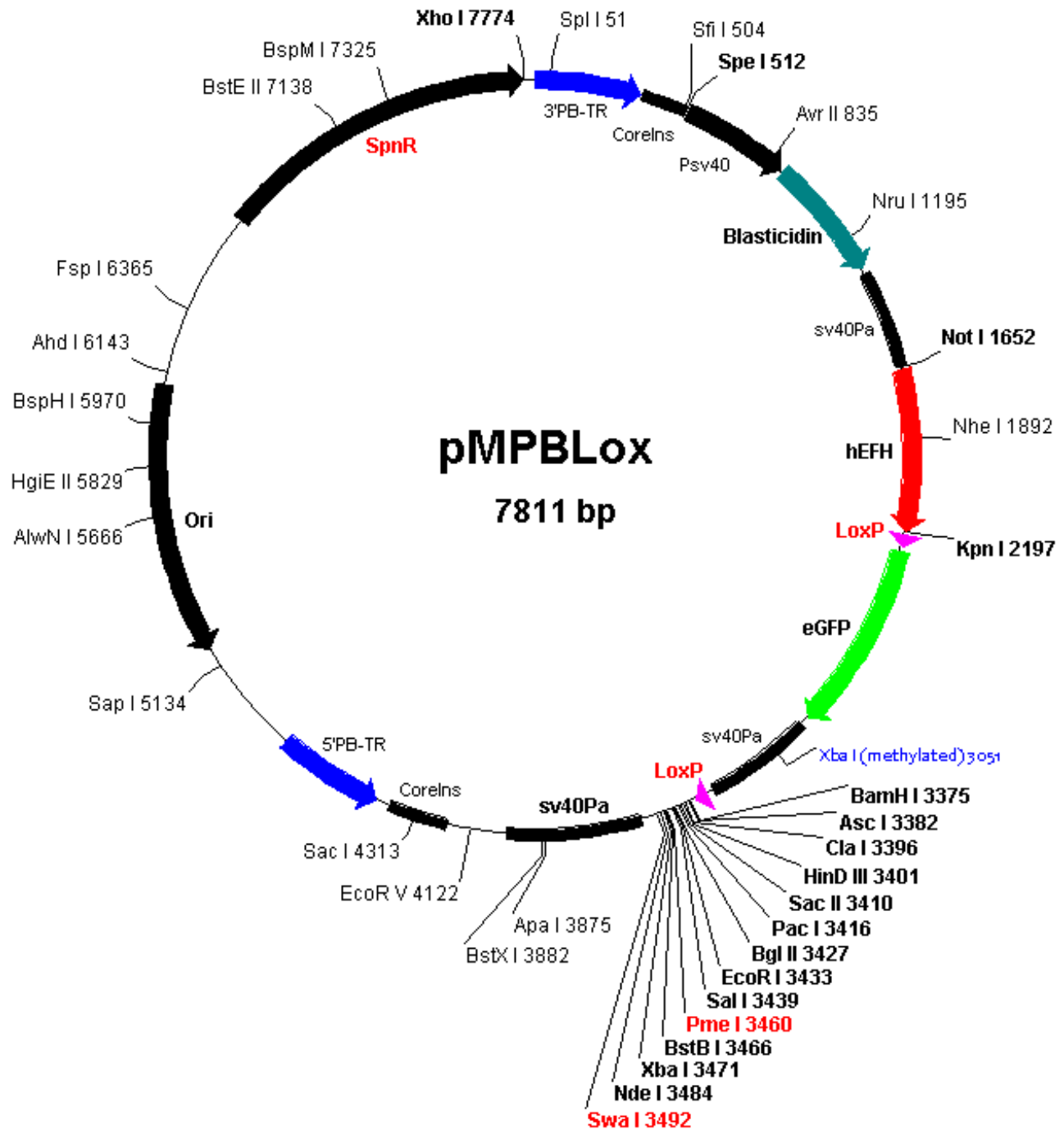


Vector: pMPBLox (MOLab PiggyBac loxP-GFP-PA-loxP vector)

Antibiotic Selection: Spectinomycin or Blasticidin-resistant

Creator(s): Ning Wang, MD & Sean Chen, MD, PhD, Molecular Oncology Lab of The University of Chicago

Date of Construction: March, 2012



pMPBlox Vector Sequence
(Spectinomycin or Blastacin-resistant)

CTGCAGAACACGCAGCTAGATTAACTCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAAATTGACCCATG
TGTTTTATCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTTACACTTACATACTAATAATA
AATTCAACAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAACAACAAAACCTCAAAATTTCTTCTATAAAGTAACAAAACTTTT
ATGAGGGACAGCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGTAGGGGGCAGCAGCGAGCCGCCGGGGCTCC
GCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCGGGCACGGGGAAGGTGGCACGGGATCGCTTT
CCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGAAAAGGCCTCCACGGCCAGACTAGTAAATGTG
TGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCTAACTCCG
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CAGAACTCGTGGTGTGGCAGTGTCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTTCGCGATCGGAAATGAGAACAGGGGCA
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GAGATCACCAAGGTAGTCGGCAAATAACCCTCGAGCCACCCAATGACCAAAAATCCCTTAACGTGAGTTA

Unique enzymes in pMPBLox:

BsiW I	C`GTAC,G	51
Spl I	C`GTAC,G	51
Sfi I	GGCCN,NNN`NGGCC	504
Spe I	A`CTAG,T	512
Avr II	C`CTAG,G	835
Bbv II	GAAGAC 7/11	1048
Bbs I	GAAGAC 8/12	1049
Nru I	TCG CGA	1195
Not I	GC`GGCC,GC	1652
Nhe I	G`CTAG,C	1892
Bsu36 I	CC`TNA,GG	1941
Kas I	G`GCGC,C	2184
Nar I	GG`CG,CC	2185
Ehe I	GGC GCC	2186
Bbe I	G,GCGC`C	2188
Acc65 I	G`GTAC,C	2193
Asp718	G`GTAC,C	2193
Kpn I	G,GTAC`C	2197
Bsp1286 I	G,DGCH`C	2922
Xmn I	GAANN NNTTC	3363
BamH I	G`GATC,C	3375
Asc I	GG`CGCG,CC	3382
Cla I	AT`CG,AT	3396
Hind III	A`AGCT,T	3401
Sac II	CC,GC`GG	3410
Bgl II	A`GATC,T	3427
EcoR I	G`AATT,C	3433
Sal I	G`TCGA,C	3439
Acc I	GT`MK,AC	3440
Pme I	CTTT AAAC	3460
BsiC I	TT`CG,AA	3466
BstB I	TT`CG,AA	3466
Nde I	CA`TA,TG	3484
Bsp120 I	G`GGCC,C	3871
Apa I	G,GGCC`C	3875

BstX I	CCAN,NNNN`NTGG	3882
EcoR V	GAT ATC	4122
Sac I	G,AGCT`C	4313
Sap I	GCTCTTC 8/11	5134
AlwN I	CAG,NNN`CTG	5666
HgiE II	ACCNNNNNNGGT -1/135829	
BspH I	T`CATG,A	5970
Ahd I	GACNN,N`NNGTC	6143
Fsp I	TGC GCA	6365
BstE II	G`GTNAC,C	7138
BspM I	ACCTGC 10/14	7325
Paer7 I	C`TCGA,G	7774
Xho I	C`TCGA,G	7774

Number of enzymes = 49

The following enzymes do not cut in pMPBLox:

Aat II	Afl II	BsmB I	Bst1107 I	Fse I
PflM I	Sca I	Tth111 I	Xca I	Xcm I

pMPBLox: sites sorted by name:

Acc I	(1)	3440			
Acc65 I	(1)	2193			
Aci I	(86)	315	336	348	370
		393	683	695	704
		716	726	737	783
		1083	1165	1232	1416
		1419	1485	1651	1655
		1756	1793	1873	1929
		1932	1947	1978	1985
		2012	2531	2572	2639
		2678	2816	2929	2989
		2992	3373	3407	3409
		3989	4012	4034	4046
		4067	4251	4284	4318
		4526	4539	4688	4795

		4800	4848	4885	4940			2481	2644	2668	2723
		5043	5099	5109	5133			3407	3695	3843	3904
		5176	5183	5204	5295			3977	4040	4041	4090
		5323	5450	5469	5590			4091	4558	4669	4989
		5700	5835	5844	6206			5410	6663	6686	6869
		6297	6488	6534	6801			6900	7207	7271	7410
		6821	6989	7086	7098			7752			
		7165	7228	7424	7427	BsaW I	(14)	352	1659	1734	2300
		7505	7552					3030	3045	3298	4028
Afl III	(5)	894	1390	3290	3451			4696	4708	5456	5603
		5250						6434	7444		
Age I	(2)	1734	2300			BseR I	(4)	831	1391	2283	2343
Aha II	(3)	1461	2185	7032		Bsg I	(6)	1151	1852	2441	2538
Ahd I	(1)	6143						2862	4800		
Alu I	(42)	16	799	853	863	BsiC I	(1)	3466			
		1066	1171	1535	1886	BsiE I	(9)	1083	1199	1655	2305
		1892	1896	2034	2175			4255	5166	5590	6513
		2289	2333	2366	2438			7359			
		2471	2687	2735	2846	BsiHKA I	(4)	2922	4313	5568	7257
		3020	3183	3403	3677	BsiW I	(1)	51			
		4311	4437	4480	4915	Bsm I	(5)	1600	3155	3248	3591
		5010	5074	5192	5418			4395			
		5508	5554	5811	6332	BsmA I	(4)	982	2038	3690	6205
		6432	6495	6742	7172	BsmF I	(16)	281	291	410	529
		7286	7658					601	665	1136	1472
Alw I	(23)	434	888	1278	1469			1683	3337	3713	3796
		1496	2163	2808	3005			3970	4089	4099	7534
		3035	3055	3291	3371	BsoF I	(70)	14	326	329	336
		3382	3949	4453	5812			387	454	783	1064
		5898	5898	5995	5996			1083	1157	1160	1163
		6460	7437	7466				1166	1169	1333	1419
AlwN I	(1)	5666						1533	1652	1655	1873
Apa I	(1)	3875						1932	1947	1978	2472
ApaL I	(2)	5564	7253					2531	2553	2837	2844
Apo I	(7)	175	233	1570	3218			2895	2898	2992	3181
		3433	3561	7721				3830	3929	3996	4047
Asc I	(1)	3382						4054	4057	4319	4438
Ase I	(6)	122	906	4786	5021			4540	4571	4574	4689
		5080	6315					4801	4848	5075	5156
Asp718	(1)	2193						5174	5177	5295	5450
Ava I	(11)	339	377	403	856			5593	5658	5661	5867
		1701	1803	3977	4003			6195	6534	6561	6656
		4041	6870	7774				6799	6884	6928	6944
Ava II	(9)	355	1123	2969	3351			7099	7166	7316	7425
		4026	6281	6503	6777			7505	7602		
		7418				Bsp120 I	(1)	3871			
Avr II	(1)	835				Bsp1286 I	(1)	2922			
BamH I	(1)	3375				BspH I	(1)	5970			
Ban I	(9)	1238	1662	1737	1993	BspM I	(1)	7325			
		2184	2193	2348	4994	BspM II	(4)	3030	3298	4696	4708
		6091				Bsr I	(22)	721	1097	1121	1769
Ban II	(6)	347	1228	1908	3875			1790	2925	3748	3858
		4041	4313					4679	5051	5657	5670
Bbe I	(1)	2188						5784	6190	6308	6351
Bbs I	(1)	1049						6618	6713	6778	7516
Bbv I	(22)	25	337	340	398			7612	7634		
		1075	1180	1544	2564	BsrB I	(5)	350	1657	4034	4942
		2848	2855	3192	3841			5183			
		3940	5669	5672	5878	BsrD I	(4)	6204	6378	7327	7620
		6572	6810	6895	6939	BsrG I	(2)	3022	3445		
		6955	7327			BssH II	(3)	3382	4889	7702	
Bbv II	(1)	1048				BssS I	(3)	1138	2493	5423	
Bcl I	(3)	886	3061	7176		BstB I	(1)	3466			
Bcn I	(20)	341	342	405	406	BstE II	(1)	7138			
		858	859	1458	2049	BstN I	(23)	291	477	549	604
		2343	2997	3697	3846			621	1268	2358	2483
		3979	3980	4043	4044			2595	2670	2724	3776
		4883	5631	6327	6674			3834	3906	4092	4670
Bfa I	(25)	17	28	318	513			4837	4990	5278	5399
		836	1073	1605	1742			5412	6632	7209	
		1893	2019	2081	2292	BstU I	(28)	1195	1485	1756	1925
		3052	3253	3370	3425			1970	2641	2959	3292
		3472	3596	4064	4423			3384	3409	3453	4251
		4434	5745	5998	6333			4357	4528	4688	4891
		7659						5097	5099	5297	5878
Bgl I	(3)	504	6263	7610				6208	6892	7165	7230
Bgl II	(1)	3427						7293	7586	7702	7704
Blp I	(2)	1359	7287			BstX I	(1)	3882			
Bpm I	(6)	1463	1520	2757	2997	BstY I	(13)	881	1489	2167	2812
		6213	7230					3039	3048	3375	3427
Bsa I	(3)	2037	3691	6204				5891	5902	5988	6000
BsaA I	(6)	895	1393	3479	4160			7459			
		4218	7735			Bsu36 I	(1)	1941			
BsaB I	(2)	1262	3066			Cac8 I	(47)	333	384	391	467
BsaH I	(3)	1461	2185	7032				562	581	634	653
BsaJ I	(45)	289	290	339	340			1059	1173	1465	1894
		403	476	502	547			1908	1929	2092	2120
		619	742	777	835			2436	2469	2517	2841
		856	962	1267	1374			2848	3384	3917	3993
		1804	2068	2311	2341			4000	4051	4298	4395

		4482	4636	4887	4891	Fsp I	(1)	6365				
		5043	5072	5181	5267	Gdi II	(11)	506	1079	1081	1370	
		5304	5864	6255	6888			1651	1653	2385	2772	
		7065	7170	7350	7519			5090	6530	7064		
		7625	7629	7704		Gsu I	(6)	1464	1519	2756	2996	
Cfr10 I	(14)	382	1463	1734	1958			6214	7229			
		2090	2181	2300	2463	Hae I	(9)	498	834	967	4629	
		3998	4749	4773	6223			4665	5265	5276	5728	
		7574	7627					7697				
Cla I	(1)	3396				Hae II	(13)	364	2065	2188	2298	
Csp6 I	(12)	52	1784	2194	2741			3425	4024	4487	4806	
		3023	3446	3480	6624			5128	5498	7045	7475	
		6857	7070	7078	7561			7624				
Dde I	(13)	795	1359	1941	2035	Hae III	(30)	498	507	776	782	
		2086	2916	2934	3036			834	967	1082	1373	
		4325	5525	5934	6100			1654	1946	2051	2386	
		7287						2486	2775	2887	3873	
Dpn I	(41)	429	883	888	1198			4629	4665	5091	5265	
		1259	1273	1475	1491			5276	5294	5728	6186	
		2169	2202	2814	2962			6266	6533	7067	7101	
		3000	3041	3050	3063			7631	7697			
		3297	3377	3429	3498	Hga I	(10)	89	1042	1468	1998	
		3955	4448	5818	5893			4224	4387	5360	5938	
		5904	5912	5990	6002			6686	7022			
		6107	6448	6466	6512	HgiA I	(4)	2922	4313	5568	7257	
		6995	7178	7358	7368	HgiE II	(1)	5829				
		7443	7461	7689	7710	Hha I	(47)	363	1063	1485	1684	
		7748						1756	1927	2064	2159	
DpnII	(41)	427	881	886	1196			2187	2297	2602	2643	
		1257	1271	1473	1489			2959	3384	3386	3424	
		2167	2200	2812	2960			4023	4359	4486	4729	
		2998	3039	3048	3061			4805	4891	4893	5034	
		3295	3375	3427	3496			5099	5127	5160	5430	
		3953	4446	5816	5891			5497	5597	5771	5880	
		5902	5910	5988	6000			6273	6366	6765	6815	
		6105	6446	6464	6510			6892	7044	7232	7293	
		6993	7176	7356	7366			7320	7474	7568	7588	
		7441	7459	7687	7708			7623	7704	7706		
		7746				HinC II	(5)	900	3167	3391	3441	
Dra I	(7)	2030	3106	3460	3492			3772				
		3725	6009	6028		Hind II	(5)	900	3167	3391	3441	
Dra III	(4)	1369	6687	7115	7735			3772				
Drd I	(3)	1051	4329	5358		HinD III	(1)	3401				
Dsa I	(8)	502	742	962	2311	Hinf I	(20)	988	1320	1409	1446	
		3407	6686	6900	7271			1965	2084	3034	3468	
Eae I	(11)	505	965	1080	1371			3646	3858	4244	4352	
		1652	2384	2773	4627			4613	5085	5150	5225	
		5089	6531	7065				5621	6138	7009	7222	
Eag I	(2)	1080	1652			HinI I	(3)	1461	2185	7032		
Ear I	(3)	2260	3354	5134		HinP I	(47)	361	1061	1483	1682	
Eco47 III	(2)	2296	3423					1754	1925	2062	2157	
Eco57 I	(8)	1060	1907	2283	2465			2185	2295	2600	2641	
		2511	2708	5797	7123			2957	3382	3384	3422	
Eco72 I	(2)	895	1393					4021	4357	4484	4727	
EcoN I	(4)	1745	1940	3359	3866			4803	4889	4891	5032	
EcoO109 I	(3)	1123	3351	3871				5097	5125	5158	5428	
EcoR I	(1)	3433						5495	5595	5769	5878	
EcoR II	(23)	289	475	547	602			6271	6364	6763	6813	
		619	1266	2356	2481			6890	7042	7230	7291	
		2593	2668	2722	3774			7318	7472	7566	7586	
		3832	3904	4090	4668			7621	7702	7704		
		4835	4988	5276	5397	Hpa I	(2)	3167	3391			
		5410	6630	7207		Hpa II	(50)	340	353	358	383	
EcoR V	(1)	4122						404	857	1456	1464	
Ehe I	(1)	2186						1660	1735	1959	2047	
Esp I	(2)	1359	7287					2059	2091	2182	2301	
Fnu4H I	(70)	14	326	329	336			2341	2404	2464	2995	
		387	454	783	1064			3031	3046	3299	3379	
		1083	1157	1160	1163			3695	3845	3978	3999	
		1166	1169	1333	1419			4024	4029	4042	4697	
		1533	1652	1655	1873			4709	4750	4760	4774	
		1932	1947	1978	2472			4882	4968	5457	5604	
		2531	2553	2837	2844			5630	5820	6224	6258	
		2895	2898	2992	3181			6325	6435	6672	7445	
		3830	3929	3996	4047			7575	7628			
		4054	4057	4319	4438	Hph I	(15)	959	2326	2331	2659	
		4540	4571	4574	4689			2683	2812	4658	5987	
		4801	4848	5075	5156			6214	6628	6686	7002	
		5174	5177	5295	5450			7149	7235	7742		
		5593	5658	5661	5867	Kas I	(1)	2184				
		6195	6534	6561	6656	Kpn I	(1)	2197				
		6799	6884	6928	6944	Mae I	(25)	17	28	318	513	
		7099	7166	7316	7425			836	1073	1605	1742	
		7505	7602					1893	2019	2081	2292	
Fok I	(22)	307	359	686	1015			3052	3253	3370	3425	
		1250	1483	1937	2340			3472	3596	4064	4423	
		2706	3694	4021	4073			4434	5745	5998	6333	
		4575	4724	4856	6109			7659				
		6290	6577	6709	6862	Mae II	(24)	50	54	304	894	
		7106	7607					1392	1849	2132	2277	

		2377	2590	2761	3478					2969	3014	3637	4174
		4078	4159	4217	4582					4234	4397	4546	4610
		4599	4816	5953	6369					4634	4864	4908	5254
		7058	7544	7734	7803					5974	6465	6475	6553
Mae III	(28)	46	248	1544	2161					6589	6832	7788	
		2177	2495	2984	3192	Nla IV	(27)			346	553	625	1124
		3535	4213	4273	4876					1240	1664	1739	1791
		5606	5669	5785	6068					1995	2074	2186	2195
		6399	6457	6610	6675					2350	2888	3353	3377
		6806	6893	6937	7132					3873	4038	4996	5282
Mbo I	(41)	7138	7240	7570	7808					5321	6093	6187	6228
		427	881	886	1196					6439	7084	7449	
		1257	1271	1473	1489	Not I	(1)			1652			
		2167	2200	2812	2960	Nru I	(1)			1195			
		2998	3039	3048	3061	Nsi I	(3)			585	657	4395	
		3295	3375	3427	3496	Nsp7524 I	(5)			84	579	651	4393
		3953	4446	5816	5891					5250			
		5902	5910	5988	6000	NspB II	(9)			1171	1886	3409	4795
		6105	6446	6464	6510					5074	5592	5837	6801
		6993	7176	7356	7366					7424			
		7441	7459	7687	7708	NspH I	(5)			88	583	655	4397
		7746								5254			
Mbo II	(19)	231	996	1053	1081	PaeR7 I	(1)			7774			
		1499	2276	2556	2601	Pal I	(30)			498	507	776	782
		2604	2797	3370	4517					834	967	1082	1373
		5122	5911	5984	7334					1654	1946	2051	2386
		7693	7696	7729						2486	2775	2887	3873
Mlu I	(2)	3290	3451							4629	4665	5091	5265
Mme I	(3)	5464	5648	7696						5276	5294	5728	6186
Mnl I	(63)	103	258	318	446					6266	6533	7067	7101
		508	766	772	795					7631	7697		
		801	809	812	824	Ple I	(2)			1973	5629		
		944	1005	1346	1347	Pme I	(1)			3460			
		1369	1486	1710	1799	Pml I	(2)			895	1393		
		1894	1936	1990	2006	PpuM I	(2)			1123	3351		
		2261	2321	2402	2408	Psp1406 I	(2)			1849	6369		
		2501	2639	2651	2702	PspA I	(5)			339	403	856	3977
		2822	3083	3122	3131					4041			
		3355	3364	3805	3938	Pst I	(3)			6	471	3917	
		4066	4310	4496	4523	Pvu I	(3)			1199	6513	7359	
		4553	4817	5099	5148	Pvu II	(3)			1171	1886	5074	
		5358	5431	5682	6082	Rsa I	(12)			53	1785	2195	2742
		6163	6309	6515	6654					3024	3447	3481	6625
		6878	6975	7015	7423					6858	7071	7079	7562
		7462	7707	7782		Rsr II	(2)			355	4026		
Msc I	(2)	967	4629			Sac I	(1)			4313			
Mse I	(36)	22	57	122	138	Sac II	(1)			3410			
		212	906	2029	2219	Sal I	(1)			3439			
		3105	3166	3287	3310	Sap I	(1)			5134			
		3390	3413	3417	3459	Sau3A I	(41)			427	881	886	1196
		3491	3717	3724	4201					1257	1271	1473	1489
		4208	4429	4642	4786					2167	2200	2812	2960
		5021	5080	5956	6008					2998	3039	3048	3061
		6013	6027	6080	6315					3295	3375	3427	3496
Msl I	(5)	6354	6971	7487	7800					3953	4446	5816	5891
		2799	3880	6395	6554					5902	5910	5988	6000
		7250								6105	6446	6464	6510
Msp I	(50)	340	353	358	383					6993	7176	7356	7366
		404	857	1456	1464					7441	7459	7687	7708
		1660	1735	1959	2047					7746			
		2059	2091	2182	2301	Sau96 I	(17)			355	1123	2049	2485
		2341	2404	2464	2995					2886	2969	3351	3871
		3031	3046	3299	3379					3872	4026	6185	6264
		3695	3845	3978	3999					6281	6503	6777	7418
		4024	4029	4042	4697					7630			
		4709	4750	4760	4774	ScrF I	(43)			291	340	341	404
		4882	4968	5457	5604					405	477	549	604
		5630	5820	6224	6258					621	857	858	1268
		6325	6435	6672	7445					1457	2048	2342	2358
		7575	7628							2483	2595	2670	2724
MspAl I	(9)	1171	1886	3409	4795					2996	3696	3776	3834
		5074	5592	5837	6801					3845	3906	3978	3979
		7424								4042	4043	4092	4670
Mun I	(2)	1727	3154							4837	4882	4990	5278
Nae I	(5)	384	1465	2092	4000					5399	5412	5630	6326
		7629								6632	6673	7209	
Nar I	(1)	2185				Sec I	(45)			289	290	339	340
Nci I	(20)	340	341	404	405					403	476	502	547
		857	858	1457	2048					619	742	777	835
		2342	2996	3696	3845					856	962	1267	1374
		3978	3979	4042	4043					1804	2068	2311	2341
		4882	5630	6326	6673					2481	2644	2668	2723
Nco I	(3)	742	962	2311						3407	3695	3843	3904
Nde I	(1)	3484								3977	4040	4041	4090
Ngom I	(5)	382	1463	2090	3998					4091	4558	4669	4989
		7627								5410	6663	6686	6869
Nhe I	(1)	1892								6900	7207	7271	7410
Nla III	(31)	71	88	583	655					7752			
		746	966	1498	1646	SfaN I	(24)			380	591	663	1036
		2315	2549	2579	2774					1093	1225	1271	1571

		1918	2412	2688	2703
		2802	3219	3562	4000
		4448	4503	4737	4835
		5346	6398	6591	6883
Sfc I	(8)	2	467	1047	3913
		5515	5706	6384	7233
Sfi I	(1)	504			
Sma I	(5)	341	405	858	3979
		4043			
SnaB I	(1)	3479			
Spe I	(1)	512			
Sph I	(3)	583	655	4397	
Spl I	(1)	51			
Srf I	(2)	405	3979		
Ssp I	(2)	3721	4381		
Stu I	(2)	498	834		
Sty I	(8)	742	835	962	2068
		2311	6663	7410	7752
Taq I	(23)	108	1256	1407	1899
		2041	2362	2656	2683
		2698	2827	3357	3396
		3440	3466	5350	6647
		6907	7007	7038	7050
		7344	7359	7775	
Tfi I	(11)	988	1320	1409	1446
		3468	3858	4352	4613
		5085	5225	7222	
Tsp45 I	(11)	46	2177	2495	2984
		4213	4273	6399	6610
		6675	7138	7240	
Tth111 II	(9)	198	2108	2795	4308
		5839	5848	5878	6895
		6902			
Vsp I	(6)	122	906	4786	5021
		5080	6315		
Xba I	(2)	3051	3471		
Xho I	(1)	7774			
Xho II	(13)	881	1489	2167	2812
		3039	3048	3375	3427
		5891	5902	5988	6000
		7459			
Xma I	(5)	339	403	856	3977
		4041			
Xma III	(2)	1080	1652		
Xmn I	(1)	3363			

Site usage in pMPBlox:

Aat II	G,ACGT`C	-	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	86
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	5
Age I	A`CCGG,T	2	Aha II	GR`CG,YC	3
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	42
Alw I	GGATC 8/9	23	AlwN I	CAG,NNN`CTG	1
Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	2
Apo I	R`AATT,Y	7	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	6	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	11	Ava II	G`GWC,C	9
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	9	Ban II	G,RCY`C	6
Bbe I	G,GCGC`C	1	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	22	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	3	Bcn I	CC,S`GG	20
Bfa I	C`TA,G	25	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	2
Bpm I	CTGGAG 22/20	6	Bsa I	GGTCTC 7/11	3
BsaA I	YAC GTR	6	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	3	BsaJ I	C`CNNG,G	45

BsaW I	W`CCGG,W	14	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	6	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	9	BsiHKA I	G,WGCW`C	4
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	5
BsmA I	GTCTC`/9	4	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	16	BsoF I	GC`N,GC	70
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	1
BspM II	T`CCGG,A	4	Bsr I	ACT,GG`	22
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	4
BsrG I	T`GTAC,A	2	BssH II	G`CGCG,C	3
BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	23	BstU I	CG CG	28
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	13
Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN NGC	47
Cfr10 I	R`CCGG,Y	14	ClA I	AT`CG,AT	1
Csp6 I	G`TA,C	12	Dde I	C`TNA,G	13
Dpn I	GA TC	41	DpnII	`GATC,	41
Dra I	TTT AAA	7	Dra III	CAC,NNN`GTG	4
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	8
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	2
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	2
EcoN I	CCTNN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	3
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	23
EcoR V	GAT ATC	1	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	70
Fok I	GGATG 14/18	22	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	6	Hae I	WGG CCW	9
Hae II	R,GCGC`Y	13	Hae III	GG CC	30
Hga I	GACCG 9/14	10	HgiA I	G,WGCW`C	4
HgiE II	ACCNNNNNNGGT -1/131	-	Hha I	G,CG`C	47
Hinc II	GTY CAC	5	Hind II	GTY CAC	5
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	20
HinI I	GR`CG,YC	3	HinP I	G`CG,C	47
Hpa I	GTT AAC	2	Hpa II	C`CG,G	50
Hph I	GGTGA 12/11	15	Kas I	G`GCGC,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	25
Mae II	A`CG,T	24	Mae III	`GTNAC,	28
Mbo I	`GATC,	41	Mbo II	GAAGA 12/11	19
Mlu I	A`CGCG,T	2	Mme I	TCCRAC 25/23	3
Mnl I	CCTC 10/10	63	Msc I	TGG CCA	2
Mse I	T`TA,A	36	Msl I	CAYNN NNRTG	5
Msp I	C`CG,G	50	MspA I	CMG CKG	9
Mun I	C`AATT,G	2	Nae I	GCC GGC	5
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	20
Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	5	Nhe I	G`CTAG,C	1
Nla III	,CATG`	31	Nla IV	GGN NCC	27
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	5
NspB II	CMG CKG	9	NspH I	R,CATG`Y	5
PaeR7 I	C`TCGA,G	1	Pal I	GG CC	30
Pf1M I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	2
Pme I	CTTT AAAC	1	Pml I	CAC GTG	2
PpuM I	RG`GWC,CY	2	Psp1406 I	AA`CG,TT	2
PspA I	C`CCGG,G	5	Pst I	C,TGCA`G	3
Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	3
Rsa I	GT AC	12	Rsr II	CG`GWC,CG	2
Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	1
Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	1
Sau3A I	`GATC,	41	Sau96 I	G`GNC,C	17
Sca I	AGT ACT	-	ScrF I	CC`N,GG	43
Sec I	C`CNNG,G	45	SfaN I	GCATC 9/13	24
Sfc I	C`TRYA,G	8	Sfi I	GGCCN,NNN`NGGCC	1
Sma I	CCC GGG	5	SnaB I	TAC GTA	1
Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
Ssp I	AAT ATT	2	Stu I	AGG CCT	2
Sty I	C`CWWG,G	8	Taq I	T`CG,A	23
Tfi I	G`AWT,C	11	Tsp45 I	`GTSAC,	11
Tth111 I	GACN`N,NGTC	-	Tth111 II	CAARCA 16/14	9
Vsp I	AT`TA,AT	6	Xba I	T`CTAG,A	2
Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNTGG-	2
Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	13
Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	2