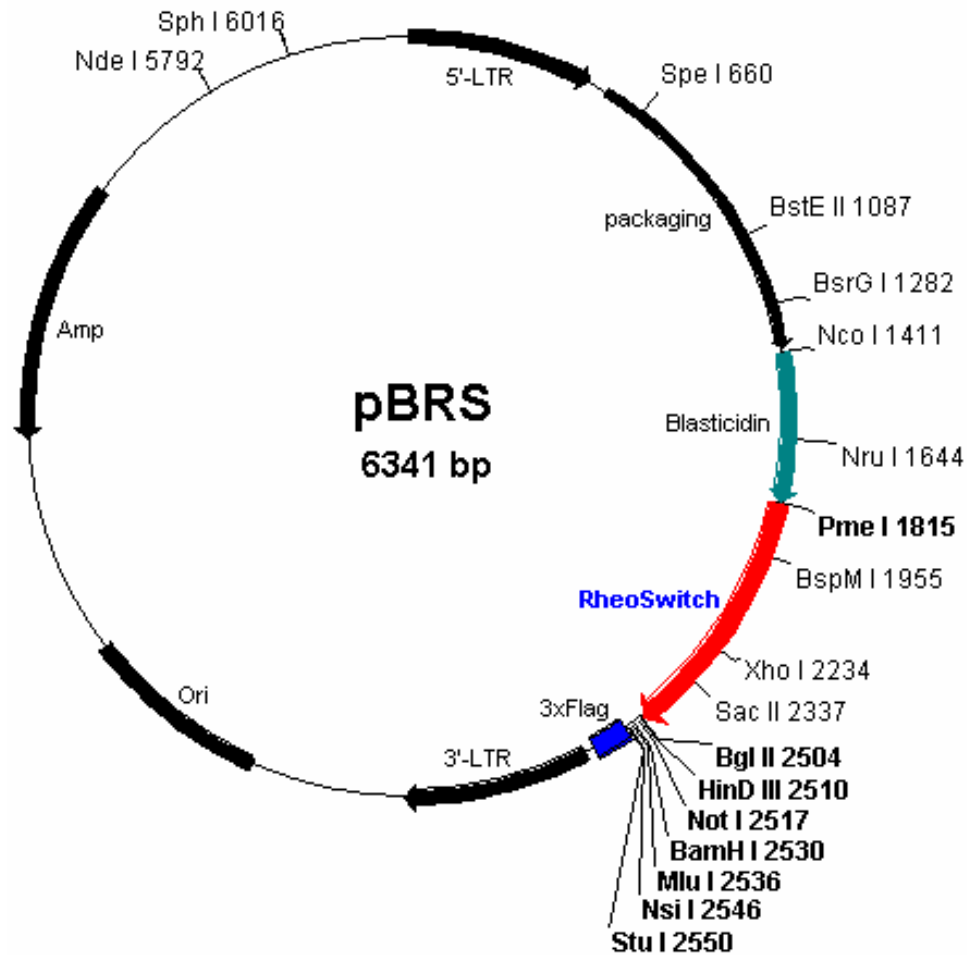


Vector: pBRS (RheoSwitch Inducible Vector)

Antibiotic Selection: Amp

Creator(s): Hong Yin, Molecular Oncology Lab of The University of Chicago

Date of Construction: May, 2008



pBRS (RhoSwitch Inducible Vector) Full-Length Sequence

TGAAAGACCC CACTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGGAACAGAGACAGCAGCAGGATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTCCCGCGCTCAGGGCCAAGAACAGATGTCCTCCAGATGCGGTCCC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTTCCAGGTTGCCCAAGGACCTGAAATGACCTGTGCTTATTTGAACTAACCAATCAGTTCGCTTCTCGCTTCT
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 AAAGCCTCTTG CTGTTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCCTCCAGATTGATGACTGCCACCTCGGGGGTCTTTCATTGGAG
 GTTCCACCGA GATTTGGAGACCCTGCCCA GGGACCACCGACCCCCCGC CGGGAGGTAA GCTGGCCAGC GGTCGTTTTCGTGTCTGTCT TGCTTTTGTG
 CGTGTTTGTGCCGCATCTAATGTTTTGCGCTGCTGTACTAGTTAGCTAAGCTGTGATCTGGCGGACCCGCTGGTGGAACTGACGATTTCTGAACACCCG
 GCCG CAACCCCTGGG AGACGTCCAGGGACTTTGGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTTCGATGTGGAATCCGACCCGCTCAGGATATGTGGTT
 CTGGTAGGAGACGAGAACCT AAAACAGTTC CCGCCTCCGT CTGAATTTTTGCTTTTCGGTT TGAACCGAAGCCGCGCGTC TTGCTGTGTC CAGCGCTGCA
 GCATCGTTCT GTGTTGTCTC TGCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTACCTTAGGTCACCTG
 GAAAGATGTCGAGCGGATCG CTCACAACCA GTCGGTAGAT GTCGAAGAAGACGTTGGGT TACCTTCTGC TCTGCAGAAT GGCCAACCTTAACTGCGGA
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 TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GGTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CTCCATCCGCCCCGCTCTCT
 CCCCCTTGAACCTCTCTCGATCCGACCCCGCTCGATCTCCCTTTATCCAGCCCTCACTCTTCTAGGCGCCGGAATTCACCATGGCCAAGCCTTTGTCTCAAGA
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 gcgg ccg cgt cga cgg atc ca CGC GT atgcat AGGCCT gcaggc gat tac aag gat gac gac gat aag ata ggcgga gat tac
 aag gat gac gac gat aag ata ggcgga gat tac aag gat gac gac gat aag atT TAATTAA
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 CTCAGGGCCAAGAACAGATGGTCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCSCCAAGGACCTGAAATGACCCGT
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 CCCCTGACGA GCATCACAAA AATCGAGCTCAAGTCAGAG GTGGCGAAAC CCGACAGGCA TATAAGATACCAGGCGTTT CCCCTGGAAGCTCCCTCGT
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 CAACACCCTGTTAGCGG TGTTTTTTTT GTTTGCAAGC AGCAGATACCGCGAGAAAA AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGGT
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 AGTCCAATTT GTTAAAGACA GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTCACAATA TCACCAGCTGAGCCTATAG AGTACGAGCCATAGATAAAA
 TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAA

Unique enzymes in pBRS:

Spe I	A`CTAG,T	660
BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
Nco I	C`CATG,G	1411
Nru I	TCG CGA	1644
BsaB I	GATNN NNATC	1711
Pme I	CTTT AAAC	1815
Mun I	C`AATT,G	1821
BspM I	ACCTGC 10/14	1955
Paer7 I	C`TCGA,G	2234
Xho I	C`TCGA,G	2234
Sac II	CC,Gc`GG	2337
Bsm I	GAATG,C`7	2363
Bgl II	A`GATC,T	2504

HinD III	A`AGCT,T	2510
Not I	GC`GGCC,GC	2517
BamH I	G`GATC,C	2530
Mlu I	A`CGCG,T	2536
Nsi I	A,TGCA`T	2546
Stu I	AGG CCT	2550
Nde I	CA`TA,TG	5792
Sph I	G,CATG`C	6016
Number of enzymes = 22		

The following enzymes do not cut in pBRS:

Age I	Apa I	Avr II	Bcl I	Blp I
BsaA I	BsiC I	BsiW I	Bsp120 I	Bsp1286 I

pBRS: sites sorted by name:									
BspM II		Bst1107 I	BstB I	BstX I	Dra III				5789
Eco72 I		Esp I	Fse I	Hpa I	Pf1M I	Bsm I	(1)		2363
Pml I		Rsr II	Sfi I	SnaB I	Spl I	BsmA I	(22)	107	475
								734	832
								1132	1150
								2272	2688
								3179	4683
								5654	6326
Aat II	(3)	745	2037	5543		BsmB I	(8)	733	831
Acc I	(3)	2037	2208	2525				1329	2271
Acc65 I	(3)	401	1993	3106		BsmF I	(12)	172	185
Aci I	(68)	197	203	566	588			764	1205
		688	727	860	901			2332	2877
		1042	1133	1199	1298	BsoF I	(38)	727	901
		1317	1355	1532	1614			925	928
		1681	1828	2070	2080			1532	1606
		2118	2150	2188	2217			1615	1618
		2334	2336	2516	2520			2337	2517
		2588	2621	2902	2908			3634	3652
		3204	3418	3521	3577			3928	4071
		3587	3611	3654	3661			4345	4673
		3682	3773	3801	3928			5134	5363
		3947	4068	4178	4313			5863	5936
		4322	4684	4775	4966	BspH I	(4)	4448	5456
		5012	5133	5177	5254	BspM I	(1)	1955	
		5363	5462	5509	5683	Bsr I	(17)	374	1030
		5722	5732	5758	5796			1570	1954
		5809	5835	5892	6151			4135	4148
Afl II	(3)	35	1006	2738				4786	4829
Afl III	(2)	2536	3728					5974	
Aha II	(10)	742	1398	2034	2280	BsrB I	(6)	1042	2118
		5158	5540	5844	6027			3661	5462
		6141	6162			BsrD I	(2)	4682	4856
Ahd I	(4)	1020	3151	3197	4621	BsrG I	(1)	1282	
Alu I	(31)	30	34	336	580	BssH II	(5)	317	368
		668	676	1515	1620			3073	
		2001	2062	2248	2512	BssS I	(4)	1587	3901
		2733	2737	3041	3360	BstE II	(1)	1087	
		3393	3488	3552	3670	BstN I	(18)	241	548
		3896	3986	4032	4289			1169	1194
		4810	4910	4973	5652			1267	1717
Alw I	(17)	5671	5916	6272				3468	3756
		453	1051	1357	1727			5963	6240
		2049	2237	2319	2526	BstU I	(27)	317	319
		2537	4290	4376	4376			905	1135
		4473	4474	4938	5253			2019	2070
		5259						2522	2538
AlwN I	(4)	2444	2453	2862	4144			3075	3575
ApaL I	(3)	4042	5288	5785				4356	4686
Apo I	(3)	872	1404	2239				5611	5613
Asc I	(2)	368	3073		4793	BstY I	(9)	2230	2504
Ase I	(4)	3371	3499	3558				4380	4466
Asp718	(3)	401	1993	3106				5263	
Ava I	(6)	331	397	498	2234	Bsu36 I	(2)	781	1018
		3036	3102			Cac8 I	(35)	28	32
Ava II	(14)	186	199	254	551			582	586
		690	1219	1572	2319			1199	1508
		2891	2904	2959	4759			2514	2552
		4981	6236					2735	3024
BamH I	(1)	2530						3550	3659
Ban I	(15)	244	401	1142	1397			4342	4733
		1687	1967	1993	2949			5914	5918
		3106	3472	4569	5843			6103	6145
		6026	6140	6161		Cfr10 I	(4)	629	4701
Ban II	(10)	338	351	1677	2003	Cla I	(2)	1883	1987
		2064	2250	3043	3056	Csp6 I	(16)	402	658
		6093	6107					1994	2055
Bbe I	(5)	1401	5847	6030	6144			2123	2155
		6165						3107	5100
Bbs I	(3)	1498	2316	2385		Dde I	(20)	75	167
Bbv I	(9)	931	939	1524	1629			781	1018
		4147	4150	4356	5050			2508	2778
		5661						3182	3253
Bbv II	(3)	1497	2315	2386		Dpn I	(32)	94	459
Bcn I	(16)	164	399	400	571			1363	1647
		724	2318	2342	2869			2012	2044
		3104	3105	4109	4805			2269	2325
Bfa I	(15)	5156	5657	5692	6043			2798	4296
		31	219	661	673			4390	4468
		1394	1522	1934	2214			4926	4944
		2465	2734	2924	4223			5265	5301
		4476	4811	6246		DpnII	(32)	92	457
Bgl I	(3)	2336	4741	5859				1361	1645
Bgl II	(1)	2504						2010	2042
Bpm I	(4)	2295	2671	4691	6309			2267	2323
Bsa I	(6)	476	530	1149	3159			2796	4294
		3180	4682					4388	4466
BsaB I	(1)	1711						4924	4942
BsaH I	(10)	742	1398	2034	2280			5263	5299
		5158	5540	5844	6027	Dra I	(4)	1815	4487
		6141	6162			Drd I	(3)	1500	3836
BsaJ I	(31)	161	240	250	397	Dsa I	(4)	694	1411
		461	497	546	547	Eae I	(13)	582	724
		694	733	734	746			1414	1529
		747	1167	1236	1245			2517	3567
		1265	1266	1411	1716			6175	
		2334	2866	2945	2955	Eag I	(4)	724	1529
		3102	3165	3467	3888	Ear I	(7)	1070	1311
		5962	6040	6046				3612	5416
BsaW I	(3)	3934	4081	4912				923	6082
BseR I	(4)	464	1293	1332	3168	Eco47 III	(2)	923	6082
Bsg I	(2)	1600	1983			Eco57 I	(4)	1509	4275
BsiE I	(12)	592	727	1532	1648	EcoN I	(2)	784	1392
		2013	2340	2520	3644	EcoO109 I	(6)	254	1219
		4068	4991	5140	5887			5597	6051
BsiHKA I	(9)	338	2003	2064	2250				
		3043	4046	5207	5292				

EcoR I	(2)	1404	2239				5955	5975				
EcoR II	(18)	239	546	733	746		92	457	1044	1176		
		1167	1192	1215	1235		1361	1645	1706	1720		
		1265	1715	2272	2944		2010	2042	2050	2230		
		3466	3754	3875	3888		2267	2323	2504	2530		
		5961	6238				2796	4294	4369	4380		
EcoR V	(3)	140	2844	6229			4388	4466	4478	4583		
Ehe I	(5)	1399	5845	6028	6142		4924	4942	4988	5246		
		6163					5263	5299	5884	6108		
Fnu4H I	(38)	727	901	917	920		1086	1299	1445	1502		
		925	928	1133	1513		1530	2320	2386	2488		
		1532	1606	1609	1612		3366	3600	4389	4462		
		1615	1618	1782	1828		5217	5295	5404	5892		
		2337	2517	2520	3553		6104					
		3634	3652	3655	3773							
		3928	4071	4136	4139	Mlu I	(1)	2536				
		4345	4673	5012	5039	Mne I	(6)	829	1106	3167	3219	
		5134	5363	5650	5759		3942	4126				
		5863	5936			Mnl I	(56)	167	216	368	387	
Fok I	(15)	423	1140	1300	1464		432	460	484	506		
		1699	2270	2581	2614		510	566	776	872		
		2647	3127	4587	4768		1168	1271	1304	1310		
		5055	5698	5942			1313	1319	1349	1352		
Fsp I	(2)	4843	5866				1367	1374	1390	1454		
Gdi II	(14)	723	725	1129	1528		1795	1796	2101	2120		
		1530	1824	2336	2338		2133	2139	2171	2190		
		2516	2518	3568	5008		2209	2310	2340	2406		
		6044	6176				2921	3073	3092	3137		
Gsu I	(4)	2294	2672	4692	6310		3164	3188	3248	3577		
Hae I	(7)	584	1111	1416	2550		3626	3836	3909	4160		
		3743	3754	4206			4560	4641	4787	4993		
Hae II	(9)	925	1401	3606	3976		5588	5646	5906	6190		
		5847	6030	6084	6144	Msc I	(3)	584	1111	1416		
		6165				Mse I	(27)	36	1007	1119	1149	
Hae III	(31)	129	173	584	726		1173	1814	2375	2379		
		762	774	987	1111		2652	2656	2739	3273		
		1132	1197	1416	1531		3371	3499	3558	4434		
		1827	2339	2519	2550		4486	4491	4505	4558		
		2833	2878	3569	3743		4793	4832	5197	5569		
		3754	3772	4206	4664		5750	5947	6217			
		4744	5011	5598	5896	Msl I	(3)	1860	4873	5032		
		6045	6053	6177		Msp I	(26)	163	398	569	630	
Hga I	(12)	381	642	895	1491		723	1401	2316	2340		
		2287	2512	3086	3838		2868	3103	3446	3935		
		4416	5148	5706	6175		4082	4108	4298	4702		
HgiA I	(9)	338	2003	2064	2250		4736	4803	4913	5155		
		3043	4046	5207	5292		5656	5690	6042	6165		
		5789					6174	6189				
HgiE II	(2)	4307	5787			MspAl I	(11)	588	1620	2336	3204	
Hha I	(39)	319	321	370	372		3552	4070	4315	5256		
		648	905	924	1400		5722	5916	6272			
		1512	2019	2021	2363	Mun I	(1)	1821				
		3024	3026	3075	3077	Nae I	(2)	631	6175			
		3352	3512	3577	3605	Nar I	(5)	1398	5844	6027	6141	
		3638	3908	3975	4075		6162					
		4249	4358	4751	4844	Nci I	(16)	163	398	399	570	
		5181	5513	5613	5716		723	2317	2341	2868		
		5846	5867	6000	6029		3103	3104	4108	4804		
		6083	6143	6164			5155	5656	5691	6042		
HinC II	(3)	2038	2209	2526		Nco I	(1)	1411				
Hind II	(3)	2038	2209	2526		Nde I	(1)	5792				
Hind III	(1)	2510				Ngom I	(2)	629	6173			
Hinf I	(19)	442	450	791	802	Nhe I	(2)	30	2733			
		1437	1769	1880	2135	Nla III	(17)	62	1205	1415	2765	
		2205	2210	3263	3285		3219	3386	3732	4452		
		3306	3563	3628	3703		4943	4953	5031	5067		
		4099	4616	6254			5460	5565	5649	6016		
HinI I	(10)	742	1398	2034	2280		6089					
		5158	5540	5844	6027	Nla IV	(35)	188	201	246	403	
		6141	6162				521	552	692	761		
HinP I	(39)	317	319	368	370		893	1144	1221	1399		
		646	903	922	1398		1573	1689	1969	1995		
		1510	2017	2019	2361		2320	2532	2893	2906		
		3022	3024	3073	3075		2951	3108	3474	3760		
		3350	3510	3575	3603		3799	4571	4665	4706		
		3636	3906	3973	4073		4917	5507	5845	6028		
		4247	4356	4749	4842		6052	6142	6163			
		5179	5511	5611	5714	Not I	(1)	2517				
		5844	5865	5998	6027	Nru I	(1)	1644				
		6081	6141	6162		Nsi I	(1)	2546				
Hpa II	(26)	163	398	569	630	Nsp7524 I	(3)	3728	5645	6012		
		723	1401	2316	2340	NspB II	(11)	588	1620	2336	3204	
		2868	3103	3446	3935		3552	4070	4315	5256		
		4082	4108	4298	4702		5722	5916	6272			
		4736	4803	4913	5155							
		5656	5690	6042	6165	NspH I	(3)	3732	5649	6016		
		6174	6189			Pac I	(2)	2379	2656			
Hph I	(13)	1157	1183	1401	4465	PaeR7 I	(1)	2234				
		4692	5106	5314	5347	Pal I	(31)	129	173	584	726	
		5631	5640	6133	6178		762	774	987	1111		
		6259					1132	1197	1416	1531		
Kas I	(5)	1397	5843	6026	6140		1827	2339	2519	2550		
		6161					2833	2878	3569	3743		
Kpn I	(3)	405	1997	3110			3754	3772	4206	4664		
Mae I	(15)	31	219	661	673		4744	5011	5598	5896		
		1394	1522	1934	2214		6045	6053	6177			
		2465	2734	2924	4223	Ple I	(5)	799	2143	2213	3271	
		4476	4811	6246			4107					
Mae II	(9)	742	1081	1122	2034	Pme I	(1)	1815				
		4431	4847	5220	5540	PpuM I	(4)	254	1219	1572	2959	
		5982				Psp1406 I	(2)	4847	5220			
Mae III	(18)	39	994	1022	1087	PspA I	(2)	397	3102			
		1231	2742	3220	4084	Pst I	(5)	921	929	1105	2449	
		4147	4263	4546	4877		2556					
		4935	5088	5276	5664	Pvu I	(4)	1648	2013	4991	5887	
						Pvu II	(4)	1620	3552	5916	6272	
						Rsa I	(16)	403	659	1284	1890	

		1995	2056	2086	2105	Ava I	C`YCGR,G	6	Ava II	G`GWC,C	14
		2124	2156	2175	2194	Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
		3108	5101	5777	6288	Ban I	G`GYRC,C	15	Ban II	G,RCY`C	10
Sac I	(5)	338	2003	2064	2250	Bbe I	G,CGGC`C	5	Bbs I	GAAGAC 8/12	3
		3043				Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	3
Sac II	(1)	2337				Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	16
Sal I	(3)	2036	2207	2524		Bfa I	C`TA,G	15	Bgl I	GCCN,NNN`NGGC	3
Sap I	(2)	3350	3612			Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Sau3A I	(32)	92	457	1044	1176	Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	6
		1361	1645	1706	1720	BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	1
		2010	2042	2050	2230	BsaH I	GR`CG,YC	10	BsaJ I	C`CNNG,G	31
		2267	2323	2504	2530	BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	4
		2796	4294	4369	4380	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
		4388	4466	4478	4583	BsiE I	CG,RY`CG	12	BsiHKA I	G,WGCW`C	9
		4924	4942	4988	5246	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1
Sau96 I	(27)	5263	5299	5884	6108	BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	8
		127	171	186	199	BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	38
		254	551	690	760	Bsp120 I	G`GGCC,C	-	Bspl286 I	G,DCGH`C	-
		773	985	1196	1219	BspH I	T`CATG,A	4	Bspm I	ACCTGC 10/14	1
		1572	2319	2831	2876	Bspm II	T`CCGG,A	-	Bsr I	ACT,GG`	17
		2891	2904	2959	4663	BsrB I	GAG CGG	6	BsrD I	GCAATG, 8	2
		4742	4759	4981	5597	BarG I	T`GTAC,A	1	BssH II	G`CGGC,C	5
		5894	6051	6236		BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
Sca I	(8)	1890	2086	2105	2124	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
		2156	2175	2194	5101	BstN I	CC`W,GG	18	BstU I	CG CG	27
ScrF I	(34)	163	241	398	399	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
		548	570	723	735	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	35
		748	1169	1194	1217	Cfr10 I	R`CCGG,Y	4	ClA I	AT`CG,AT	2
		1237	1267	1717	2274	Csp6 I	G`TA,C	16	Dde I	C`TNA,G	20
		2317	2341	2868	2946	Dpn I	GA TC	32	DpnII	`GATC,	32
		3103	3104	3468	3756	Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-
		3877	3890	4108	4804	Drd I	GACNN,NN`NNGTC	3	Dea I	C`CRYG,G	4
		5155	5656	5691	5963	Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	4
		6042	6240			Ear I	CTCTTC 7/10	7	Eco47 III	AGC GCT	2
Sec I	(31)	161	240	250	397	Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-
		461	497	546	547	EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	6
		694	733	734	746	EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	18
		747	1167	1236	1245	EcoR V	GAT ATC	3	Ehe I	GGC GCC	5
		1265	1266	1411	1716	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	38
		2334	2866	2945	2955	Fok I	GGATG 14/18	15	Fse I	GG,CCGG`CC	-
		3102	3165	3467	3888	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	14
		5962	6040	6046		Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	7
SfaN I	(20)	185	444	641	938	Hae II	R,CGC`Y	9	Hae III	GG CC	31
		1485	1542	1674	1720	Hga I	GAGCG 9/14	12	HgiA I	G,WGCW`C	9
		2890	3148	3824	4876	HgiE II	ACCNNNNNNGGT	-1/132	Hha I	G,CG`C	39
		5069	5316	5677	5769	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
		5807	5845	6161	6173	HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	19
Sfc I	(12)	15	917	925	1101	HinI I	GR`CG,YC	10	HinP I	G`CG,C	39
		1496	2445	2552	2718	Hpa I	GTT AAC	-	Hpa II	C`CG,G	26
		3993	4184	4862	6280	Hph I	GGTGA 12/11	13	Kas I	G`GGC,C	5
Sma I	(2)	399	3104			Kpn I	CG,GTAC`C	3	Mae I	C`TA,G	15
Spe I	(1)	660				Mae II	A`CG,T	9	Mae III	`GTNAC,	18
Sph I	(1)	6016				Mbo I	`GATC,	32	Mbo II	GAAGA 12/11	17
Ssp I	(2)	3271	5425			Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Stu I	(1)	2550				Mnl I	CCTC 10/10	56	Msc I	TGG CCA	3
Sty I	(6)	250	461	1245	1411	Mse I	T`TA,A	27	Msl I	CAYNN NNRTG	3
		2955	3165			Msp I	C`CG,G	26	MspAl I	CMG CKG	11
Taq I	(17)	794	1038	1349	1360	Mun I	C`AATT,G	1	Nae I	GCC GGC	2
		1705	1883	1987	2037	Nar I	GG`CG,CC	5	Nci I	CC`S,G	16
		2075	2138	2145	2208	Nco I	C`CATG,G	1	Nde I	CA`TA,TG	1
		2235	2525	3266	3828	NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
		5272				Nla III	,CATG`	17	Nla IV	GGN NCC	35
Tfi I	(8)	442	802	1437	1769	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
		1880	3306	3563	3703	Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	3
Tsp45 I	(6)	1022	1231	4877	5088	NspB II	CMG CKG	11	NspH I	R,CATG`Y	3
		5664	5975			Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	1
Tth111 I	(4)	390	811	1217	3095	Pal I	GG CC	31	PflM I	CCAN,NNN`NTGG	-
Tth111 II	(8)	146	422	613	632	Ple I	GAGTC 9/10	5	Pme I	CTTT AAAC	1
		2850	4317	4326	4356	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Vsp I	(4)	3371	3499	3558	4793	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
Xba I	(2)	218	2923			Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	4
Xho I	(1)	2234				Pvu II	CAG CTG	4	Rsa I	GT AC	16
Xho II	(9)	2230	2504	2530	4369	Rer II	CG`GWC,CG	-	Sac I	G,AGCT`C	5
		4380	4466	4478	5246	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	3
		5263				Sap I	GCCTTTC 8/11	2	Sau3A I	`GATC,	32
Xma I	(2)	397	3102			Sau96 I	G`GNC,C	27	Sca I	AGT ACT	8
Xma III	(4)	724	1529	2337	2517	ScrF I	CC`N,GG	34	Sec I	C`CNNG,G	31
Xmn I	(3)	3334	3372	5220		SfaN I	GCATC 9/13	20	Sfc I	C`TRYA,G	12
						Sfi I	GCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
						SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
						Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
						Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
						Stu I	AGG CCT	1	Sty I	C`CWGG,G	6
						Taq I	T`CG,A	17	Tfi I	G`AWT,C	8
						Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	4
						Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	4
						Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
						Xcm I	CCANNNN,NN`NNNTGG-	-	Xho I	C`TCGA,G	1
						Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	2
						Xma III	C`GGCC,G	4	Xmn I	GAANN NNTTTC	3

Site usage in pBRS:

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	3
Acc65 I	G`GTAC,C	3	Aci I	C`CG,C	68
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	31
Alw I	GGATC 8/9	17	AlwN I	CAG,NNN`CTG	4
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	3