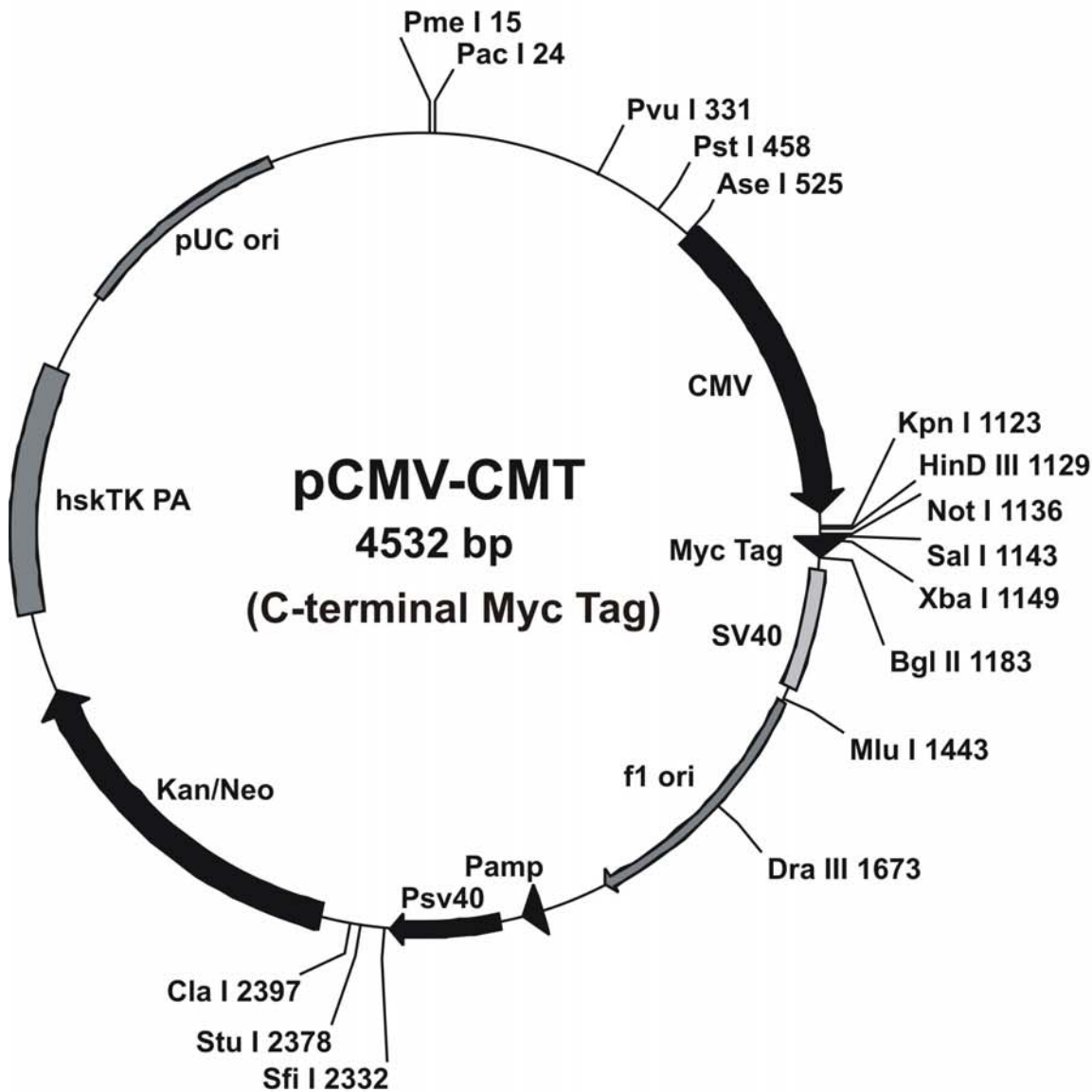


Name of Vector: pCMV-CMT
Antibiotic Selection: Kan
Created by: Wei Jiang and Qing Luo
(He Lab @ The University of Chicago)
Date of Creation: February 2004



Linker Sequence

Kozak

Kpn I Hind III Not I Sal I Xba I

GGT ACC ATG GAA GCT TGC GGC CGC GTC GAC TCT AGA GGA GGC GGC GGA GGT
M E A C G R V D S R G G G G G

Myc Tag Bgl II

GTC GAG GGA GAA CAA AAA CTC ATC TCA GAA GAG GAT CTG TGAGATCT
V E G E Q K L I S E E D L -

pCMV-CMT Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagtctctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttggtgagtactcaccagtacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacctgatgataa 300
cactgcggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacacaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgcttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGGTTACATAACTTACGGTAAATG 600
GCCCCCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTG 960
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCAAAATGTCGTAACA 1020
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGC GGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGCGAGGAGAACAAAACTCATCTCAGAAGA 1200
GGATCTGTGagatctatccgatccaccggannnnnnTAACTGATCATAATCAGCCATACC 1260
ACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAA 1320
CATAAAATGAATGCAATTGTTGTTGTTAACTTGTATTATGCAGCTTATAATGGTTACAAA 1380
TAAAGCAATAGCATCACAATTTTCAAAATAAAGCATTTTTTTCACTGCATTCTAGTTGT 1440
GGTTTGTCCAAACTCATCAATGTATCTTAAACCGGTAAATTGTAAGCGTTAATATTTTTGTT 1500
AAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTTAAACCAATAGGCCGAAATCGG 1560
CAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTG 1620
GAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTA 1680
TCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTG 1740
CCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAA 1800
GCCGGCGAACGTGGCGAGAAAGGAAGGAAAGCGAAAGGAGCGGGCGCTAGGGCGCT 1860
GGCAAGTGTAGCGGTCACGCTGCGCGTAAACCACCACCCCGCGCTTAATGCGCCGCT 1920
ACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAAATGTGCGCGGAACCCCTATTTGTTTATT 1980
TTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCTGATAAATGCTTCA 2040
ATAATATTGAAAAAGGAAGAGTCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAG 2100
TTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTC 2160
AATTAGTCAGCAACCAGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAA 2220
AGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCGCCCC 2280
CTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTTAT 2340
GCAGAGGCCGAGGCCGCTCGGCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTT 2400
GGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGAT 2460
TGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTA 2520
TGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCA 2580
GGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGA 2640
CGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCTTGCAGCTGTGCTCGA 2700
CGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCT 2760
CCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCG 2820
GCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGA 2880
GCGAGCACGTAICTGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCA 2940
TCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGA 3000
GGATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCG 3060
CTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGC 3120
GTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT 3180
GCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGA 3240

GTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCCAACCTGCCA 3300
 TCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGTTGGGCTTCGGAATCGTTTTTC 3360
 CGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCAC 3420
 CCTAGGGGGAGGCTAACTGAAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATG 3480
 ACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACGCGGG 3540
 GTTCGGTCCCAGGGCTGGCACTCTGTGCATACCCACCGAGACCCCATTTGGGGCCAATAC 3600
 GCCCGCGTTTTCTTCCTTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTC 3660
 GCAGCCAACGTCGGGGCGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAG 3720
 ATTGATTTAAAACCTTCATTTTTTAATTTAAAGGATCTAGGTGAAGATCCTTTTTGATAAT 3780
 CTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA 3840
 AAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACA 3900
 AAAAAACCACCGCTACCAGCGGTGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTT 3960
 CCGAAGGTAACCTGGCTTACAGCAGCGCAGATACCAATACTGTCCTTCTAGTGTAGCCG 4020
 TAGTTAGGCCACCCTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATC 4080
 CTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA 4140
 CGATAGTTACCGGATAAGGCGCAGCGGTGGGGTGAACGGGGGTTTCGTGCACACAGCCC 4200
 AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGC 4260
 GCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACA 4320
 GGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTTGTTCGGG 4380
 TTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA 4440
 TGGAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGT 4500
 CACATGTTCTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4560

Unique enzymes in CMVCMT

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,NNAGS	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	1211
Pf1M I	CCAN,NNN`NTGG	1230
BstX I	CCAN,NNNN`NTGG	1231
Bcl I	T`GATC,A	1242
Mun I	C`AATT,G	1335
Hpa I	GTT AAC	1348
Mlu I	A`CGCG,T	1471
Dra III	CAC,NNN`GTG	1701
Sfi I	GGCCN,NNN`NGGCC	2360
Stu I	AGG CCT	2406
Cla I	AT`CG,AT	2425
Kas I	G`GCGC,C	2584
Nar I	GG`CG,CC	2585
Ehe I	GGC GCC	2586
Bbe I	G,GCGC`C	2588
Msc I	TGG CCA	2667
Tth111 I	GACN`N,NGTC	2703
Rsr II	CG`GWC,CG	3101
BsiC I	TT`CG,AA	3267
BstB I	TT`CG,AA	3267
Bsa I	GGTCTC 7/11	3574
EcoO109 I	RG`GNC,CY	3683

Number of enzymes = 41

CMVCMT: 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	1845
		1872	1900	1903	1917
		1960	2007	2070	2255
		2267	2276	2288	2298
		2309	2355	2494	2557
		2651	2715	2816	2819
		3059	3099	3104	3154
		3170	3196	3252	3321
		3324	3390	3472	3537
		3604	3677	3911	3920
		4055	4165	4286	4305
		4432	4460	4551	
Afl III	(2)	1471	4503		
Aha II	(8)	160	640	693	776
		962	2585	3287	3366
Alu I	(16)	347	410	510	1084
		1131	1364	1531	1788
		2083	2371	2691	3149
		3946	4203	4249	4339
Alw I	(17)	60	66	381	1099
		1209	1216	2452	2763
		2830	3009	3374	3401
		3760	3761	3858	3858
		3944			
AlwN I	(2)	3686	4094		
ApaL I	(2)	28	4189		
Apo I	(3)	1399	1503	1514	
Ase I	(1)	525			
Asp718	(1)	1119			
Ava II	(3)	336	3101	3546	
Avr II	(2)	2407	3422		
Ban I	(5)	983	1119	1738	2584
		2619			
Ban II	(3)	1776	2950	3660	
Bbe I	(1)	2588			
Bbv I	(7)	468	1373	2658	2700
		3221	3674	4174	
Bcl I	(1)	1242			
Bcn I	(6)	165	516	2590	2750
		3363	4127		
Bfa I	(9)	507	1110	1150	1434
		1852	2408	3423	3757
		4010			
Bgl I	(4)	608	730	801	2360
Bgl II	(1)	1211			
Bpm I	(2)	3368	3425		
Bsa I	(1)	3574			

The following enzymes do not cut in CMVCMT

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	Sma II	Sma I	Spe I
Spl I	Srf I	Xca I	Xcm I	Xho I

BsaA I	(3)	858	1701	2889				2652	2689	2730	2817
BsaB I	(2)	1247	2444					2820	2823	3059	3155
BsaH I	(8)	160	640	693	776			3196	3210	3324	3663
		962	2585	3287	3366			3678	3889	4095	4098
BsaJ I	(16)	878	1123	2119	2191			4163	4306	4461	
		2314	2349	2358	2407	Fok I	(6)	261	2258	2452	2909
		2748	3017	3422	3549			2934	3388		
		3550	3652	3653	4343	Fsp I	(2)	477	2687		
BsaW I	(6)	404	1226	2616	3460	Gdi II	(7)	308	1135	1137	2490
		4150	4297					2492	3055	3082	
BseR I	(2)	1168	2403			Gsu I	(2)	3369	3424		
BsiC I	(1)	3267				Hae I	(5)	2406	2667	4029	4481
BsiE I	(5)	182	331	1139	2494			4492			
		4169				Hae II	(4)	1852	1860	2588	4263
BsiHKA I	(5)	32	117	2698	2888	Hae III	(21)	309	602	795	1138
		4193						1551	1693	2348	2354
Bsm I	(2)	1336	1429					2363	2406	2493	2667
BsmA I	(5)	951	2010	2428	3447			3058	3085	3594	3651
		3575						3684	4029	4463	4481
BsmF I	(10)	693	844	1012	2101			4492			
		2173	2237	2736	3268	Hga I	(8)	167	1043	1131	1919
		3377	3532					3294	3373	3814	4392
BsoF I	(35)	185	280	307	457	HgiA I	(5)	32	117	2698	2888
		1136	1139	1160	1362			4193			
		1881	1903	1917	2355	HgiE II	(2)	1224	3914		
		2494	2546	2557	2647	Hha I	(22)	141	478	1851	1859
		2652	2689	2730	2817			1885	1907	1916	1929
		2820	2823	3059	3155			1960	2579	2587	2651
		3196	3210	3324	3663			2688	2954	3214	3390
		3678	3889	4095	4098			3476	3879	3988	4162
		4163	4306	4461				4262	4329		
Bspl286 I	(2)	117	2888			HinC II	(3)	158	1145	1348	
BspH I	(2)	2011	3783			Hind II	(3)	158	1145	1348	
BspM I	(3)	2472	2853	3303		Hind III	(1)	1129			
Bsr I	(11)	54	226	493	814	Hinf I	(12)	928	1146	1628	1650
		1615	2293	2528	2729			2060	3070	3204	3256
		3975	4089	4102				3314	3351	4133	4529
BsrB I	(4)	1845	2009	3198	3252	HinI I	(8)	160	640	693	776
BsrD I	(2)	466	2818					962	2585	3287	3366
Bsss I	(4)	31	3177	3303	4330	HinP I	(22)	139	476	1849	1857
BstB I	(1)	3267						1883	1905	1914	1927
BstN I	(11)	608	801	2121	2176			1958	2577	2585	2649
		2193	2972	3551	3654			2686	2952	3212	3388
		4344	4357	4478				3474	3877	3986	4160
		4460						4260	4327		
BstU I	(17)	141	578	1141	1473	Hpa I	(1)	1348			
		1509	1885	1905	1929	Hpa II	(20)	163	405	515	1227
		1960	2651	2952	3390			1803	2490	2567	2589
		3474	3537	3606	3879			2617	2748	2838	2905
		4460						3086	3361	3369	3461
BstX I	(1)	1231						3935	4125	4151	4298
BstY I	(12)	53	70	1103	1202	Hph I	(6)	215	893	1703	2764
		1211	2756	3002	3394			3655	3771		
		3753	3765	3851	3862						
Bsu36 I	(2)	2065	3697			Kas I	(1)	2584			
Cac8 I	(29)	454	604	797	1133	Kpn I	(1)	1123			
		1804	1847	1861	2134	Mae I	(9)	507	1110	1150	1434
		2153	2206	2225	2479			4010	1852	2408	3423
		2665	2884	2950	2956			98	471	640	652
		2984	2988	3029	3033	Mae II	(16)	693	776	857	962
		3087	3370	3557	3604			1645	1657	1700	1810
		3660	3682	3893	4453			2701	2888	3669	3802
		4490						39	227	380	438
Cfr10 I	(4)	1802	2904	3085	3368	Mae III	(16)	579	666	1015	1373
Cla I	(1)	2425						1874	1886	2705	3011
Cap6 I	(9)	218	736	761	816			3701	3967	4083	4146
		849	900	1057	1120	Mbo I	(27)	53	70	328	374
		2890						392	1103	1114	1202
Dde I	(8)	199	1193	2065	2367			1211	1220	1242	2422
		3248	3697	3820	4229			2426	2445	2756	2834
Dpn I	(27)	55	72	330	376			2915	2924	3002	3378
		394	1105	1116	1204			3394	3753	3765	3843
		1213	1222	1244	2424			3851	3862	3937	
		2428	2447	2758	2836			104	1208	1840	2068
		2917	2926	3004	3380			2945	3155	3237	3404
		3396	3755	3767	3845			3604	3774	3847	
		3853	3864	3939							
DpnII	(27)	53	70	328	374	Mlu I	(1)	1471			
		392	1103	1114	1202	Mme I	(3)	1677	4111	4295	
		1211	1220	1242	2422	Mnl I	(30)	327	1059	1146	1149
		2426	2445	2756	2834			1158	1166	1193	1264
		2915	2924	3002	3378			1303	1312	1729	2060
		3394	3753	3765	3843			2338	2344	2367	2373
		3851	3862	3937				2381	2384	2396	2436
Dra I	(5)	15	122	1287	3729			2500	2636	2993	3185
		3748						3391	3423	3705	4075
		4326						4326	4399		
Dra III	(1)	1701				Msc I	(1)	2667			
Drd I	(3)	1656	2612	4401		Mse I	(20)	14	20	24	121
Dsa I	(4)	878	1123	2314	3017			486	525	1286	1347
Eae I	(6)	307	1136	2491	2665			1468	1489	1500	1512
		3056	3083					1523	1540	1638	1909
Eag I	(2)	1136	2491					3728	3742	3747	3799
Ear I	(4)	1192	2052	2929	3139			288	883	1231	3022
Eco57 I	(3)	2730	3162	3962		Msl I	(4)	288	883	1231	3022
EcoN I	(1)	339				Msp I	(20)	163	405	515	1227
EcoO109 I	(1)	3683						1803	2490	2567	2589
EcoR II	(11)	606	799	2119	2174			2617	2748	2838	2905
		2191	2970	3549	3652			3086	3361	3369	3461
		4342	4355	4476				3935	4125	4151	4298
Ehe I	(1)	2586				MspAl I	(5)	64	2083	2691	3920
Fnu4H I	(35)	185	280	307	457			4165			
		1136	1139	1160	1362	Mun I	(1)	1335			
		1881	1903	1917	2355	Nae I	(3)	1804	3087	3370	
		2494	2546	2557	2647	Nar I	(1)	2585			

Nci I	(6)	164	515	2589	2749	Avr II	C`CTAG,G	2	BamH I	G`GATC,C	-
Nco I	(4)	362	4126			Ban I	G`GYRC,C	5	Ban II	G,RCY`C	3
Nde I	(1)	878	1123	2314	3017	Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	-
NgoM I	(3)	752				Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
Nla III	(20)	1802	3085	3368		Bcl I	T`GATC,A	1	Bcn I	CC,s`GG	6
		257	293	371	381	Bfa I	C`TA,G	9	Bgl I	GCCN,NNN`NGGC	4
		822	882	1127	2015	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
		2155	2227	2318	2459	Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
		2804	2990	3021	3047	BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
		3403	3787	4507	4558	BsaH I	GR`CG,YC	8	BsaJ I	C`C`NNG,G	16
Nla IV	(16)	403	985	1121	1740	BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	2
		1761	1773	1964	2125	Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	1
		2197	2586	2621	3469	BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
		3548	3593	4436	4475	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
Not I	(1)	1136				BsmA I	GTCTC`/9	5	BsmB I	CGTCTC 7/11	-
Nsi I	(3)	2157	2229	4560		BsmF I	GGAC 15/19	10	BsoF I	GC`N,GC	35
Nsp7524 I	(4)	2151	2223	2986	4503	Bsp120 I	G`GGCC,C	2	Bsp1286 I	G,DGCH`C	2
NspB II	(5)	64	2083	2691	3920	BspH I	T`CATG,A	-	BspM I	ACCTGC 10/14	3
		4165				BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
NspH I	(4)	2155	2227	2990	4507	BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
Pac I	(1)	24				BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	-
Pal I	(21)	309	602	795	1138	BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
		1551	1693	2348	2354	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
		2363	2406	2493	2667	BstN I	CC`W,GG	11	BstU I	CG CG	17
		3058	3085	3594	3651	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	12
		3684	4029	4463	4481	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	29
		4492				Cfr10 I	R`CCGG,Y	4	Clal I	AT`CG,AT	1
PflM I	(1)	1230				Csp6 I	G`TA,C	9	Dde I	C`TNA,G	8
Ple I	(2)	1636	2068			Dpn I	GA TC	27	DpnII	`GATC,	27
Pme I	(1)	15				Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Psp1406 I	(2)	98	471			Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Pst I	(1)	458				Eae I	Y`GGCC,R	6	Eag I	C`GGCC,G	2
Pvu I	(1)	331				Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	-
Pvu II	(2)	2083	2691			Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
Rsa I	(9)	219	737	762	817	EcoN I	CCTNN`N,NNAGG	1	EcoO109 I	RG`GNC,CY	1
		850	901	1058	1121	EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	11
		2891				EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Rsr II	(1)	3101				Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	35
Sal I	(1)	1143				Fok I	GGATG 14/18	6	Fse I	GG,CCGG`CC	-
Sap I	(2)	2929	3139			Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
Sau3A I	(27)	53	70	328	374	Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	5
		392	1103	1114	1202	Hae II	R,GC`C`Y	4	Hae III	GG CC	21
		1211	1220	1242	2422	Hga I	GACGC 9/14	8	HgaI I	G,WGCW`C	5
		2426	2445	2756	2834	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	22
		2915	2924	3002	3378	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
		3394	3753	3765	3843	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12
		3851	3862	3937		HinI I	GR`CG,YC	8	HinP I	G`CG,C	22
Sau96 I	(9)	336	601	794	1692	Hpa I	GT AAC	1	Hpa II	C`CG,C	20
		3101	3546	3592	3650	Hph I	GGTGA 12/11	6	Kas I	G`CGCG,C	1
		3683				Kpn I	G,GTAC`C	1	Mae I	C`TA,G	9
Sca I	(1)	219				Mae II	A`CG,T	16	Mae III	`GTNAC,	16
ScrF I	(17)	164	515	608	801	Mbo I	`GATC,	27	Mbo II	GAAGA 12/11	11
		2121	2176	2193	2589	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
		2749	2972	3362	3551	Mnl I	CCTC 10/10	30	Msc I	TGG CCA	1
		3654	4126	4344	4357	Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
		4478				Msp I	C`CG,G	20	MspA1 I	CMG CKG	5
Sec I	(16)	878	1123	2119	2191	Mun I	C`AATT,G	1	Nae I	GCC GGC	3
		2314	2349	2358	2407	Nar I	GG`CG,CC	1	Nci I	CC`s,GG	6
		2748	3017	3422	3549	Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
		3550	3652	3653	4343	NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
SfaN I	(13)	247	440	876	1400	Nla III	,CATG`	20	Nla IV	GGN NCC	16
		2163	2235	2544	2799	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
		2883	2947	3015	3222	Nsi I	A,GTCA`T	3	Nsp7524 I	R`CATG,Y	4
		4407				NspB II	CMG CKG	5	NspH I	R,CATG`Y	4
Sfc I	(4)	454	1920	4047	4238	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
Sfi I	(1)	2360				Pal I	GG CC	21	PflM I	CCAN,NNN`NTGG	1
SnaB I	(1)	858				Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Sph I	(3)	2155	2227	2990		Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
Ssp I	(2)	1493	2046			Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
Stu I	(1)	2406				Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Sty I	(6)	878	1123	2314	2407	Pvu II	CAG CTG	2	Rsa I	GT AC	9
		3017	3422			Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Taq I	(14)	46	1144	1171	1734	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
		2425	2698	2854	2878	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	27
		2914	3076	3267	3312	Sau96 I	G`GNC,C	9	Sca I	AGT ACT	1
		3567	4405			ScrF I	CC`N,GG	17	Sec I	C`C`NNG,G	16
Tfi I	(5)	3070	3204	3314	3351	SfaN I	GCATC 9/13	13	Sfc I	C`TRYA,G	4
		4529				Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Tsp45 I	(5)	227	438	1874	2705	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	-
		3011				Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Tth111 I	(1)	2703				Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Tth111 II	(4)	3021	3881	3911	3920	Stu I	AGG CCT	1	Sty I	C`C`WVG,G	6
Vsp I	(1)	525				Taq I	T`CG,A	14	Tfi I	G`AWT,C	5
Xba I	(1)	1149				Tsp45 I	`GTSAC,	5	Tth111 I	GACN`N,NGTC	1
Xho II	(12)	53	70	1103	1202	Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	1
		1211	2756	3002	3394	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
		3753	3765	3851	3862	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Xma III	(2)	1136	2491			Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	-
Xmn I	(1)	100				Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1

Site usage in CMVCMT:

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	17	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`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	-	Ava II	G`GWC,C	3