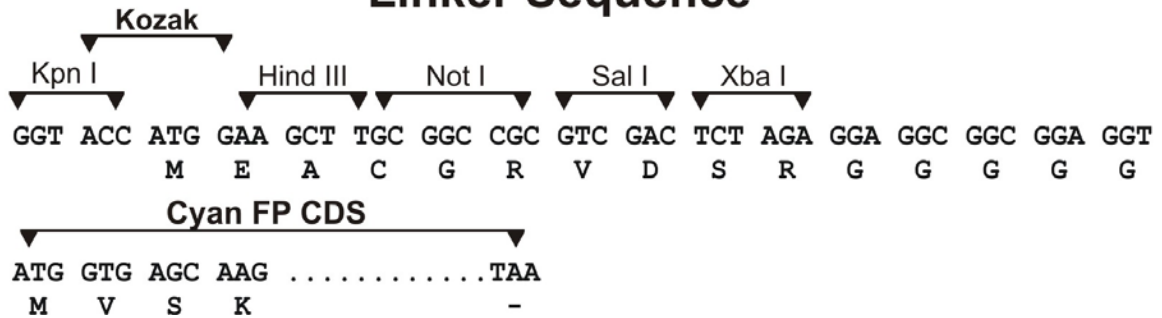


**Name of Vector:** pCMV-CFP(CFP by Miyawaki)  
**Antibiotic Selection:** Kan  
**Created by:** Wei Jiang and Hue Luu  
 (He Lab @ The University of Chicago)  
**Date of Creation:** September 2004



### Linker Sequence



# pCMV-CFP Full-length Sequence and Restriction Sites

(Modified Cyan FP by Atsushi Miyawaki)

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60  
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120  
taaagttctgctatgtggcgcggtattatcccgtgttgacgccgggcaagagcaactcgg 180  
tcgccgcatacactattctcagaatgacttgggtgagtaactcaccagtcacagaaaagca 240  
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgagtgataa 300  
cactgcgcccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360  
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420  
catacacaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480  
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540  
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600  
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660  
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720  
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780  
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTTA 840  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT 900  
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960  
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020  
ACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080  
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtaccATGGAAGCTTGCGGCCG 1140  
CGTCGACTCTAGAGGAGGCGGCGGAGGTatggtgagcaagggcgaggagctgttaccggg 1200  
ggtggtgcccacctggtcgagctggacggcgacgtaaacggccacaagttcagcgtgtc 1260  
cggcgagggcgagggcgatgccacctacggcaagctgacctgaagttcatctgcaccac 1320  
cggcaagctgcccgtgcccctggcccaccctcgtgaccaccctgacctggggcgctgcagtg 1380  
cttcagccgctaccccgaccacatgaagcagcagcacttcttcaagtccgccatgcccga 1440  
aggctacgtccaggagcgcaccatcttcttcaaggacgacggcaactacaagaccgcgc 1500  
cgaggtgaagttcgagggcgacaccctggtgaaccgcatcgagctgaagggcatcgactt 1560  
caaggaggacggcaacatcctggggcacaagctggagtacaactacatcagccacaacgt 1620  
ctatatcaccgcccgaacagcagaagaacggcatcaaggccaacttcaagatccgccacaa 1680  
catcgaggacggcagcgtgcagctcgccgaccactaccagcagaacacccccatcggcga 1740  
cggccccgtgctgctgcccgcacaaccactacctgagcaccacagtcggccctgagcaaga 1800  
ccccaacgagaagcgcgatcacatggtcctgctggagttcgtgaccgcccgggatcac 1860  
tctcggcatggacgagtaaGGATCCGCTAGCGAATTCTCGAGACTAGTGATCtatccgat 1920  
ccaccggannnnnnTAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTG 1980  
CTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTG 2040  
TTGTTAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATT 2100  
TCACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATG 2160  
TATCTTAACCGGTAAATTTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTTGT 2220  
TAAATCAGCTCATTTTTTAAACCAATAGGCCGAAAATCGGCAAAAATCCCTTATAAATCAAAA 2280  
GAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAG 2340  
AACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCACTACGT 2400  
GAACCATCACCTAATCAAGTTTTTTGGGGTGCAGGTGCCGTAAAGCACTAAATCGGAAC 2460  
CCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAG 2520  
GAAGGGAAGAAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTG 2580  
CGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACT 2640  
TTTTGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATG 2700  
TATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGT 2760  
CCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTGAGTTAGGGTGTGGAAAGTCCCCAG 2820  
GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTG 2880  
GAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAG 2940  
CAACCATAGTCCCGCCCCTAACTCCGCCCATCCGCCCCTAACTCCGCCCAGTCCGCCC 3000  
ATTCTCCGCCCCTATGGCTGACTAATTTTTTTTATTTATGTCAGAGGCCGAGGCCCTCGG 3060  
CCTCTGAGCTATTCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCCTAGGCTTTTGCAAAG 3120  
ATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCA 3180  
GGTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATC 3240

GGCTGCTCTGATGCCGCGTGTTCGGCTGTCAGCGCAGGGGCGCCCGTTCTTTTTGTC 3300  
AAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGG 3360  
CTGGCCACGACGGGCGTTTCTTGGCGAGCTGTGCTCGACGTTGTCACCTGAAGCGGGAAGG 3420  
GACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCT 3480  
GCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCT 3540  
ACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAA 3600  
GCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAA 3660  
CTGTTCCGCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCTGACCCATGGC 3720  
GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGT 3780  
GGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCT 3840  
GAAGAGCTTGGCGCGAATGGGCTGACCGCTTCTCCTCGTGCTTTACGGTATCGCCGCTCCC 3900  
GATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGG 3960  
GGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCACCCG 4020  
CCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCC 4080  
TCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAA 4140  
CACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATA 4200  
AAACGCACGGTGTGGGTGCTTTGTTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCACT 4260  
CTGTCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGCTTTCTTCTTTTCCC 4320  
CACCCACCCCAAGTTCCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCCGGGGCGGCAG 4380  
GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTT 4440  
AATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACAAAATCCCTTAAC 4500  
GTGAGTTTTTCTGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAG 4560  
ATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCAGGCTACCAGCGG 4620  
TGGTTTGTGGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCA 4680  
GAGCGCAGATAACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGA 4740  
ACTCTGTAGCACCGCCTACATACTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCA 4800  
GTGGCGATAAGTCTGCTTACCAGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGC 4860  
AGCGGTCCGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACA 4920  
CCGAAGTGAATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAA 4980  
AGGCGGACAGGTATCCGGTAAGCGGCAGGGTCCGGAACAGGAGAGCGCACGAGGGAGCTTC 5040  
CAGGGGGAAACCGCTGGTATCTTTATAGTCTTGTGCGGGTTTTCGCCACCTCTGACTTGAGC 5100  
GTCGATTTTTGTGATGCTCGTTCAGGGGGCGGAGCCATGGAAAACGCCAGCAACGCGG 5160  
CCTTTTTACGGTTCCCTGGCCTTTTGTGTCCTTTTGTGCTCACATGTTCTTTCTGCGTTAT 5220  
CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5258

**Unique enzymes in CMVCFP.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
BamH I	G`GATC,C	1881
Nhe I	G`CTAG,C	1887
EcoR I	G`AATT,C	1893
Ava I	C`YCGR,G	1898
Paer7 I	C`TCGA,G	1898
Xho I	C`TCGA,G	1898
Spe I	A`CTAG,T	1904
Pf1M I	CCAN,NNN`NTGG	1928
BstX I	CCAN,NNNN`NTGG	1929
Bcl I	T`GATC,A	1940
Mun I	C`AATT,G	2033
Hpa I	GTT AAC	2046
Mlu I	A`CGCG,T	2169
Dra III	CAC,NNN`GTG	2399
Sfi I	GGCCN,NNN`NGGCC	3058
Stu I	AGG CCT	3104
Cla I	AT`CG,AT	3123
Kas I	G`GCGC,C	3282

Nar I	GG`CG,CC	3283
Ehe I	GGC GCC	3284
Bbe I	G,CGC`C	3286
Msc I	TGG CCA	3365
Tth111 I	GACN`N,NGTC	3401
Rsr II	CG`GWC,CG	3799
BslC I	TT`CG,AA	3965
BstB I	TT`CG,AA	3965
Bsa I	GGTCTC 7/11	4272
EcoO109 I	RG`GNC,CY	4381
Number of enzymes = 47		

**The following enzymes do not cut in CMVCFP:**

Afl II	Age I	Ahd I	Apa I	Asc I
Bbs I	Bbv II	Bgl II	Blp I	BsiW I
BsmB I	Bsp120 I	BspM II	BsrG I	BssH II
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

**CMVCFP.TXT: sites sorted by name:**

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
AcI I	(73)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1388
		1429	1496	1535	1630
		1673	1786	1846	1849
		1885	2543	2570	2598
		2601	2615	2658	2705
		2768	2953	2965	2974
		2986	2996	3007	3053



HinP I	(25)	139	476	1457	1498	PflM I	(1)	1928					
		1814	2547	2555	2581	Ple I	(2)	2334	2766				
		2603	2612	2625	2656	Pme I	(1)	15					
		3275	3283	3347	3384	Psp1406 I	(2)	98	471				
		3650	3910	4086	4172	Pst I	(1)	458					
		4575	4684	4858	4958	Pvu I	(1)	331					
		5025				Pvu II	(2)	2781	3389				
Hpa I	(1)	2046				Rsa I	(10)	219	737	762	817		
Hpa II	(24)	163	405	515	1198			850	901	1058	1121		
		1261	1321	1852	1925			1599	3589				
		2501	3188	3265	3287	Rsr II	(1)	3799					
		3315	3446	3536	3603	Sal I	(1)	1143					
		3784	4059	4067	4159	Sap I	(2)	3627	3837				
		4633	4823	4849	4996	Sau3A I	(30)	53	70	328	374		
Hph I	(11)	215	893	1183	1188			392	1103	1114	1669		
		1516	1540	1620	2401			1817	1855	1881	1909		
		3462	4353	4469				1918	1940	3120	3124		
Kas I	(1)	3282						3143	3454	3532	3613		
Kpn I	(1)	1123						3622	3700	4076	4092		
Mae I	(11)	507	1110	1150	1888			4451	4463	4541	4549		
		1905	2132	2550	3106			4560	4635				
		4121	4455	4708		Sau96 I	(12)	336	601	794	1342		
Mae II	(19)	98	471	640	652			1743	1826	2390	3799		
		693	776	857	962			4244	4290	4348	4381		
		1234	1447	1618	2343	Sca I	(1)	219					
		2355	2398	2508	3399	ScrF I	(25)	164	515	608	801		
		3586	4367	4500				1199	1215	1340	1367		
Mae III	(18)	39	227	380	438			1452	1527	1581	1853		
		579	666	1015	1352			2819	2874	2891	3287		
		1841	2071	2572	2584			3447	3670	4060	4249		
		3403	3709	4399	4665			4352	4824	5042	5055		
		4781	4844					5176					
Mbo I	(30)	53	70	328	374	Sec I	(22)	878	1123	1198	1338		
		392	1103	1114	1669			1366	1501	1525	1580		
		1817	1855	1881	1909			2817	2889	3012	3047		
		1918	1940	3120	3124			3056	3105	3446	3715		
		3143	3454	3532	3613			4120	4247	4248	4350		
		3622	3700	4076	4092			4351	5041				
		4451	4463	4541	4549	SfaN I	(17)	247	440	876	1269		
		4560	4635					1545	1560	1659	2098		
Mbo II	(14)	104	1413	1458	1461			2861	2933	3242	3497		
		1654	2538	2766	3643			3581	3645	3713	3920		
		3853	3935	4102	4302			5105					
		4472	4545			Sfc I	(4)	454	2618	4745	4936		
Mlu I	(1)	2169				Sfi I	(1)	3058					
Mme I	(3)	2375	4809	4993		SnaB I	(1)	858					
Mnl I	(36)	327	1059	1146	1149	Spe I	(1)	1904					
		1158	1178	1259	1265	Sph I	(3)	2853	2925	3688			
		1358	1496	1508	1559	Ssp I	(2)	2191	2744				
		1679	1962	2001	2010	Stu I	(1)	3104					
		2427	2758	3036	3042	Sty I	(6)	878	1123	3012	3105		
		3065	3071	3079	3082			3715	4120				
		3094	3134	3198	3334	Taq I	(19)	46	1144	1219	1513		
		3691	3883	4089	4121			1540	1555	1684	1899		
		4403	4773	5024	5097			2432	3123	3396	3552		
Msc I	(1)	3365						3576	3612	3774	3965		
Mse I	(20)	14	20	24	121			4010	4265	5103			
		486	525	1984	2045	Tfi I	(5)	3768	3902	4012	4049		
		2166	2187	2198	2210			5227					
		2221	2238	2336	2607	Tsp45 I	(7)	227	438	1352	1841		
		4426	4440	4445	4497			2572	3403	3709			
Msl I	(4)	288	883	1929	3720	Tth111 I	(1)	3401					
Msp I	(24)	163	405	515	1198	Tth111 II	(5)	1652	3719	4579	4609		
		1261	1321	1852	1925			4618					
		2501	3188	3265	3287	Vsp I	(1)	525					
		3315	3446	3536	3603	Xba I	(1)	1149					
		3784	4059	4067	4159	Xho I	(1)	1898					
		4633	4823	4849	4996	Xho II	(12)	53	70	1103	1669		
MspA1 I	(5)	64	2781	3389	4618			1881	3454	3700	4092		
		4863						4451	4463	4549	4560		
Mun I	(1)	2033				Xma III	(2)	1136	3189				
Nae I	(3)	2502	3785	4068		Xmn I	(1)	100					
Nar I	(1)	3283											
Nci I	(8)	164	515	1199	1853								
		3287	3447	4060	4824								
Nco I	(4)	878	1123	3012	3715								
Nde I	(1)	752											
NgoM I	(3)	2500	3783	4066									
Nhe I	(1)	1887											
Nla III	(24)	257	293	371	381								
		822	882	1127	1406								
		1436	1826	1871	2713								
		2853	2925	3016	3157								
		3502	3688	3719	3745								
		4101	4485	5205	5256								
Nla IV	(19)	403	985	1121	1207								
		1745	1883	2438	2459								
		2471	2662	2823	2895								
		3284	3319	4167	4246								
		4291	5134	5173									
Not I	(1)	1136											
Nsi I	(3)	2855	2927	5258									
Nsp7524 I	(4)	2849	2921	3684	5201								
NspB II	(5)	64	2781	3389	4618								
		4863											
NspH I	(4)	2853	2925	3688	5205								
Pac I	(1)	24											
Paer7 I	(1)	1898											
Pal I	(25)	309	602	795	1138								
		1243	1343	1659	1744								
		2249	2391	3046	3052								
		3061	3104	3191	3365								
		3756	3783	4292	4349								
		4382	4727	5161	5179								
		5190											

### Site usage in CMVCFP.TXT:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	73
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	23
Alw I	GGATC 8/9	20	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	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	1	Ava II	G`GWC,C	4
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	6	Ban II	G,`RGY`C	3
Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	8
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	4	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	22
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	3
Bsg I	GTGCAG 22/20	3	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	6
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	43
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	3
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	12

BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2	Mse I	T`TA, A	20	Msl I	CAYNN NNRTG	4
BsrG I	T`GTAC, A	-	BssH II	G`CGCG, C	-	Msp I	C`CG, G	24	MspA1 I	CMG CKG	5
BssS I	C`TCGT, G	5	Bst1107 I	GTA TAC	-	Mun I	C`AATT, G	1	Nae I	GCC GGC	3
BstB I	TT`CG, AA	1	BstE II	G`GTNAC, C	-	Nar I	GG`GG, CC	1	Nci I	CC`S, GG	8
BstN I	CC`W, GG	17	BstU I	CG CG	19	Nco I	C`CATG, G	4	Nde I	CA`TA, TG	1
BstX I	CCAN, NNNN`NTGG	1	BstY I	R`GATC, Y	12	NgoM I	G`CCGG, C	3	Nhe I	G`CTAG, C	1
Bsu36 I	CC`TNA, GG	2	Cac8 I	GCN NGC	35	Nla III	,CATG`	24	Nla IV	GGN NCC	19
Cfr10 I	R`CCGG, Y	5	Cla I	AT`CG, AT	1	Not I	GC`GGCC, GC	1	Nru I	TCG CGA	-
Csp6 I	G`TA, C	10	Dde I	C`TNA, G	9	Nsi I	A, TGCA`T	3	Nsp7524 I	R`CATG, Y	4
Dpn I	GA TC	30	DpnII	`GATC,	30	NspB II	CMG CKG	5	NspH I	R, CATG`Y	4
Dra I	TTT AAA	5	Dra III	CAC, NNN`GTG	1	Pac I	TTA, AT`TAA	1	PaeR7 I	C`TCGA, G	1
Drd I	GACNN, NN`NNGTC	3	Dsa I	C`CRYG, G	4	Pal I	GG CC	25	PflM I	CCAN, NNN`NTGG	1
Eae I	Y`GGCC, R	7	Eag I	C`GGCC, G	2	Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-	Pml I	CAC GTG	-	PpuM I	RG`GWC, CY	-
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-	Psp1406 I	AA`CG, TT	2	PspA I	C`CCGG, G	-
EcoN I	CCTNN`N, NNAGG	1	Eco109 I	RG`GNC, CY	1	Pst I	C, TGCA`G	1	Pvu I	CG, AT`CG	1
EcoR I	G`AATT, C	1	EcoR II	`CCWGG,	17	Pvu II	CAG CTG	2	Rsa I	GT AC	10
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1	Rsr II	CG`GWC, CG	1	Sac I	G, AGCT`C	-
Esp I	GC`TNA, GC	-	Fnu4H I	GC`N, GC	43	Sac II	CC, GC`GG	-	Sal I	G`TCGA, C	1
Fok I	GGATG 14/18	8	Fse I	GG, CCGG`CC	-	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	30
Fsp I	TGC GCA	2	Gdi II	`YGGC, CG	8	Sau96 I	G`GNC, C	12	Sca I	AGT ACT	1
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	6	ScrF I	CC`N, GG	25	Sec I	C`CNNG, G	22
Hae II	R, GCGC`Y	4	Hae III	GG CC	25	SfaN I	GATC 9/13	17	Sfc I	C`TRYA, G	4
Hga I	GACGC 9/14	8	HgiA I	G, WGCW`C	6	Sfi I	GGCCN, NNN`NGGCC	1	Sma I	CCC GGG	-
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G, CG`C	25	SnaB I	TAC GTA	1	Spe I	A`CTAG, T	1
HinC II	GTY RAC	3	Hind II	GTY RAC	3	Sph I	G, CATG`C	3	Sp1 I	C`GTAC, G	-
Hind III	A`AGCT, T	1	Hinf I	G`ANT, C	12	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
HinI I	GR`CG, YC	8	HinP I	G`CG, C	25	Stu I	AGG CCT	1	Sty I	C`CWWG, G	6
Hpa I	GTT AAC	1	Hpa II	C`CG, G	24	Taq I	T`CG, A	19	Tfi I	G`AWT, C	5
Hph I	GGTGA 12/11	11	Kas I	G`GCGC, C	1	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N, NGTC	1
Kpn I	G, GTAC`C	1	Mae I	C`TA, G	11	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA, AT	1
Mae II	A`CG, T	19	Mae III	`GTNAC,	18	Xba I	T`CTAG, A	1	Xca I	GTA TAC	-
Mbo I	`GATC,	30	Mbo II	GAAGA 12/11	14	Xcm I	CCANNNN, N`NNNNTGG-	-	Xho I	C`TCGA, G	1
Mlu I	A`CGCG, T	1	Mme I	TCCRAC 25/23	3	Xho II	R`GATC, Y	12	Xma I	C`CCGG, G	-
Mnl I	CCTC 10/10	36	Msc I	TGG CCA	1	Xma III	C`GGCC, G	2	Xmn I	GAANN NNTTG	1