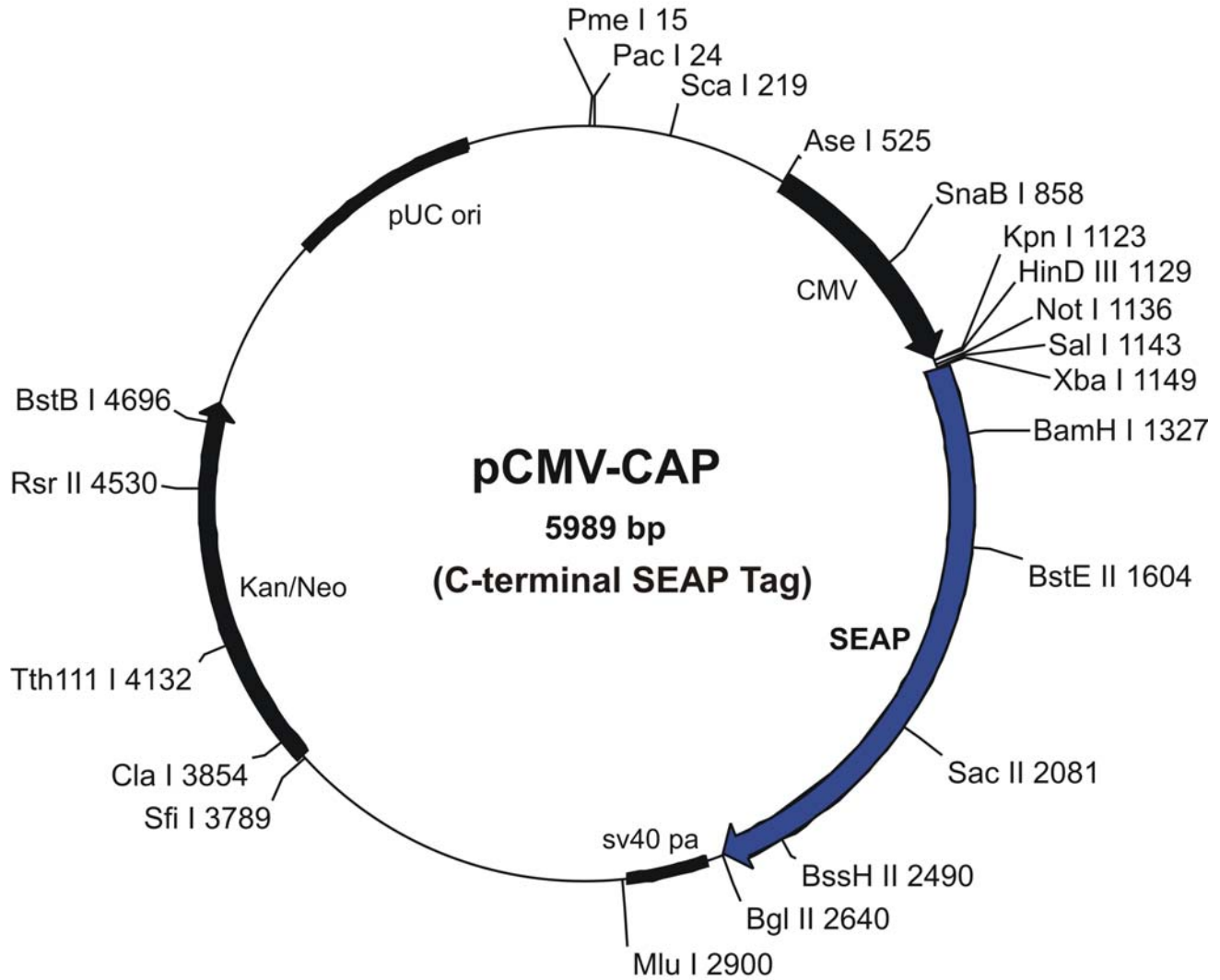
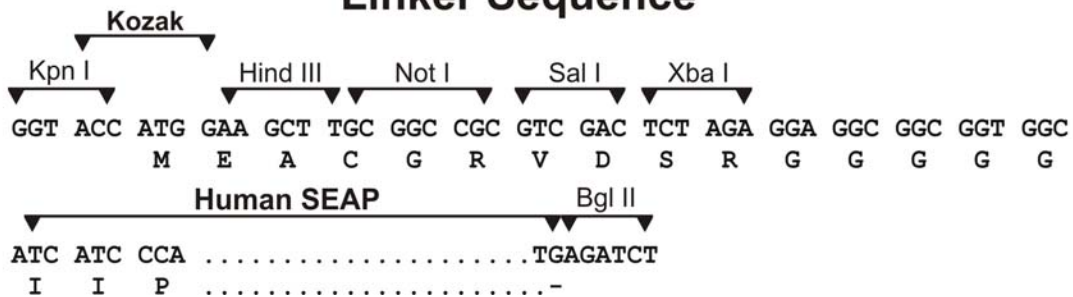


Name of Vector: pCMV-CAP
Antibiotic Selection: Kan
Created by: Jay Shrestha
 (He Lab @ The University of Chicago)
Date of Creation: June 2004



Linker Sequence



pCMV-CAP Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttgggtgagtaactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgagtgataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
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CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTTCTTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTG 960
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CGTCGACTCTAGAGGAGGCGGCGGtgccatcatcccagttgaggaggagaaccggaactt 1200
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CAGCAACGCGGCTTTTTTACGGTTCC`TGGCCTTTTGTGCTGGCCTTTTGTCTCACATGTTCTT 5940
TCCTGCGTTATCCCCTGATTCTGTGGATAAACCGTATTACCGCCATGCAT 5989

Unique enzymes in pCMV-CAP:

Pme I	CTTT AAAC	15	Xba I	T`CTAG,A	1149
Pac I	TTA,AT`TAA	24	BamH I	G`GATC,C	1327
Xmn I	GAANN NNTTC	100	BstE II	G`GTNAC,C	1604
Sca I	AGT ACT	219	Sac II	CC,GC`GG	2081
Pvu I	CG,AT`CG	331	BsmB I	CGTCTC 7/11	2151
EcoN I	CCTNN`N,NNAGG	339	Bbs I	GAAGAC 8/12	2243
Ase I	AT`TA,AT	525	Bbv II	GAAGAC 7/11	2244
Vsp I	AT`TA,AT	525	Xcm I	CCANNNN,N`NNNNTGG2294	
SnaB I	TAC GTA	858	BssH II	G`CGCG,c	2490
Acc65 I	G`GTAC,C	1119	Bgl II	A`GATC,T	2640
Asp718	G`GTAC,C	1119	Bcl I	T`GATC,A	2671
Kpn I	G,GTAC`C	1123	Mun I	C`AATT,G	2764
Hind III	A`AGCT,T	1129	Hpa I	GTT AAC	2777
Not I	GC`GGCC,GC	1136	Mlu I	A`CGCG,T	2900
Sal I	G`TCGA,C	1143	Sfi I	GGCCN,NNN`NGGCC	3789
			Cla I	AT`CG,AT	3854
			Tth111 I	GACN`N,NGTC	4132

Rsr II	CG`GWC,CG	4530				3548	3620	3743	3778
BsiC I	TT`CG,AA	4696				3787	3836	4177	4446
BstB I	TT`CG,AA	4696				4851	4978	4979	5081
Number of enzymes = 35									
The following enzymes do not cut in pCMV-CAP:									
Afl II	Age I	Ahd I	Apa I	Asc I					
BsiW I	Bsp120 I	BspM II	BsrG I	Bst1107 I					
Eco47 III	Eco72 I	EcoR I	EcoR V	Fse I					
Nhe I	Nru I	PaeR7 I	Pml I	PpuM I					
Spe I	Spl I	Srf I	Xca I	Xho I					
pCMV-CAP: sites sorted by name:									
Aat II	(4)	643	696	779	965				
Acc I	(3)	1144	1308	1423					
Acc65 I	(1)	1119							
Aci I	(86)	64	141	185	306				
		352	576	604	616				
		630	797	888	921				
		1025	1046	1107	1135				
		1139	1159	1162	1208				
		1234	1264	1385	1471				
		1513	1517	1543	1664				
		1699	1703	1916	2078				
		2080	2190	2410	2481				
		2494	2499	2563	2584				
		2605	2623	3274	3301				
		3329	3332	3346	3389				
		3436	3499	3684	3696				
		3705	3717	3727	3738				
		3784	3923	3986	4080				
		4144	4245	4248	4488				
		4528	4533	4583	4599				
		4625	4681	4750	4753				
		4819	4901	4966	5033				
		5106	5340	5349	5484				
		5594	5715	5734	5861				
		5889	5980						
Afl III	(4)	1430	1786	2900	5932				
Aha II	(13)	160	640	693	776				
		962	1681	2176	2380				
		2598	2620	4014	4716				
		4795							
Alu I	(22)	347	410	510	1084				
		1131	1244	1320	1736				
		1925	2198	2284	2793				
		2960	3217	3512	3800				
		4120	4578	5375	5632				
		5678	5768						
Alw I	(20)	60	66	381	1099				
		1323	1334	1758	1995				
		2645	3881	4192	4259				
		4438	4803	4830	5189				
		5190	5287	5287	5373				
AlwN I	(4)	1812	2049	5115	5523				
ApaL I	(2)	28	5618						
Apo I	(3)	2828	2932	2943					
Ase I	(1)	525							
Asp718	(1)	1119							
Ava I	(3)	2314	2418	2630					
Ava II	(9)	336	1382	1843	1943				
		2021	2336	2355	4530				
		4975							
Avr II	(3)	1766	3836	4851					
BamH I	(1)	1327							
Ban I	(12)	983	1119	1230	1641				
		1714	1896	2379	2597				
		2610	3167	4013	4048				
Ban II	(7)	1927	2286	2418	2578				
		3205	4379	5089					
Bbe I	(3)	2383	2601	4017					
Bbs I	(1)	2243							
Bbv I	(13)	468	1227	1259	1521				
		1634	1745	2441	2802				
		4087	4129	4650	5103				
		5603							
Bbv II	(1)	2244							
Bcl I	(1)	2671							
Bcn I	(14)	165	516	1195	1902				
		2146	2316	2317	2385				
		2632	2633	4019	4179				
		4792	5556						
Bfa I	(10)	507	1110	1150	1767				
		2863	3281	3837	4852				
		5186	5439						
Bgl I	(4)	608	730	801	3789				
Bgl II	(1)	2640							
Blp I	(2)	2064	2220						
Bpm I	(4)	2002	2592	4797	4854				
Bsa I	(3)	1974	2451	5003					
BsaA I	(3)	858	3130	4318					
BsaB I	(2)	2676	3873						
BsaH I	(13)	160	640	693	776				
		962	1681	2176	2380				
		2598	2620	4014	4716				
		4795							
BsaJ I	(34)	878	1123	1219	1225				
		1226	1286	1372	1378				
		1456	1766	1835	1892				
		1939	2078	2117	2303				
		2314	2446	2630	2631				
BsaW I	(6)	404	2655	4045	4889				
		5579	5726						
BseR I	(5)	1168	1197	1200	2223				
		3832							
Bsg I	(5)	1237	1528	1641	1890				
		2544							
BsiC I	(1)	4696							
BsiE I	(6)	182	331	1139	2388				
		3923	5598						
BsiHKA I	(8)	32	117	1927	2286				
		2371	4127	4317	5622				
Bsm I	(2)	2765	2858						
BsmA I	(10)	951	1973	1979	2003				
		2152	2452	3439	3857				
		4876	5004						
BsmB I	(1)	2151							
BsmF I	(12)	693	844	1012	1856				
		2331	3530	3602	3666				
		4165	4697	4806	4961				
BsoF I	(52)	185	280	307	457				
		1136	1139	1160	1216				
		1234	1245	1248	1264				
		1321	1510	1513	1544				
		1623	1734	2050	2081				
		2430	2495	2563	2623				
		2791	3310	3332	3346				
		3784	3923	3975	3986				
		4076	4081	4118	4159				
		4246	4249	4252	4488				
		4584	4625	4639	4753				
		5092	5107	5318	5524				
		5527	5592	5735	5890				
Bsp1286 I	(2)	117	4317						
BspH I	(3)	2126	3440	5212					
BspM I	(3)	3901	4282	4732					
Bsr I	(16)	54	226	493	814				
		1177	1359	1527	1673				
		2022	3044	3722	3957				
		4158	5404	5518	5531				
BsrB I	(5)	2410	3274	3438	4627				
		4681							
BsrD I	(2)	466	4247						
BssH II	(1)	2490							
BssS I	(5)	31	1615	4606	4732				
		5759							
BstB I	(1)	4696							
BstE II	(1)	1604							
BstN I	(27)	608	801	1227	1287				
		1325	1374	1707	1719				
		1847	1893	1941	1981				
		2305	2359	2448	2511				
		2571	2595	3550	3605				
		3622	4401	4980	5083				
		5773	5786	5907					
BstU I	(24)	141	578	1141	1210				
		1543	2080	2490	2492				
		2494	2625	2902	2938				
		3314	3334	3358	3389				
		4080	4381	4819	4903				
		4966	5035	5308	5889				
BstX I	(2)	1497	2660						
BstY I	(13)	53	70	1103	1327				
		1999	2640	4185	4431				
		4823	5182	5194	5280				
		5291							
Bsu36 I	(2)	3494	5126						

		1762	1999	2161	2640			4890	5364	5554	5580
		2649	2671	3851	3855			5727			
		3874	4185	4263	4344	Hph I	(10)	215	893	1324	1669
		4353	4431	4807	4823			2193	2646	3132	4193
		5182	5194	5272	5280			5084	5200		
		5291	5366			Kas I	(3)	2379	2597	4013	
Dra I	(5)	15	122	2716	5158	Kpn I	(1)	1123			
		5177				Mae I	(10)	507	1110	1150	1767
Dra III	(3)	1658	2522	3130				2863	3281	3837	4852
Drd I	(3)	3085	4041	5830				5186	5439		
Dsa I	(8)	878	1123	1378	1456	Mae II	(21)	98	471	640	652
		2078	2117	3743	4446			693	776	857	962
Eae I	(8)	307	1136	1375	2385			1687	1759	2248	2476
		3920	4094	4485	4512			2548	3074	3086	3129
Eag I	(3)	1136	2385	3920				3239	4130	4317	5098
Ear I	(5)	2097	2449	3481	4358			5231			
		4568				Mae III	(21)	39	227	380	438
Eco57 I	(3)	4159	4591	5391				579	666	1015	1313
EcoN I	(1)	339						1604	1952	2228	2393
EcoO109 I	(3)	1223	1359	5112				2802	3303	3315	4134
EcoR II	(27)	606	799	1225	1285			4440	5130	5396	5512
		1323	1372	1705	1717			5575			
		1845	1891	1939	1979	Mbo I	(30)	53	70	328	374
		2303	2357	2446	2509			392	1103	1114	1327
		2569	2593	3548	3603			1762	1999	2161	2640
		3620	4399	4978	5081			2649	2671	3851	3855
		5771	5784	5905				3874	4185	4263	4344
Ehe I	(3)	2381	2599	4015				4353	4431	4807	4823
Esp I	(2)	2064	2220					5182	5194	5272	5280
Fnu4H I	(52)	185	280	307	457			5291	5366		
		1136	1139	1160	1216	Mbo II	(19)	104	1275	1354	1870
		1234	1245	1248	1264			2079	2085	2244	2283
		1321	1510	1513	1544			2465	2649	3269	3497
		1623	1734	2050	2081			4374	4584	4666	4833
		2430	2495	2563	2623			5033	5203	5276	
		2791	3310	3332	3346	Mlu I	(1)	2900			
		3784	3923	3975	3986	Mme I	(4)	1767	3106	5540	5724
		4076	4081	4118	4159	Mnl I	(49)	327	1059	1146	1149
		4246	4249	4252	4488			1175	1178	1205	1214
		4584	4625	4639	4753			1283	1544	1639	1703
		5092	5107	5318	5524			1705	1767	2035	2039
		5527	5592	5735	5890			2093	2099	2179	2201
Fok I	(9)	261	1158	1310	2403			2204	2234	2256	2271
		3687	3881	4338	4363			2348	2465	2693	2732
		4817						2741	3158	3489	3767
Fsp I	(2)	477	4116					3773	3796	3802	3810
Gdi II	(9)	308	1135	1137	2384			3813	3825	3865	3929
		2386	3919	3921	4484			4065	4422	4614	4820
		4511						4852	5134	5504	5755
Gsu I	(4)	2001	2591	4798	4853			5828			
Hae I	(8)	1377	2328	2556	3835	Msc I	(2)	1377	4096		
		4096	5458	5910	5921	Mse I	(21)	14	20	24	121
Hae II	(7)	1892	2383	2601	3281			486	525	1522	2715
		3289	4017	5692				2776	2897	2918	2929
Hae III	(34)	309	602	795	1138			2941	2952	2969	3067
		1224	1361	1377	1461			3338	5157	5171	5176
		1575	1777	2194	2301			5228			
		2313	2328	2387	2497	Msl I	(6)	288	883	1560	1758
		2556	2980	3122	3777			2660	4451		
		3783	3792	3835	3922	Msp I	(29)	163	405	515	1194
		4096	4487	4514	5023			1639	1901	2144	2315
		5080	5113	5458	5892			2384	2388	2608	2631
		5910	5921					2656	3232	3919	3996
Hga I	(11)	167	1043	1131	1688			4018	4046	4177	4267
		2183	2627	3348	4723			4334	4515	4790	4798
		4802	5243	5821				4890	5364	5554	5580
HgiA I	(8)	32	117	1927	2286			5727			
		2371	4127	4317	5622	MspAl I	(7)	64	1320	2080	3512
HgiE II	(3)	1661	2653	5343				4120	5349	5594	
Hha I	(31)	141	478	1891	2059	Mun I	(1)	2764			
		2382	2492	2494	2507	Nae I	(5)	1640	2609	3233	4516
		2546	2600	2627	3280			4799			
		3288	3314	3336	3345	Nar I	(3)	2380	2598	4014	
		3358	3389	4008	4016	Nci I	(14)	164	515	1194	1901
		4080	4117	4383	4643			2145	2315	2316	2384
		4819	4905	5308	5417			2631	2632	4018	4178
		5591	5691	5758				4791	5555		
HinC II	(3)	158	1145	2777		Nco I	(6)	878	1123	1378	2117
Hind II	(3)	158	1145	2777				3743	4446		
Hind III	(1)	1129				Nde I	(2)	752	1394		
Hinf I	(15)	928	1146	1568	1862	NgoM I	(5)	1638	2607	3231	4514
		2010	3057	3079	3489			4797			
		4499	4633	4685	4743	Nla III	(32)	257	293	371	381
		4780	5562	5958				822	882	1127	1382
HinI I	(13)	160	640	693	776			1434	1751	1790	1799
		962	1681	2176	2380			1931	1967	1991	2121
		2598	2620	4014	4716			2130	2168	2555	3444
		4795						3584	3656	3747	3888
HinP I	(31)	139	476	1889	2057			4233	4419	4450	4476
		2380	2490	2492	2505			4832	5216	5936	5987
		2544	2598	2625	3278			403	985	1121	1206
		3286	3312	3334	3343	Nla IV	(36)	1232	1329	1360	1448
		3356	3387	4006	4014			1643	1716	1802	1844
		4078	4115	4381	4641			1898	1914	1945	2023
		4817	4903	5306	5415			2073	2302	2381	2415
		5589	5689	5756				2575	2599	2612	3169
Hpa I	(1)	2777						3190	3202	3393	3554
Hpa II	(29)	163	405	515	1194			3626	4015	4050	4898
		1639	1901	2144	2315			4977	5022	5865	5904
		2384	2388	2608	2631	Not I	(1)	1136			
		2656	3232	3919	3996	Nsi I	(3)	3586	3658	5989	
		4018	4046	4177	4267	Nsp7524 I	(6)	1430	1786	3580	3652
		4334	4515	4790	4798			4415	5932		

NspB II	(7)	64	1320	2080	3512	Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	3
		4120	5349	5594		Acc65 I	G`GTAC,C	1	AcI I	C`CG,C	86
NspH I	(6)	1434	1790	3584	3656	Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	4
		4419	5936			Age I	A`CCGG,T	-	Aha II	GR`CG,YC	13
Pac I	(1)	24				Ahd I	GACNN,N`NNGTC	-	Alu I	AG CT	22
Pal I	(34)	309	602	795	1138	Alw I	GGATC 8/9	20	AlwN I	CAG,NNN`CTG	4
		1224	1361	1377	1461	Apa I	G,GGCC`C	-	ApaL I	G`TGA,C,C	2
		1575	1777	2194	2301	Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	-
		2313	2328	2387	2497	Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
		2556	2980	3122	3777	Ava I	C`YCGR,G	3	Ava II	G`GWC,C	9
		3783	3792	3835	3922	Avr II	C`CTAG,G	3	BamH I	G`GATC,C	1
		4096	4487	4514	5023	Ban I	G`GYRC,C	12	Ban II	G,RCGY`C	7
		5080	5113	5458	5892	Bbe I	G,CGCC`C	3	Bbs I	GAAGAC 8/12	1
		5910	5921			Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	1
Pf1M I	(3)	1443	1964	2659		Bcl I	T`GTAC,A	1	Bcn I	CC,S`GG	14
Ple I	(2)	3065	3497			Bfa I	C`TA,G	10	Bgl I	GCCN,NNN`NGGC	4
Pme I	(1)	15				Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	2
Psp1406 I	(2)	98	471			Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	3
PspA I	(2)	2314	2630			BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
Pst I	(2)	458	1249			BsaH I	GR`CG,YC	13	BsaJ I	C`CNNG,G	34
Pvu I	(1)	331				BsaW I	W`CCGG,W	6	BseI I	GAGGAG 16/14	5
Pvu II	(3)	1320	3512	4120		Bsg I	GTCGAG 22/20	5	BsiC I	TT`CG,AA	1
Rsa I	(12)	219	737	762	817	BsiE I	CG,RY`CG	6	BsiHKA I	G,WGCW`C	8
		850	901	1058	1121	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
		1674	1785	1818	4320	BsmA I	GTCTC`9	10	BsmB I	CGTCTC 7/11	1
Rsr II	(1)	4530				BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	52
Sac I	(2)	1927	2286			Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
Sac II	(1)	2081				BspH I	T`CATG,A	3	BspM I	ACTCTG 10/14	3
Sal I	(1)	1143				BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	16
Sap I	(2)	4358	4568			BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
Sau3A I	(30)	53	70	328	374	BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1
		392	1103	1114	1327	BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
		1762	1999	2161	2640	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
		2649	2671	3851	3855	BstN I	CC`W,GG	27	BstU I	CG CG	24
		3874	4185	4263	4344	BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	13
		4353	4431	4807	4823	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	50
		5182	5194	5272	5280	Cfr10 I	R`CCGG,Y	6	Cla I	AT`CG,AT	1
Sau96 I	(22)	336	601	794	1223	Csp6 I	G`TA,C	12	Dde I	C`TNA,G	13
		1359	1382	1573	1843	Dpn I	GA TC	30	DpnII	`GATC,	30
		1943	2021	2192	2300	Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	3
		2312	2336	2355	2496	Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	8
		3121	4530	4975	5021	Eae I	Y`GGCC,R	8	Eag I	C`GGCC,G	3
		5079	5112			Ear I	CTCTTC 7/10	5	Eco47 III	AGC GCT	-
Sca I	(1)	219				Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
ScrF I	(41)	164	515	608	801	EcoN I	CCTNN`N,NNAGG	1	EcoO109 I	RG`GNC,CY	3
		1194	1227	1287	1325	EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	27
		1374	1707	1719	1847	EcoR V	GAT ATC	-	Ehe I	GGC GCC	3
		1893	1901	1941	1981	Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	52
		2145	2305	2315	2316	Fok I	GGATG 14/18	9	Fse I	GG,CCGG`CC	-
		2359	2384	2448	2511	Fsp I	TG GCA	2	Gdi II	`YGGC,CG	9
		2571	2595	2631	2632	Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	8
		3550	3605	3622	4018	Hae II	R,CGCC`Y	7	Hae III	GG CC	34
		4178	4401	4791	4980	Hga I	GACCC 9/14	11	HgiA I	G,WGCW`C	8
		5083	5555	5773	5786	HgiE II	ACCCNNNNNGGT -1/133	-	Hha I	G,CG`C	31
		5907				Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Sec I	(34)	878	1123	1219	1225	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	15
		1226	1286	1372	1378	HinI I	GR`CG,YC	13	HinP I	G`CG,C	31
		1456	1766	1835	1892	Hpa I	GTT AAC	1	Hpa II	C`CG,G	29
		1939	2078	2117	2303	Hph I	GGTGA 12/11	10	Kas I	G`CGCG,C	3
		2314	2446	2630	2631	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	10
		3548	3620	3743	3778	Mae II	A`CG,T	21	Mae III	`GTNAC,	21
		3787	3836	4177	4446	Mbo I	`GATC,	30	Mbo II	GAAGA 12/11	19
		4851	4978	4979	5081	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	4
		5082	5772			Mnl I	CCTC 10/10	49	Msc I	TGG CCA	2
SfaN I	(15)	247	440	876	1176	Mse I	T`TA,A	21	Msl I	CAYNN NNRTG	6
		2118	2829	3592	3664	Msp I	C`CG,G	29	MspAl I	CMG CKG	7
		3973	4228	4312	4376	Mun I	C`AATT,G	1	Nae I	GCC GGC	5
		4444	4651	5836		Nar I	GG`CG,CC	3	Nci I	CC`S,GG	14
Sfc I	(6)	454	1245	1829	3349	Nco I	C`CATG,G	6	Nde I	CA`TA,TG	2
		5476	5667			Ngom I	G`CCGG,C	5	Nhe I	G`CTAG,C	-
Sfi I	(1)	3789				Nla III	,CATG`	32	Nla IV	GGN NCC	36
Sma I	(2)	2316	2632			Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
SnaB I	(1)	858				Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	6
Sph I	(3)	3584	3656	4419		NspB II	CMG CKG	7	NspH I	R,CATG`Y	6
Ssp I	(2)	2922	3475			Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
Stu I	(2)	2328	3835			Pal I	GG CC	34	Pf1M I	CCAN,NNN`NTGG	3
Sty I	(10)	878	1123	1378	1766	Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
		1835	2117	3743	3836	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
		4446	4851			Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
Taq I	(15)	46	1144	2113	2170	Pst I	C,TGCA`G	2	Pvu I	CG,AT`CG	1
		3163	3854	4127	4283	Pvu II	CAG CTG	3	Rsa I	GT AC	12
		4307	4343	4505	4696	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
		4741	4996	5834		Sac II	CC,CG`GG	1	Sal I	G`TCGA,C	1
Tfi I	(7)	1568	1862	4499	4633	Sap I	GGCTCTC 8/11	2	Sau3A I	`GATC,	30
		4743	4780	5958		Sau96 I	G`GNC,C	22	Sca I	AGT ACT	1
Tsp45 I	(8)	227	438	1313	1952	ScrF I	CC`N,GG	41	Sec I	C`CNNG,G	34
		2228	3303	4134	4440	SfaN I	GCATC 9/13	15	Sfc I	C`TRYA,G	6
Tth111 I	(1)	4132				Sfi I	GCCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Tth111 II	(5)	1442	4450	5310	5340	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	-
		5349				Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Vsp I	(1)	525				Srf I	GCCC GGCC	-	Ssp I	AAT ATT	2
Xba I	(1)	1149				Stu I	AGG CCT	2	Sty I	C`CWGG,G	10
Xcm I	(1)	2294				Taq I	T`CG,A	15	Tfi I	G`AWT,C	7
Xho II	(13)	53	70	1103	1327	Tsp45 I	`GTSAC,	8	Tth111 I	GACN`N,NGTC	1
		1999	2640	4185	4431	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
		4823	5182	5194	5280	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
		5291				Xcm I	CCANNNN,N`NNNNTGG1	-	Xho I	C`TCGA,G	2
Xma I	(2)	2314	2630	3920		Xho II	R`GATC,Y	13	Xma I	C`CCGG,G	2
Xma III	(3)	1136	2385			Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	1
Xmn I	(1)	100									

Site usage in pCMV-CAP: