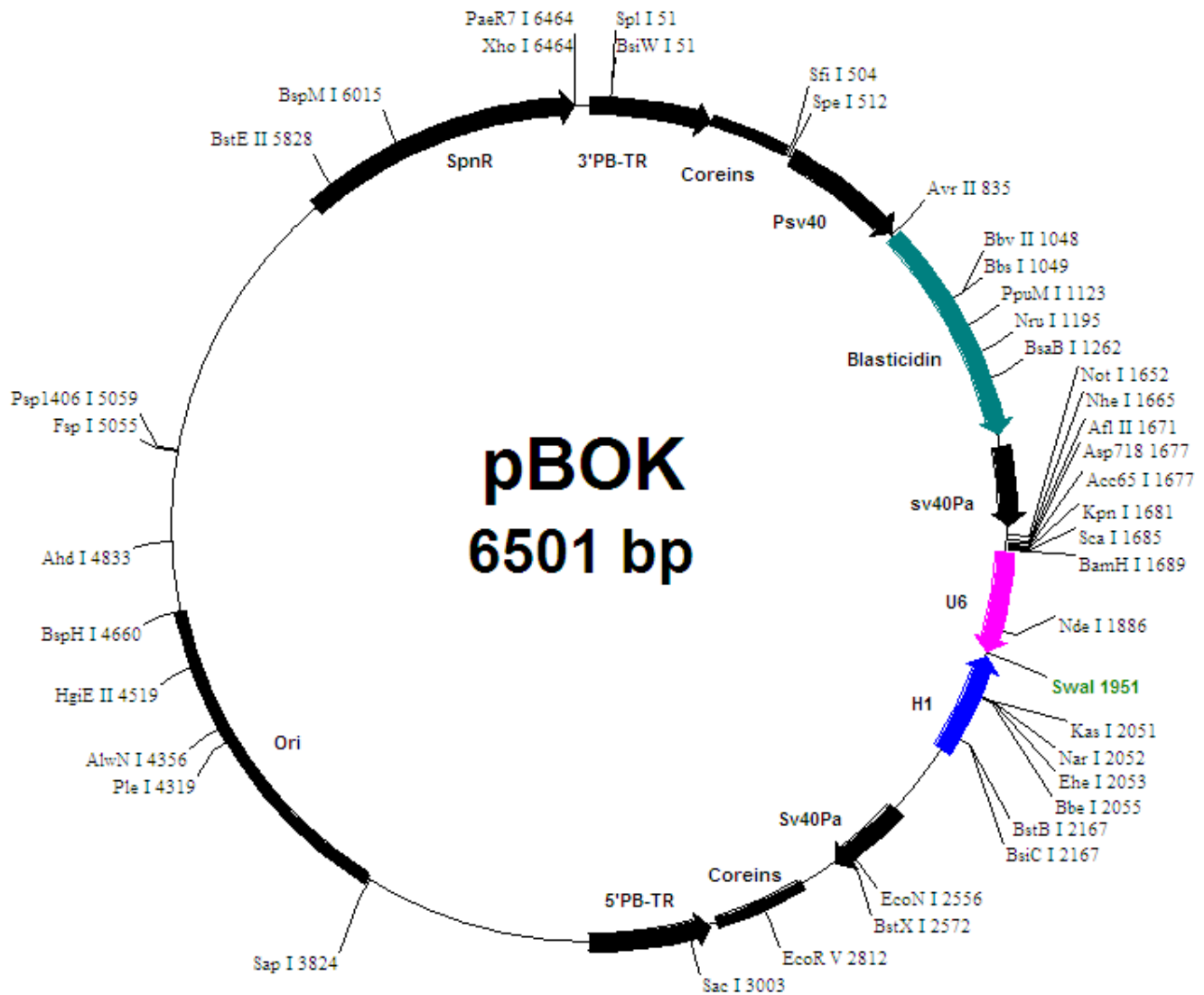


Vector: pBOK (*piggyBac* one-step siRNA knockdown destination vector)

Antibiotic Selection: Spn

Creator(S): Fang Deng & Zhengjian Yan, Molecular Oncology Laboratory of The University of Chicago Medical Center

Date of Construction: October, 2013



pBOK Full-Length Sequence

CTGCAGAACACGCAGCTAGATTAA**CCCTAGAAAAGATAATCATATTTGTGACGTACGTTAAAGATAATCATGCGTAAAAATTGAC**
GCATGTGTTTTATCGGTCTGTATATCGAGGTTTTATTTATTTAATTTGAATAGATATTAAGTTTTATTATATTTACACTTACAT
 ACTAATAATAAAATTCACAAAACAATTTATTTATGTTTTATTTATTTATTTAAAAAAAACAAAACTCAAAATTTCTTCTATAA
 AGTAACAAAACTTTTATGAGGGACAGCCCCCCCCAAAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGC
 AGCGAGCCGCCGGGGCTCCGCTCCGGTCCGGCGCTCCCCCGCATCCCCGAGCCGGCAGCGTGCGGGGACAGCCCGGGCAC
 GGGGAAGGTGGCACGGGATCGCTTTCTCTGAACGCTTCTCGCTGCTCTTTGAGCCTGCAGACACCTGGGGGGATACGGGGA
 AAAGGCTCCACGGCCAGACTAGT**AATGTGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGC**
AAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCA
TCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCATCCCCGCCCTAACCTCCGCCAGTTCCGCCAATTCCTCCG
 CCCCATGGCTGACTAATTTTTTTTTATTTATGTCAGAGGCCGAGGCCCTCTGCCTCTGAGCTATTCCAGAAGTAGTGAGGAG
 GCTTTTTTGGAGGCCTAGGCTTTTTGCAAAAAGCTCCCGGGAGCTTGTATATCCATTTTCGGATCTGATCAGCACGTGTTGAC
AATTAATCATCGGCATAGTATATCGGCATAGTATAATACGACAAGGTGAGGAACTAAACCATGGCCAAGCCTTTGTCTCAAG
AAGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGC
TCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGACCTTGTGCAGAACTCGTGGTGTCTG
GGCACTGCTGCTGTCGCGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCCT
GCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGTGGACAGCCGACGGC
AGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTCTGGCCGAGGAGCAGGACTGACACGT
GCTACGAGATTTTCGATTCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATC
CTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGTTTATTGTCAGCTTATAAATGGTTACAAAATAAGCA
ATAGCATCACAAATTTACAAAATAAAGCAATTTTTTCACTGCATTTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTA
TCATGCTGGGCGCCG**GACGTCGCTAGCCTTAAG**GGTACCAGTACT**ggatccaggctcgggcaggaagaggccattttccc**
atgattccttcatattttgcata**acgatacaaggctg**tttagagagata**aattagaattaatttgactg**taaacacaaagatat
tagtacaaa**atac**gtgagtagaa**agtaataat**ttcttgggtag**tttgcag**ttttaa**attatg**ttttaa**atggactat**cat
atgcttaccgta**acttg**aaag**at**ttt**cg**at**ttctt**ggct**ttat**at**ctt**gtg**gaa**agga**ATTTAAAT**tggtct**cat**acaga
acttataag**attcc**caaat**ccaa**agac**at**tt**ca**g**tt**at**g**gtg**att**cccagaa**ac**atag**cg**acat**g**caaat**att**gcag
gcgcc**act**cccct**gt**ccct**ca**gac**ct**ctt**ct**gccaggg**gc**ac**gc**g**ct**gggt**gt**ccc**gc**ctag**tg**ac**act**ggg**ccc**
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 CCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCC
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AGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCCTGACTCCCCGTCG
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CTGCAATTTGGAGAATGGCAGCGCAATGACATTCTTGCAGGTATCTTCGAGCCAGCCACGATCGACATTGATCTGGCTATCT
TGCTGACAAAAGCAAGAGAACATAGCGTTGCCCTGGTAGGTCCAGCGCGGAGGAACCTTTTGATCCGGTTCCCTGAACAGGA
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ACGTTGTCCCGCATTTGGTACAGCGCAGTAACCGGCAAAAATCGCGCCGAAGGATGTCGCTGCCGACTGGGCAATGGAGCGCC
TGCCGGCCAGTATCAGCCCGTCATACTTGAAGCTAGACAGGCTTATCTTGGACAAGAAGAAGATCGCTTGGCTTCGCGCGC
AGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATCACCAGGTAGTCGGCAAATAACCCCTCGAGCCACCCATGA
CCAAAATCCCTTAACGTGAGTTA

Unique enzymes in pBOK:

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
PpuM I	RG`GWC,CY	1123
Nru I	TCG CGA	1195
BsaB I	GATNN NNATC	1262
Not I	GC`GGCC,GC	1652
Nhe I	G`CTAG,C	1665
Afl II	C`TTAA,G	1671
Acc65 I	G`GTAC,C	1677
Asp718	G`GTAC,C	1677
Kpn I	G,GTAC`C	1681
Sca I	AGT ACT	1685
BamH I	G`GATC,C	1689
Nde I	CA`TA,TG	1886
SwaI	ATTT AAAT	1951
Kas I	G`GCGC,C	2051
Nar I	GG`CG,CC	2052
Ehe I	GGC GCC	2053
Bbe I	G,GCGC`C	2055
BsiC I	TT`CG,AA	2167
BstB I	TT`CG,AA	2167
EcoN I	CCTNN`N,NNAGG	2556
BstX I	CCAN,NNNN`NTGG	2572
EcoR V	GAT ATC	2812
Sac I	G,AGCT`C	3003
Sap I	GCTCTTC 8/11	3824
Ple I	GAGTC 9/10	4319
AlwN I	CAG,NNN`CTG	4356
HgiE II	ACCNNNNNNGGT -1/134519	
BspH I	T`CATG,A	4660
Ahd I	GACNN,N`NNGTC	4833
Fsp I	TGC GCA	5055
Psp1406 I	AA`CG,TT	5059
BstE II	G`GTNAC,C	5828
BspM I	ACCTGC 10/14	6015
Paer7 I	C`TCGA,G	6464
Xho I	C`TCGA,G	6464

Number of enzymes = 42

The following enzymes do not cut in pBOK:

Acc I	Age I	Asc I	Bgl II	BsmB I
Bsp1286 I	BsrG I	Bst1107 I	Bsu36 I	Cla I
Eco47 III	EcoR I	Fse I	Hind III	Hpa I
Mlu I	Mun I	PacI	PflM I	Pme I
Sac II	Sal I	SnaB I	Tth111 I	Xba I

pBOK: sites sorted by name:

Aat II	(2)	1663	2160		
Acc65 I	(1)	1677			
Aci I	(69)	315	336	348	370
		393	683	695	704
		716	726	737	783
		1083	1165	1232	1416
		1419	1485	1651	1655
		2112	2131	2146	2679
		2702	2724	2736	2757
		2941	2974	3008	3216
		3229	3378	3485	3490
		3538	3575	3630	3733
		3789	3799	3823	3866
		3873	3894	3985	4013
		4140	4159	4280	4390
		4525	4534	4896	4987
		5178	5224	5491	5511
		5679	5776	5788	5855
		5918	6114	6117	6195
		6242			
Afl II	(1)	1671			
Afl III	(3)	894	1390	3940	
Aha II	(5)	1461	1660	2052	2157
		5722			
Ahd I	(1)	4833			
Alu I	(27)	16	799	853	863
		1066	1171	1535	2176
		2367	3001	3127	3170
		3605	3700	3764	3882
		4108	4198	4244	4501
		5022	5122	5185	5432
		5862	5976	6348	
Alw I	(17)	434	888	1278	1469
		1496	1685	1696	2639
		3143	4502	4588	4588
		4685	4686	5150	6127
		6156			
AlwN I	(1)	4356			
Apa I	(2)	2131	2565		
ApaL I	(2)	4254	5943		

		5856	6006	6115	6195		1257	1271	1473	1489
		6292					1689	2186	2643	3136
Fok I	(19)	307	359	686	1015		4506	4581	4592	4600
		1250	1483	2384	2711		4678	4690	4795	5136
		2763	3265	3414	3546		5154	5200	5683	5866
		4799	4980	5267	5399		6046	6056	6131	6149
		5552	5796	6297			6377	6398	6436	
Fsp I	(1)	5055				Mbo II	(15)	231	996	1053
Gdi II	(9)	506	1079	1081	1370		1499	1717	2071	3207
		1651	1653	3780	5220		3812	4601	4674	6024
		5754					6383	6386	6419	
Gsu I	(4)	1464	1519	4904	5919	Mme I	(3)	4154	4338	6386
Hae I	(9)	498	834	967	3319	Mnl I	(46)	103	258	318
		3355	3955	3966	4418		508	766	772	795
		6387					801	809	812	824
Hae II	(10)	364	2055	2714	3177		944	1005	1346	1347
		3496	3818	4188	5735		1369	1486	1702	2077
		6165	6314				2085	2495	2628	2756
Hae III	(26)	498	507	776	782		3000	3186	3213	3243
		834	967	1082	1373		3507	3789	3838	4048
		1654	1713	2129	2563		4121	4372	4772	4853
		3319	3355	3781	3955		4999	5205	5344	5568
		3966	3984	4418	4876		5665	5705	6113	6152
		4956	5223	5757	5791		6397	6472		
		6321	6387			Msc I	(2)	967	3319	
Hga I	(9)	89	1042	1468	2914	Mse I	(32)	22	57	122
		3077	4050	4628	5376		212	906	1672	1779
		5712					1858	1871	1950	2172
HgiA I	(3)	3003	4258	5947			2181	2407	2414	2891
HgiE II	(1)	4519					2898	3119	3332	3476
Hha I	(38)	363	1063	1485	2054		3711	3770	4646	4698
		2093	2099	2101	2713		4703	4717	4770	5005
		3049	3176	3419	3495		5044	5661	6177	6490
		3581	3583	3724	3789	Msl I	(4)	2570	5085	5244
		3817	3850	4120	4187	Msp I	(34)	340	353	358
		4287	4461	4570	4963		404	857	1456	1464
		5056	5455	5505	5582		2385	2535	2668	2689
		5734	5922	5983	6010		2714	2719	2732	3387
		6164	6258	6278	6313		3399	3440	3450	3464
		6394	6396				3572	3658	4147	4294
HinC II	(2)	900	2462				4320	4510	4914	4948
Hind II	(2)	900	2462				5015	5125	5362	6135
Hinf I	(19)	988	1320	1409	1446		6265	6318		
		1726	1978	2135	2336	MspA1 I	(7)	1171	3485	3764
		2548	2934	3042	3303		4527	5491	6114	4282
		3775	3840	3915	4311	Nae I	(4)	384	1465	2690
		4828	5699	5912		Nar I	(1)	2052		6319
HinI I	(5)	1461	1660	2052	2157	Nci I	(17)	340	341	404
		5722					857	858	1457	2386
HinP I	(38)	361	1061	1483	2052		2535	2668	2669	2732
		2091	2097	2099	2711		2733	3572	4320	5016
		3047	3174	3417	3493		5363			
		3579	3581	3722	3787	Nco I	(2)	742	962	
		3815	3848	4118	4185	Nde I	(1)	1886		
		4285	4459	4568	4961	NgoM I	(4)	382	1463	2688
		5054	5453	5503	5580	Nhe I	(1)	1665		6317
		5732	5920	5981	6008	Nla III	(27)	71	88	583
		6162	6256	6276	6311		746	966	1498	1646
		6392	6394				1726	2038	2327	2864
Hpa II	(34)	340	353	358	383		2924	3087	3236	3300
		404	857	1456	1464		3324	3554	3598	3944
		2385	2535	2668	2689		4664	5155	5165	5243
		2714	2719	2732	3387		5279	5522	6478	
		3399	3440	3450	3464	Nla IV	(20)	346	553	625
		3572	3658	4147	4294		1240	1679	1691	2053
		4320	4510	4914	4948		2129	2563	2728	3686
		5015	5125	5362	6135		3972	4011	4783	4877
		6265	6318				4918	5129	5774	6139
Hph I	(11)	959	2021	3348	4677	Not I	(1)	1652		
		4904	5318	5376	5692	Nru I	(1)	1195		
		5839	5925	6432		Nsi I	(3)	585	657	3085
Kas I	(1)	2051				Nsp7524 I	(6)	84	579	651
Kpn I	(1)	1681					3083	3940		2034
Mae I	(17)	17	28	318	513	NspB II	(7)	1171	3485	3764
		836	1073	1605	1666		4527	5491	6114	4282
		2116	2286	2754	3113	NspH I	(6)	88	583	655
		3124	4435	4688	5023		3087	3944		2038
		6349				PaeR7 I	(1)	6464		
Mae II	(21)	50	54	304	894	Pal I	(26)	498	507	776
		1392	1660	1817	2002		834	967	1082	1373
		2157	2768	2849	2907		1654	1713	2129	2563
		3272	3289	3506	4643		3319	3355	3781	3955
		5059	5748	6234	6424		3966	3984	4418	4876
		6493					4956	5223	5757	5791
Mae III	(25)	46	248	1544	1896		6321	6387		
		2118	2225	2903	2963	Ple I	(1)	4319		
		3566	4296	4359	4475	Pml I	(2)	895	1393	
		4758	5089	5147	5300	PpuM I	(1)	1123		
		5365	5496	5583	5627	Psp1406 I	(1)	5059		
		5822	5828	5930	6260	PspA I	(5)	339	403	856
		6498					2731			2667
Mbo I	(31)	427	881	886	1196	Pst I	(3)	6	471	2607

pBOK Vector

Pvu I	(3)	1199	5203	6049
Pvu II	(2)	1171	3764	
Rsa I	(9)	53	1679	1685 1809
		5315	5548	5761 5769
		6252		
Rsr II	(2)	355	2716	
Sac I	(1)	3003		
Sap I	(1)	3824		
Sau3A I	(31)	427	881 886	1196
		1257	1271 1473	1489
		1689	2186 2643	3136
		4506	4581 4592	4600
		4678	4690 4795	5136
		5154	5200 5683	5866
		6046	6056 6131	6149
		6377	6398 6436	
Sau96 I	(15)	355	1123 1711	2127
		2128	2561 2562	2716
		4875	4954 4971	5193
		5467	6108 6320	
Sca I	(1)	1685		
ScrF I	(37)	291	340 341	404
		405	477 549	604
		621	857 858	1268
		1457	1694 2087	2386
		2466	2524 2535	2596
		2668	2669 2732	2733
		2782	3360 3527	3572
		3680	3968 4089	4102
		4320	5016 5322	5363
		5899		
Sec I	(38)	289	290 339	340
		403	476 502	547
		619	742 777	835
		856	962 1267	1374
		2086	2139 2385	2533
		2594	2667 2730	2731
		2780	2781 3248	3359
		3679	4100 5353	5376
		5559	5590 5897	5961
		6100	6442	
SfaN I	(18)	380	591 663	1036
		1093	1225 1271	1571
		2252	2690 3138	3193
		3427	3525 4036	5088
		5281	5573	
Sfc I	(8)	2	467 1047	2603
		4205	4396 5074	5923
Sfi I	(1)	504		
Sma I	(5)	341	405 858	2669
		2733		
Spe I	(1)	512		
Sph I	(3)	583	655 3087	
Spl I	(1)	51		
Srf I	(2)	405	2669	
Ssp I	(3)	2043	2411 3071	
Stu I	(2)	498	834	
Sty I	(7)	742	835 962	2139
		5353	6100 6442	
SwaI	(1)	1951		
Taq I	(14)	108	1256 1407	1913
		2167	4040 5337	5597
		5697	5728 5740	6034
		6049	6465	
Tfi I	(13)	988	1320 1409	1446
		1726	1978 2135	2548
		3042	3303 3775	3915
		5912		
Tsp45 I	(9)	46	2118 2903	2963
		5089	5300 5365	5828
		5930		
Tth111 II	(7)	198	2998 4529	4538
		4568	5585 5592	
Vsp I	(7)	122	906 1779	3476
		3711	3770 5005	
Xho I	(1)	6464		
Xho II	(8)	881	1489 1689	4581
		4592	4678 4690	6149
Xma I	(5)	339	403 856	2667
		2731		
Xma III	(2)	1080	1652	

Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	69
Afl II	C`TTAA,G	1	Afl III	A`CRYG,T	3
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	5
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	27
Alw I	GGATC 8/9	17	AlwN I	CAG,NNN`CTG	1
Apa I	G,GGCC`C	2	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	6	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	7	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	9	Ava II	G`GWC,C	7
Avr II	C`CTAG,G	1	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	5	Ban II	G,RCY`C	6
Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	18	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	17
Bfa I	C`TA,G	17	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	2
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	3
BsaA I	YAC GTR	6	BsaB I	GATNN NNAATC	1
BsaH I	GR`CG,YC	5	BsaJ I	C`CNNG,G	38
BsaW I	W`CCGG,W	8	BseI I	GAGGAG 16/14	2
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	8	BsiHKA I	G,WGCW`C	3
BsiW I	C`GTAC,G	1	Bsm I	GAATG,C 7	3
BsmA I	GTCCT`/9	4	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	15	BsoF I	GC`N,GC	57
Bsp120 I	G`GGCC,C	2	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	1
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	22
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	4
BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	3
BssS I	C`TCGT,G	2	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	20	BstU I	CG CG	23
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	8
Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	40
Cfr10 I	R`CCGG,Y	8	Clal I	AT`CG,AT	-
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	7
Dpn I	GA TC	31	DpnII	`GATC,	31
Dra I	TTT AAA	7	Dra III	CAC,NNN`GTG	4
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	6
Eae I	Y`GGCC,R	9	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	2
EcoN I	CCTNN`N,NNAGG	1	Eco1019 I	RG`GNC,CY	3
EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	20
EcoR V	GAT ATC	1	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	2	Fnu4H I	GC`N,GC	57
Fok I	GGATG 14/18	19	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	1	Gdi II	`YGGC,CG	9
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	9
Hae II	R,CGCC`Y	10	Hae III	GG CC	26
Hga I	GACGC 9/14	9	HgiA I	G,WGCW`C	3
HgiE II	ACCNNNNNNGGT	-1/131	Hha I	G,CG`C	38
HinC II	GTY RAC	2	Hind II	GTY RAC	2
Hind III	A`AGCT,T	-	Hinf I	G`ANT,C	19
HinI I	GR`CG,YC	5	HinP I	G`CG,C	38
Hpa I	GTT AAC	-	Hpa II	C`CG,G	34
Hph I	GGTGA 12/11	11	Kas I	G`CGCC,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	17
Mae II	A`CG,T	21	Mae III	`GTNAC,	25
Mbo I	`GATC,	31	Mbo II	GAAGA 12/11	15
Mlu I	A`CGCC,T	-	Mme I	TCCRAC 25/23	3
Mnl I	CCTC 10/10	46	Msc I	TGG CCA	2
Mse I	T`TA,A	32	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	34	MspAl I	CMG CKG	7
Mun I	C`AATT,G	-	Nae I	GCC GGC	4
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	17
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	4	Nhe I	G`CTAG,C	1
Nla III	,CATG`	27	Nla IV	GGN NCC	20
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	6
NspB II	CMG CKG	7	NspH I	R,CATG`Y	6
PacI	TTA`AT,TAA	-	Paer7 I	C`TCGA,G	1
Pal I	GG CC	26	Pf1M I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	1	Pme I	CTTT AAAC	-
Pml I	CAC GTG	2	PpuM I	RG`GWC,CY	1
Psp1406 I	AA`CG,TT	1	PspA I	C`CCGG,G	5
Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	3
Pvu II	CAG CTG	2	Rsa I	GT AC	9
Rsr II	CG`GWC,CG	2	Sac I	G,AGCT`C	1
Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	-
Sap I	GCTCTTC 8/11	1	Sau3A I	`GATC,	31
Sau96 I	G`GNC,C	15	Sca I	AGT ACT	1
ScrF I	CC`N,GG	37	Sec I	C`CNNG,G	38
SfaN I	GCATC 9/13	18	Sfc I	C`TRYA,G	8
Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	5
SnaB I	TAC GTA	-	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	3
Stu I	AGG CCT	2	Sty I	C`CWVG,G	7
SwaI	ATTT AAAT	1	Taq I	T`CG,A	14
Tfi I	G`AWT,C	13	Tsp45 I	`GTSAC,	9
Tth111 I	GACN`N,NGTC	-	Tth111 II	CAARCA 16/14	7
Vsp I	AT`TA,AT	7	Xba I	T`CTAG,A	-
Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNTGG-	-
Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	8
Xma I	C`CCGG,G	5	Xma III	C`GGCC,G	2

Site usage in pBOK:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	-
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