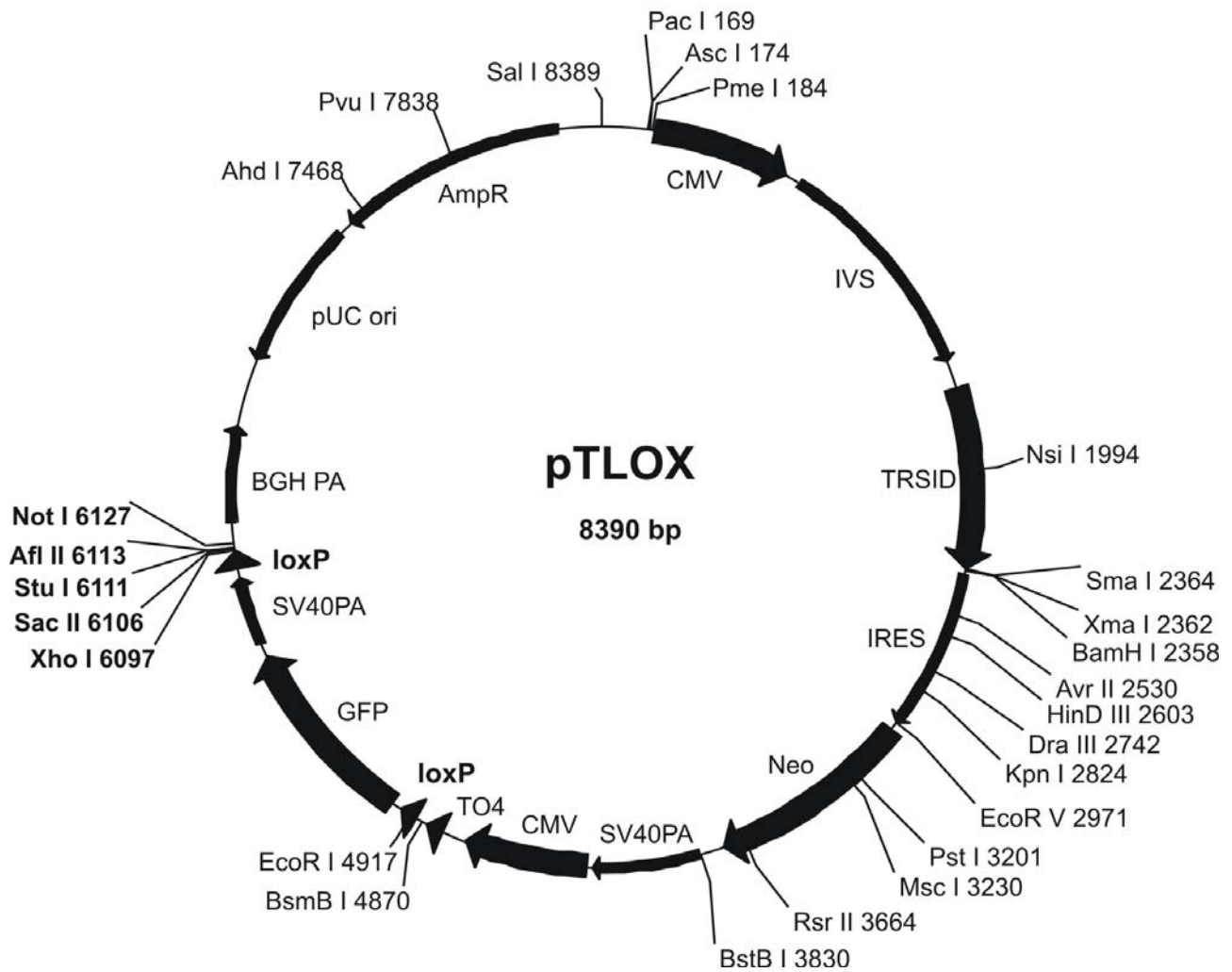


Name of Vector: pTLOX
Antibiotic Selection: Amp
Created by: Jae Yoon Park, Wei Jiang and Qing Luo
(He Lab @ The University of Chicago)
Date of Creation: July 2003



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
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CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT	660
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ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACA	780
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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
Pme I	CTTT AAAC		390	557	648	681
Nsi I	A,TGCA`T		785	806	1748	2103
BamH I	G`GATC,C		2188	2224	2238	2241
PspA I	C`CCGG,G		2244	2277	2294	2297
Xma I	C`CCGG,G		2376	2418	2649	2681
Sma I	CCC GGG		2719	3057	3120	3130
Avr II	C`CTAG,G		3214	3278	3379	3382
Hind III	A`AGCT,T		3622	3662	3667	3717
Eco72 I	CAC GTG		3733	3759	3815	3884
Pml I	CAC GTG		3887	3953	4250	4278
Dra III	CAC,NNN`GTG		4290	4304	4471	4562
Acc65 I	G`GTAC,C		4595	4699	4720	5254
Asp718	G`GTAC,C		5295	5362	5401	5539
Kpn I	G,GTAC`C		5652	5712	5715	6103
EcoR V	GAT ATC		6105	6126	6130	6139
Kas I	G`GCGC,C		6365	6389	6427	6437
Nar I	GG`CG,CC		6461	6504	6511	6532
Ehe I	GGC GCC		6623	6651	6778	6797
Bbe I	G,GCGC`C	Afl II	(1) 6113			
Pst I	C,TGCA`G	Afl III	(6) 256	2694	2869	4170
Msc I	TGG CCA		6013	6578		
Tth111 I	GACN`N,NGTC	Age I	(2) 5023	6119		
Rsr II	CG`GWC,CG	Aha II	(15) 400	453	536	722
BsiC I	TT`CG,AA		1762	3148	3850	3929
BstB I	TT`CG,AA		4314	4367	4450	4636
BsmB I	CGTCTC 7/11		4879	8005	8387	
EcoR I	G`AATT,C	Ahd I	(1) 7468			
BsrG I	T`GTAC,A	Alu I	(38) 136	844	919	1172
Hpa I	GTT AAC		1521	1649	1703	1825
Paer7 I	C`TCGA,G		2121	2310	2605	2964
Xho I	C`TCGA,G		3254	3712	4003	4758
Sac II	CC,GC`GG		4800	4848	5012	5056
Stu I	AGG CCT		5089	5161	5194	5410
Afl II	C`TTAA,G		5458	5569	5743	5906
Not I	GC`GGCC,GC		6096	6402	6520	6746
Ahd I	GACNN,N`NNGTC		6836	6882	7139	7657
Pvu I	CG,AT`CG		7757	7820		
Sal I	G`TCGA,C	Alw I	(28) 12	17	926	2354
Acc I	GT`MK,AC		2365	2843	2989	3013
			3326	3393	3572	3937
			3964	4118	4125	5531
			5728	5758	5778	6014
			7140	7223	7223	7320
			7321	7785	8100	8106
		AlwN I	(4) 81	1524	2267	6994
		Apa I	(2) 1480	2496		
		ApaL I	(4) 33	2856	6892	8135
		Apo I	(8) 128	994	1187	1195
			1344	4038	4917	5941

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
						4199	6408	7640	
					Asp718	(1) 2820			
					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

Ban II	(7)	7416				3547	3953	4172	4252
		846	1480	2496	3513	5364	5682	6015	6105
		4760	4802	6374		6126	6425	6427	6625
Bbe I	(1)	3151				7203	7533	8026	8358
Bbs I	(4)	2505	2619	4915	6345	BstY I (18)	13	2358	2836
Bbv I	(14)	1727	2658	3221	3263		3319	3565	3957
		3784	4012	5287	5571		4820	5535	5762
		5578	5915	6997	7000		7216	7227	7313
		7203	7897				8093	8110	8110
Bbv II	(4)	2506	2618	4914	6344	Cac8 I (37)	123	176	364
Bcl I	(5)	2135	2179	2987	5784		921	1174	1354
		6143					1827	2155	2644
Bcn I	(13)	1476	2231	2364	2365		3228	3447	3513
		2497	3153	3313	3926		3547	3551	3592
		5066	5720	6959	7652		3650	3933	4278
		8003					5159	5192	5240
Bfa I	(18)	278	857	924	1609		5571	6173	6350
		1704	1983	2531	2898		6509	6595	6632
		4073	4192	5015	5775		7580		
		5976	6093	6165	7073	Cfr10 I (8)	2432	3467	3648
		7323	7658				5023	5186	6119
Bgl I	(9)	368	490	561	2681		929	4121	
		4282	4404	4475	6108	Cla I (2)	44	241	496
		7588				Csp6 I (23)	576	609	660
Bgl II	(3)	13	4778	4820			1227	1277	1899
Bpm I	(8)	2292	2310	3931	3988		2821	3453	4410
		4894	5480	5720	7538		4490	4523	4574
Bsa I	(3)	904	4164	7529			5464	5746	7947
BsaA I	(5)	618	1842	2695	3452	Dde I (19)	40	110	208
		4532					1463	1766	1875
BsaB I	(6)	2256	3005	4777	4819		2354	3811	5639
		4840	5789				5759	6275	6384
BsaH I	(15)	400	453	536	722		7259	7425	7965
		1762	3148	3850	3929	Dpn I (49)	7	15	23
		4314	4367	4450	4636		932	2047	2137
		4879	8005	8387			2360	2838	2843
BsaJ I	(21)	638	1065	1524	2141		2989	3008	3321
		2362	2530	2851	2912		3480	3489	3567
		3311	3580	4154	4552		3959	4120	4124
		5034	5064	5204	5367		4822	4843	4868
		5391	5446	6103	6213		5537	5685	5723
		6738					5773	5786	6020
BsaW I	(9)	3179	5023	5753	5768		7146	7218	7229
		6021	6119	6784	6931		7315	7327	7432
		7759					7791	7837	8095
BseR I	(5)	1115	2769	4143	5006		8148		
		5066				DpnII (49)	5	13	21
Bsg I	(4)	2167	5164	5261	5585		930	2045	2135
BsiC I	(1)	3830					2358	2836	2841
BsiE I	(9)	2281	3057	5028	6124		2987	3006	3319
		6130	6494	6918	7838		3478	3487	3565
		7987					3957	4118	4122
BsiHKA I	(11)	37	846	2860	3261		4820	4841	4866
		3451	4760	4802	5645		5535	5683	5721
		6896	8054	8139			5771	5784	6018
Bsm I	(6)	1994	2525	2564	4068		7144	7216	7227
		5878	5971				7313	7325	7430
BsmA I	(10)	711	905	1126	1555		7789	7835	8093
		2989	4163	4625	4871		8146		
		7530	8304			Dra I (6)	184	1194	5829
BsmB I	(1)	4870					7353	8045	7334
BsmF I	(13)	453	604	772	972	Dra III (1)	2742		
		1037	2931	3299	3831	Drd I (2)	3175	6686	
		3940	4367	4518	4686	Dsa I (7)	638	1065	2912
		6060					4552	5034	6103
BsoF I	(58)	62	229	1650	1716	Eae I (12)	2278	2409	2682
		2103	2239	2242	2268		3228	3619	3646
		2278	2295	2418	2647		5496	6127	6417
		2682	2720	3057	3109	Eag I (3)	2278	3054	6127
		3120	3131	3210	3215	Ear I (6)	3492	3702	4983
		3252	3293	3380	3383		6462	8263	6077
		3386	3622	3718	3759	Eco47 III (2)	2009	5019	
		3773	3887	4001	5195	Eco57 I (11)	928	1266	2823
		5254	5276	5560	5567		3725	5006	5188
		5618	5621	5715	5904		5431	7125	8136
		6103	6127	6130	6403	Eco72 I (1)	2695		
		6484	6502	6505	6623	EcoN I (2)	1813	6082	
		6778	6921	6986	6989	EcoO109 I (6)	959	1477	2492
		7192	7520	7859	7886		2901	6074	2848
		7981	8210			EcoR I (1)	4917		
Bsp120 I	(2)	1476	2492			EcoR II (19)	366	559	1391
Bsp1286 I	(2)	3451	5645				2502	2661	3533
BspH I	(3)	1075	7295	8303			4473	4871	5079
BspM I	(4)	2718	3035	3416	3866		5316	5391	5445
BspM II	(2)	5753	6021				6604	6725	6738
Bsr I	(17)	76	574	879	2411	EcoR V (1)	2971		
		2731	3091	3292	4488	Ehe I (1)	3149		
		5648	6985	6998	7112	Fnu4H I (58)	62	229	1650
		7515	7633	7676	7943		2103	2239	2242
		8115					2278	2295	2418
BsrB I	(5)	2294	3761	3815	6511		2682	2720	3057
		8309					3120	3131	3210
BsrD I	(4)	2490	3381	7529	7703		3252	3293	3380
BsrG I	(1)	5745					3386	3622	3718
BssH II	(2)	174	3545				3773	3887	4001
BssS I	(5)	3740	3866	5216	6751		5254	5276	5560
		8132					5618	5621	5715
BstB I	(1)	3830					6103	6127	6130
BstN I	(19)	368	561	1393	1525		6484	6502	6505
		2504	2663	3535	4282		6778	6921	6986
		4475	4873	5081	5206		7192	7520	7859
		5318	5393	5447	6215		7981	8210	
		6606	6727	6740					
BstU I	(24)	121	176	236	258	Fok I (16)	1375	1387	2244
		338	1885	3214	3515		2821	3013	3472
							3951	4869	5063

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`CWVG,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