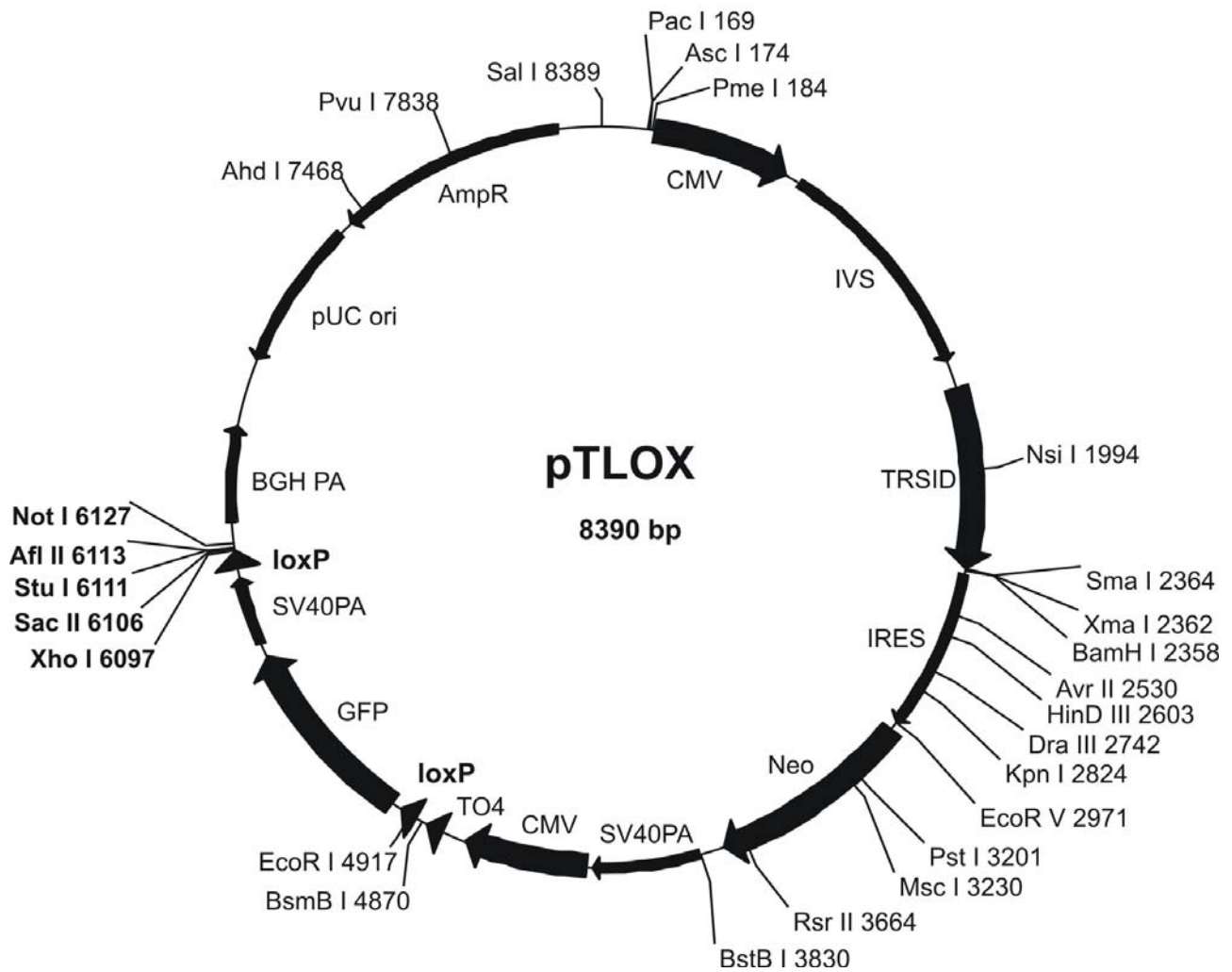


Name of Vector: pTLOX  
Antibiotic Selection: Amp  
Created by: Jae Yoon Park, Wei Jiang and Qing Luo  
(He Lab @ The University of Chicago)  
Date of Creation: July 2003



## pTLOX Vector Sequence

**(Note: The vector was NOT fully sequenced. Please notify us if you find any discrepancies)**

GACGGATCGGGAGATCTCCCGATCCCCTATGGTGCACCTCTCAGTACAATCTGCTCTGATG	60
CCGCATAGTTAAGCCAGTATCTGCTCCCTGCTTGTGTGTTGGAGGTCGCTGAGTAGTGCG	120
CGAGCAAAATTTAAGCTACAACAAGGCAAGGCTTGACCGACAATTAATTAAGGCGCGCCG	180
TTTAAACTAATTGCATGAAGAATCTGCTTAGGGTTAGGCGTTTTGCGCTGCTTCGCGATG	240
TACGGGCCAGATATAACGCTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTA	300
CGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCGCGCTTACATAACTTACGGTAAATG	360
GCCCCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTTC	420
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA	480
CTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA	540
ATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCTTA	600
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT	660
ACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTG	720
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTGTAACA	780
ACTCCGCCCATTTGACGCAAAATGGGCGGTAGGCGGTGACGGTGGGAGGTCTATATAAGCA	840
GAGCTCTCTGGCTAAGTACGAGAACCCACTGCTTACTGGCTTATCGAAATTAATACGACTC	900
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AATTTTGTCTTTCTTTCACTTTCTACTCTGTTGACAACCATTGTCTCCTCTTATTTTCTTTT	1140
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CTTTTGTATTTTGTGTCAGATTGTAAGTACTTTCTCTAATCACTTTTTTTTTCAAGGCAATC	1260
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GCCGTGTTGCGGCTGTGACGCGAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCC	3180
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AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC 8390

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**Unique enzymes in pTLOX:**

			4317	4370	4453	4639
			8390			
		Asc I	(1) 8390			
		Acc65 I	(1) 2820			
		Aci I	(90) 62	336	364	376
Asc I	GG`CGCG,CC	174	390	557	648	681
Pme I	CTTT AAAC	184	785	806	1748	2103
Nsi I	A,TGCA`T	1994	2188	2224	2238	2241
BamH I	G`GATC,C	2358	2244	2277	2294	2297
PspA I	C`CCGG,G	2362	2376	2418	2649	2681
Xma I	C`CCGG,G	2362	2719	3057	3120	3130
Sma I	CCC GGG	2364	3214	3278	3379	3382
Avr II	C`CTAG,G	2530	3622	3662	3667	3717
HinD III	A`AGCT,T	2603	3733	3759	3815	3884
Eco72 I	CAC GTG	2695	3887	3953	4250	4278
Pml I	CAC GTG	2695	4290	4304	4471	4562
Dra III	CAC,NNN`GTG	2742	4595	4699	4720	5254
Acc65 I	G`GTAC,C	2820	5295	5362	5401	5539
Asp718	G`GTAC,C	2820	5652	5712	5715	6103
Kpn I	G,GTAC`C	2824	6105	6126	6130	6139
EcoR V	GAT ATC	2971	6365	6389	6427	6437
Kas I	G`GCGC,C	3147	6461	6504	6511	6532
Nar I	GG`CG,CC	3148	6623	6651	6778	6797
Ehe I	GGC GCC	3149	6918	7028	7163	7172
Bbe I	G,GCGC`C	3151	7531	7622	7813	7859
Pst I	C,TGCA`G	3201	7980	8024	8101	8210
Msc I	TGG CCA	3230	8309	8356		
Tth111 I	GACN`N,NGTC	3266	Afl II	(1) 6113		
Rsr II	CG`GWC,CG	3664	Afl III	(6) 256	2694	2869
BsiC I	TT`CG,AA	3830		6013	6578	4170
BstB I	TT`CG,AA	3830	Age I	(2) 5023	6119	
BsmB I	CGTCTC 7/11	4870	Aha II	(15) 400	453	536
EcoR I	G`AATT,C	4917		1762	3148	3850
BsrG I	T`GTAC,A	5745		4314	4367	4450
Hpa I	GTT AAC	5890		4879	8005	8387
Paer7 I	C`TCGA,G	6097	Ahd I	(1) 7468		
Xho I	C`TCGA,G	6097	Alu I	(38) 136	844	919
Sac II	CC,GC`GG	6106		1521	1649	1703
Stu I	AGG CCT	6111		2121	2310	2605
Afl II	C`TTAA,G	6113		3254	3712	4003
Not I	GC`GGCC,GC	6127		4800	4848	5012
Ahd I	GACNN,N`NNGTC	7468		5089	5161	5194
Pvu I	CG,AT`CG	7838		5458	5569	5743
Sal I	G`TCGA,C	8389		6096	6402	6520
Acc I	GT`MK,AC	8390		6836	6882	7139
				7757	7820	7657
			Alw I	(28) 12	17	926
				2365	2843	2989
				3326	3393	3572
				3964	4118	4125
				5728	5758	5778
				7140	7223	7223
				7321	7785	8100
				81	1524	2267
			AlwN I	(4) 81	1524	2267
			Apa I	(2) 1480	2496	
			ApaL I	(4) 33	2856	6892
			Apo I	(8) 128	994	1187
				1344	4038	4917
			Asc I	(1) 174		
			Ase I	(7) 165	285	890
				4199	6408	7640
			Asp718	(1) 2820		
			Ava I	(2) 2362	6097	
			Ava II	(8) 959	1069	2221
				5692	6074	7606
			Avr II	(1) 2530		
			BamH I	(1) 2358		
			Ban I	(9) 743	1789	2672
				3147	3182	5071
						6221

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

Blp I	BsiW I	Bst1107 I	BstE II	BstX I	Asc I	(1) 174			
Bsu36 I	Esp I	Fse I	Nhe I	Sfi I	Ase I	(7) 165	285	890	2370
					Asp718	(1) 2820	6408	7640	
					Ava I	(2) 2362	6097		
					Ava II	(8) 959	1069	2221	3664
						5692	6074	7606	7828
					Avr II	(1) 2530			
					BamH I	(1) 2358			
Aat II	(9) 403	456	539	725	Ban I	(9) 743	1789	2672	2820
						3147	3182	5071	6221

**pTLOX: sites sorted by name:**

Aat II	(9) 403	456	539	725	Asc I	(1) 174			
					Ase I	(7) 165	285	890	2370
					Asp718	(1) 2820	6408	7640	
					Ava I	(2) 2362	6097		
					Ava II	(8) 959	1069	2221	3664
						5692	6074	7606	7828
					Avr II	(1) 2530			
					BamH I	(1) 2358			
					Ban I	(9) 743	1789	2672	2820
						3147	3182	5071	6221



*pTLOX map/sequence/restriction sites*

Fsp I	(2)	6374	7434	7615	7902					2081	2506	2623	3508
Gdi II	(14)	3250	7690							3718	3800	3967	4919
		2277	2279	2408	2683					4999	5279	5324	5327
		3053	3055	3618	3645					5520	6093	6349	6450
		5108	5495	6126	6128					7087	7236	7309	8064
		6418	7855							8142	8251		
Gsu I	(8)	2291	2309	3932	3987	Mlu I	(3)	256				6013	
Hae I	(5)	4893	5479	5719	7539	Mme I	(5)	81	1644			2729	6792
		3230	6111	6593	6604			6976					
		7056				Mnl I	(58)	96		819		1003	1082
Hae II	(5)	2011	3151	5021	6456			1135		1442		1490	1652
		6826						2267		2335		2390	2396
Hae III	(34)	247	362	555	1478			2483		2554		2605	2685
		1916	2170	2280	2411			2789		2860		2876	2997
		2432	2494	2507	2684			3063		3199		3556	3748
		2850	2902	3056	3230			3954		4158		4163	4733
		3621	3648	4276	4469			4909		4984		5044	5125
		5109	5209	5498	5610			5131		5224		5362	5374
		6111	6129	6419	6593			5425		5545		5806	5845
		6604	6622	7056	7511			5854		6078		6087	6101
		7591	7858					6159		6201		6247	6322
Hga I	(9)	803	1769	3857	3936			6379		6427		6476	6686
		4717	4886	6688	7263			6759		7010		7407	7488
		7995						7634		7840			
HgiA I	(11)	37	846	2860	3261	Msc I	(1)	3230					
		3451	4760	4802	5645	Mse I	(32)	70	132	165	169		
		6896	8054	8139				183	285	890	1162		
HgiE II	(2)	6210	7157					1193	1313	1633	1654		
Hha I	(31)	121	176	178	228			1677	2206	2370	2887		
		1641	2010	3142	3150			4199	4942	5828	5889		
		3214	3251	3517	3547			6010	6033	6114	6408		
		3549	3777	3953	5020			7281	7333	7338	7352		
		5325	5366	5682	6427			7405	7640	7679	8044		
		6455	6488	6758	6825	Msl I	(11)	643	1496	1776	1885		
		6925	7099	7205	7598			2262	2320	3585	4557		
		7691	8028	8360				5522	7720	7879			
Hinc II	(4)	262	1111	4176	5890	Msp I	(32)	1474	2229	2363	2433		
Hind II	(4)	262	1111	4176	5890			2496	3053	3152	3180		
Hind III	(1)	2603						3311	3401	3468	3649		
Hinf I	(20)	201	688	897	1465			3924	3932	5024	5064		
		1582	1666	2765	3633			5127	5187	5718	5754		
		3767	3819	3877	3914			5769	6022	6120	6785		
		4164	4602	5757	6413			6932	6958	7148	7549		
		6478	6553	6949	7463			7583	7650	7760	8002		
HinI I	(15)	400	453	536	722	MspAl I	(8)	2649	3254	6105	6141		
		1762	3148	3850	3929			6402	6920	7165	8103		
		4314	4367	4450	4636								
		4879	8005	8387		Mun I	(2)	1301	5877				
HinP I	(31)	119	174	176	226	Nae I	(2)	3650	3933				
		1639	2008	3140	3148	Nar I	(1)	3148					
		3212	3249	3515	3545	Nci I	(13)	1475	2230	2363	2364		
		3547	3775	3951	5018			2496	3152	3312	3925		
		5323	5364	5680	6425			5065	5719	6958	7651		
		6453	6486	6756	6823			8002					
		6923	7097	7203	7596	Nco I	(5)	638	1065	3580	4552		
		7689	8026	8358				5034					
Hpa I	(1)	5890				Nde I	(3)	512	2184	4426			
Hpa II	(32)	1474	2229	2363	2433	NgoM I	(2)	3648	3931				
		2496	3053	3152	3180	Nla III	(35)	198	582	642	1002		
		3311	3401	3468	3649			1069	1079	1495	1501		
		3924	3932	5024	5064			1737	2319	2333	2864		
		5127	5187	5718	5754			2873	3367	3553	3584		
		5769	6022	6120	6785			3610	3966	4114	4496		
		6932	6958	7148	7549			4556	5038	5272	5302		
		7583	7650	7760	8002			5497	5692	5737	6356		
Hph I	(16)	653	959	1055	2131			6582	7299	7790	7800		
		3327	4567	5049	5054	Nla IV	(29)	745	7914	8307			
		5382	5406	5535	7312			7878	7914	8307			
		7539	7953	8161	8194								
								1478	1479	1791	2222		
Kas I	(1)	3147						2360	2494	2653	2674		
Kpn I	(1)	2824						2822	2849	2903	3149		
Mae I	(18)	278	857	924	1609			3184	4659	5073	5611		
		1704	1983	2531	2898			6076	6223	6610	6649		
		4073	4192	5015	5775			7418	7512	7553	7764		
		5976	6093	6165	7073			8354					
		7323	7658			Not I	(1)	6127					
Mae II	(30)	400	412	453	536	Nru I	(2)	236	1885				
		617	722	1532	1841	Nsi I	(1)	1994					
		2402	2623	2694	2738	Nsp7524 I	(6)	1733	2860	2869	3549		
		2894	2920	3264	3451			6352	6578				
		4314	4326	4367	4450	NspB II	(8)	2649	3254	6105	6141		
		4531	4636	5000	5100			6402	6920	7165	8103		
		5313	5484	7278	7694	NspH I	(6)	1737	2864	2873	3553		
		8067	8387					6356	6582				
Mae III	(25)	339	426	775	1149	PaeR7 I	(1)	6097					
		1181	1421	2332	2403	Pal I	(34)	247	362	555	1478		
		3268	3574	4012	4253			1916	2170	2280	2411		
		4340	4689	5218	5707			2432	2494	2507	2684		
		5915	6934	6997	7113			2850	2902	3056	3230		
		7393	7724	7782	7935			3621	3648	4276	4469		
		8123						5109	5209	5498	5610		
Mbo I	(49)	5	13	21	926			6111	6129	6419	6593		
		930	2045	2135	2179			6604	6622	7056	7511		
		2358	2836	2841	2982	PflM I	(2)	2771	2771	2832			
		2987	3006	3319	3397	Ple I	(3)	1473	2773	6957			
		3478	3487	3565	3941	Pme I	(1)	184					
		3957	4118	4122	4778	Pml I	(1)	2695					
		4820	4841	4866	4923	PpuM I	(2)	959	6074				
		5535	5683	5721	5762	Psp1406 I	(3)	2402	7694	8067			
		5771	5784	6018	6143	PspA I	(1)	2362					
		7144	7216	7227	7235	Pst I	(1)	3201					
		7313	7325	7430	7771	Pvu I	(1)	7838					
		7789	7835	8093	8110	Pvu II	(2)	3254	6402				
		8146				Rsa I	(23)	45	242	497	522		
Mbo II	(26)	209	1057	1498	2054			577	610	661	818		

		1228	1278	1900	1910	Age I	A`CCGG,T	2	Aha II	GR`CG,YC	15
		2822	3454	4411	4436	Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	38
		4491	4524	4575	4732	Alw I	GGATC 8/9	28	AlwN I	CAG,NNN`CTG	4
		5465	5747	7948		Apa I	G,GGCC`C	2	ApaL I	G`TGCA,C	4
Rsr II	(1)	3664				Apo I	R`AATT,Y	8	Asc I	GG`CGCG,CC	1
Sac I	(3)	846	4760	4802		Ase I	AT`TA,AT	7	Asp718	G`GTAC,C	1
Sac II	(1)	6106				Ava I	C`YCGR,G	2	Ava II	G`GWC,C	8
Sal I	(1)	8389				Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Sap I	(3)	3492	3702	6462		Ban I	G`GYRC,C	9	Ban II	G,RCGY`C	7
Sau3A I	(49)	5	13	21	926	Bbe I	G,GGCC`C	1	Bbs I	GAAGAC 8/12	4
		930	2045	2135	2179	Bbv I	GCAGC 13/17	14	Bbv II	GAAGAC 7/11	4
		2358	2836	2841	2982	Bcl I	T`GATC,A	5	Bcn I	CC,S`GG	13
		2987	3006	3319	3397	Bfa I	C`TA,G	18	Bgl I	GCCN,NNN`NGGC	9
		3478	3487	3565	3941	Bgl II	A`GATC,T	3	Blp I	GC`TNA,GC	-
		3957	4118	4122	4778	Bpm I	CTGGAG 22/20	8	Bsa I	GGTCTC 7/11	3
		4820	4841	4866	4923	BsaA I	YAC GTR	5	BsaB I	GATNN NNATC	6
		5535	5683	5721	5762	BsaH I	GR`CG,YC	15	BsaJ I	C`CNRG,G	21
		5771	5784	6018	6143	BsaW I	W`CCGG,W	9	BseR I	GAGGAG 16/14	5
		7144	7216	7227	7235	Bsg I	GTGCAG 22/20	4	BsiC I	TT`CG,AA	1
		7313	7325	7430	7771	BsiE I	CG,RY`CG	9	BsiHKA I	G,WGCW`C	11
		7789	7835	8093	8110	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	6
		8146				BsmA I	CTCTC`/9	10	BsmB I	CGTCTC 7/11	1
Sau96 I	(24)	245	361	554	959	BsmF I	GGGAC 15/19	13	BsoF I	GC`N,GC	58
		1069	1476	1477	2221	Bsp120 I	G`GGCC,C	2	Bsp1286 I	G,DGCH`C	2
		2492	2493	2506	2848	BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	4
		2901	3664	4275	4468	BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	17
		5208	5609	5692	6074	BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	4
		7510	7589	7606	7828	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	2
Sca I	(2)	1228	7948			BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
ScrF I	(32)	368	561	1393	1475	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
		1525	2230	2363	2364	BstN I	CC`W,GG	19	BstU I	CG CG	24
		2496	2504	2663	3152	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	18
		3312	3535	3925	4282	Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	37
		4475	4873	5065	5081	Cfr10 I	R`CCGG,Y	8	Clal I	AT`CG,AT	2
		5206	5318	5393	5447	Csp6 I	G`TA,C	23	Dde I	C`TNA,G	19
		5719	6215	6606	6727	Dpn I	GA TC	49	DpnII	`GATC,	49
		6740	6958	7651	8002	Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	1
Sec I	(21)	638	1065	1524	2141	Drd I	GACNN,NN`NNGTC	2	Dsa I	C`CRYG,G	7
		2362	2530	2851	2912	Eae I	Y`GGCC,R	12	Eag I	C`GGCC,G	3
		3311	3580	4154	4552	Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2
		5034	5064	5204	5367	Eco57 I	CTGAAG 21/19	11	Eco72 I	CAC GTG	1
		5391	5446	6103	6213	EcoN I	CCTNN`N,NNAGG	2	EcoO109 I	RG`GNC,CY	6
SfaN I	(24)	49	636	2062	2255	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	19
		2800	3107	3362	3446	EcoR V	GAT ATC	1	Ehe I	GGC GCC	1
		3510	3578	3785	4039	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	58
		4550	5135	5411	5426	Fok I	GGATG 14/18	16	Fse I	GG,CCGG`CC	-
		5525	5942	6271	6353	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	14
		6674	7723	7916	8163	Gsu I	CTGGAG 21/19	8	Hae I	WGG CCW	5
Sfc I	(9)	903	1516	1588	1918	Hae II	R,GGCC`Y	5	Hae III	GG CC	34
		2627	3197	6843	7034	Hga I	GACCG 9/14	9	HgiA I	G,WGCW`C	11
		7709				HgiE II	ACCCNNNNNGGT -1/132	-	Hha I	G,GC`C	31
Sma I	(1)	2364				Hinc II	GTY RAC	4	Hind II	GTY RAC	4
SnaB I	(3)	618	1842	4532		Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	20
Spe I	(2)	277	4191			HinI I	GR`CG,YC	15	HinP I	G`CG,C	31
Sph I	(2)	3553	6356			Hpa I	GTT AAC	1	Hpa II	C`CG,G	32
Spl I	(3)	1331	1365	8272		Hph I	GGTGA 12/11	16	Kas I	G`CGCG,C	1
Stu I	(1)	6111				Kpn I	G,GTAC`C	1	Mae I	C`TA,G	18
Sty I	(7)	638	1065		2530	Mae II	A`CG,T	30	Mae III	`GTNAC,	25
		3580	4552	5034		Mbo I	`GATC,	49	Mbo II	GAAGA 12/11	26
Taq I	(28)	884	929	1669	1759	Mlu I	A`CCGG,T	3	Mme I	TCCRAC 25/23	5
		1942	2125	2881	3261	Mnl I	CCTC 10/10	58	Msc I	TGG CCA	1
		3417	3441	3477	3639	Mse I	T`TA,A	32	Msl I	CAYNN NNRTG	11
		3830	3875	4121	4162	Msp I	C`CG,G	32	MspA1 I	CMG CKG	8
		4844	5085	5379	5406	Mun I	C`AATT,G	2	Nae I	GCC GGC	2
		5421	5550	6080	6098	Nar I	GG`CG,CC	1	Nci I	CC`S,GG	13
		6152	6678	8119	8390	Nco I	C`CATG,G	5	Nde I	CA`TA,TG	3
Tfi I	(9)	201	1666	3633	3767	NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	-
		3877	3914	4164	6413	Nla III	,CATG`	35	Nla IV	GGN NCC	29
		6553				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	2
Tsp45 I	(6)	3268	3574	5218	5707	Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	6
		7724	7935			NspB II	CMG CKG	8	NspH I	R,CATG`Y	6
Tth111 I	(1)	3266				PaeR7 I	C`TCGA,G	1	Pal I	GG CC	34
Tth111 II	(9)	81	1430	2632	3584	Pf1M I	CCAN,NNN`NTGG	2	Ple I	GAGTC 9/10	3
		5518	6175	7167	7173	Pme I	CTTT AAAC	1	Pml I	CAC GTG	1
		7203				PpuM I	RG`GWC,CY	2	Psp1406 I	AA`CG,TT	3
Vsp I	(7)	165	285	890	2370	PspA I	C`CCGG,G	1	Pst I	C,TGCA`G	1
		4199	6408	7640		Pvu I	CG,AT`CG	1	Pvu II	CAG CTG	2
Xba I	(2)	1608	5774			Rsa I	GT AC	23	Rsr II	CG`GWC,CG	1
Xho I	(1)	6097				Sac I	G,AGCT`C	3	Sac II	CC,GC`GG	1
Xho II	(18)	13	2358	2836	2982	Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	3
		3319	3565	3957	4778	Sau3A I	`GATC,	49	Sau96 I	G`GNC,C	24
		4820	5535	5762	5771	Sca I	AGT ACT	2	ScrF I	GC`N,GG	32
		7216	7227	7313	7325	Sec I	C`CNRG,G	21	SfaN I	GCATC 9/13	24
		8093	8110			Sfc I	C`TRYA,G	9	Sfi I	GGCCN,NNN`NGGCC	-
Xma I	(1)	2362				Sma I	CCC GGG	1	SnaB I	TAC GTA	3
Xma III	(3)	2278	3054	6127		Spe I	A`CTAG,T	2	Sph I	G,CATG`C	2
Xmn I	(4)	2371	2591	6086	8067	Spl I	C`GTAC,G	-	Srf I	GCCC GGGC	-
						Ssp I	AAT ATT	3	Stu I	AGG CCT	1
						Sty I	C`CWG,G	7	Taq I	T`CG,A	28
						Tfi I	G`AWT,C	9	Tsp45 I	`GTSAC,	6
						Tth111 I	GACN`N,NGTC	1	Tth111 II	CAARCA 16/14	9
						Xba I	AT`TA,AT	7	Xba I	T`CTAG,A	2
						Xco I	GTA TAC	-	Xcm I	CCANNNN,N`NNNNTGG-	-
						Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	18
						Xma I	C`CCGG,G	1	Xma III	C`GGCC,G	3

Site usage in pTLOX:

Aat II	G,ACGT`C	9	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	90
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	6