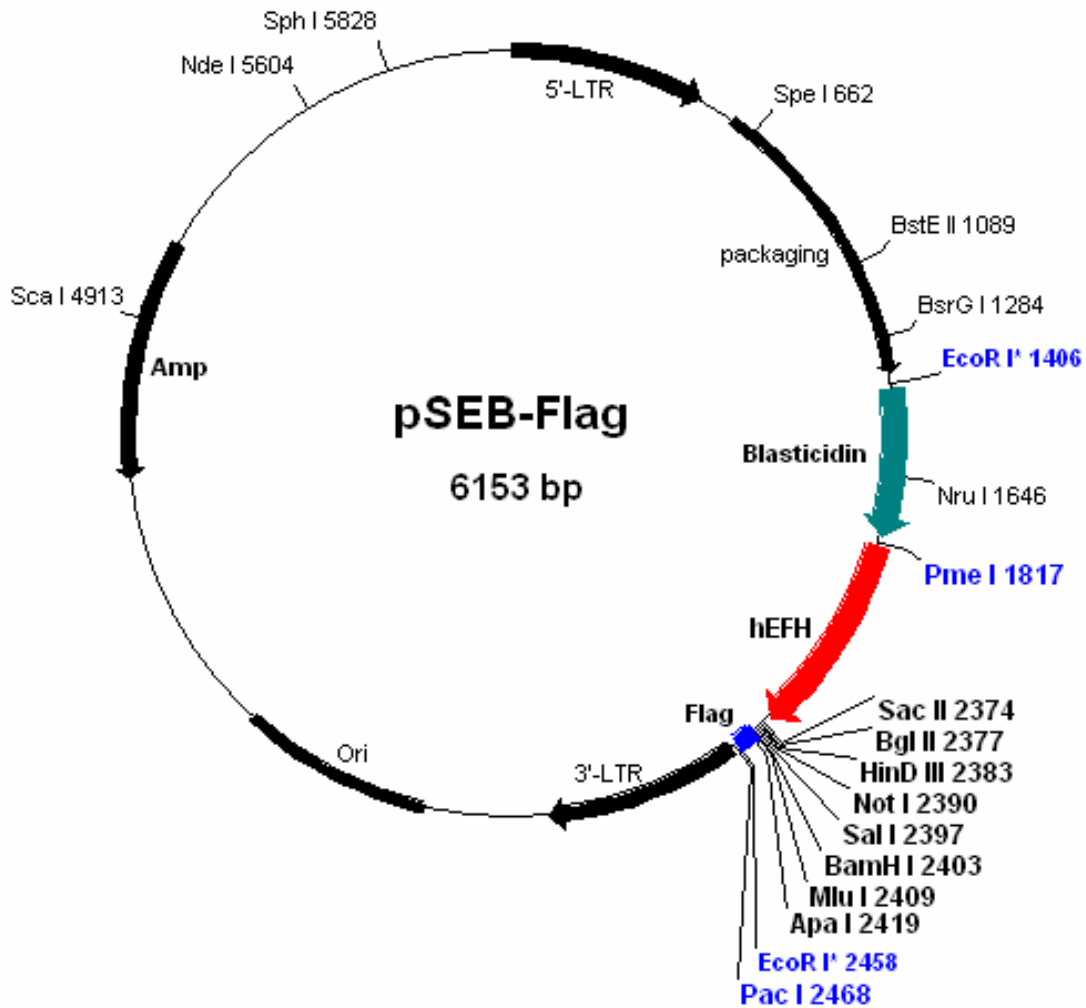


Vector: pSEB-Flag

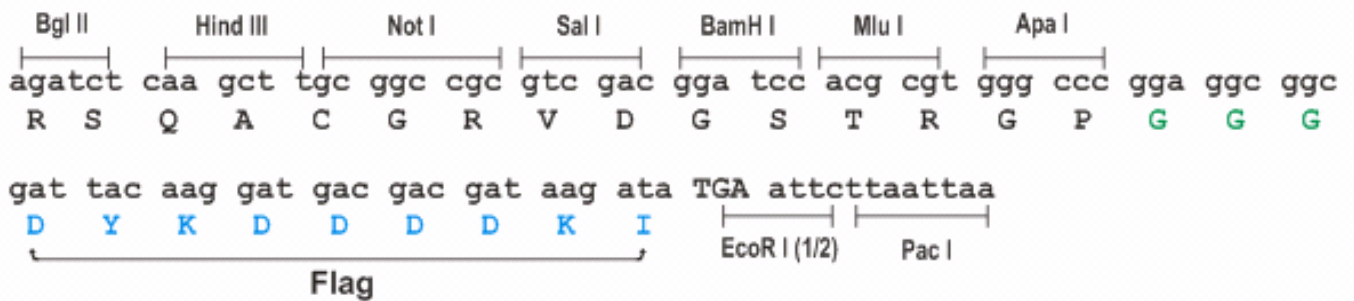
Antibiotic Selection: Amp

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

Date of Construction: Dec, 2005



Linker Sequence



pSEB-Flag (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACAC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGT AGATCAAGG
 TTCAAGACAGCAGACAGCAGAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCGGTCCC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCCAGGACCTGAAATGACCTTGTCCTTATTGAACTAACCAATCAGTTCGCTTCTCGCTTCT
 GTTCGCGCGTCTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCCAGTCTCCGATAGACTGCGTCCCGGGTACCCGATTTCCCAAT
 AAAGCCTCTG CTGTTTGCAT CGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG
 GTTCCACC GA TATTGGAGACCCCTGCCA GGGACCACCGACCCCGCCG CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGTCTTTGTG
 CGTGTTTGTGCCGGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTTGGTGAAGTACTGACGAGTTCCTGAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGACGAGAACCT AAAACGTACT CCGCCTCCGT CTGAATTTTGTCTTTCGGTT TGAACCCGAAGCCCGCGCT TTGTCTGCTG CAGCGCTGCA
 GCATCGTTCT GTGTTGTCT TGTCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTACCTTAGGTCAGT
 GAAAGATGTGAGCGGATCG CTCACAAACA GTCGGTAGAT FTCAAGAAAGAGACTGTTGGT TACCTTCTGC TCTGCAGAAAT GGCCAACCTTAAACGTCGGA
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 TCGTACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTAGACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT
 CCCCTTGAACCTCTCCTGTTGACCCCGCTCGATCTCCCTTATTCACGCCCTCACTCTTCTCTAGGCGCCGGAATTCACCATG GCCAAGCCTTTGTCTCAAGA
 AGAATCCACCCTCATTGAAAGACGACGGTACAATCAACAGCATCCCATCTCTGAAGACTACAGCTCGCCAGCGCAGCTCTCTTAGCCAGCGCCGATCTCTC
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 GCCGACGGCAGTTGGGATTCTGTAATTGCTGCCCTCTGTTTATGTTGGGAGGGCTaa **gtttaaacatg** **cagCGTCCCGTGCCTCAGTGGGAGAGCGCACAT**
CGCCACAGTCCCGAGAAGTTGGGGGAGGGTCCGCAATGAACCGGTGCCTAGAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGCTGCTACTGGTCCGCT
CCTTTTCCCGAGGGTGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACCGGGTTGGCCGAGAACACAGCTGAAGCTAGCTT**CG**
AGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGCGCCATCCACGCGGTTGAGTCCGCTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAT
CGCTCCGCTCTAGGTAAGTTAAAGCTCAGGTCCGACCGCGGCTTGTCCGCGCTCCCTTGAGGCTACCTAGACTCAGCCGCTTCCAGCTTTGCCTGA
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gcyg ccg cgt cya cgg atc cA CGC GT GGGCC gga ggc ggc gat tac aag gat gac gat aag ata TGA attc**taattaa**
CGATAAAAATAAAAGATTTTATTAGTCTCCAGAAAAGGGGGAATGAAAGACCCACCTGTAGTGTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAGGCATG
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TTAGCTCCCGTCCCAAC ATCAAGGGCA GTTACATGAT CCCCATGTT GTGCAAAAA GCGGTTAGCTCTTCCGGT TCCGATCTTGTGAGAAGTA
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AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTCCCGCGCTCAAT ACGGGATAAT ACCGCGCCACATAGCAGAACTTTAAAAGTG
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CATACTCTTCTTTTTCAAT ATATTGAAG CATTATACAG GGTATTGTCTCATGAGCGG ATACATATTGAATGATTT AGAAAATAAACAATAAGG
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GTCTCGCGG TTTCCGGTAT GACGGTAAAACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG TCTGTAAGCGGATCCCGGGAGCAGACAAGC
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AGTCAATTT GTTAAAGACA GGATATCAGTGGTCCAGCT CTAGTTTTGA CTCACAATA TCACCAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA
TAAAAGATTT TATTAGTCT CCAGAAAAG GGGGGA

Unique enzymes in pSEB-Flag:

Spe I	A ⁺ CTAG,T	662
BstE II	G ⁺ TNAC,C	1089
BsrG I	T ⁺ GTAC,A	1284
Nco I	C ⁺ CATG,G	1413
Bbv II	GAAGAC 7/11	1499
Bbs I	GAAGAC 8/12	1500
Nru I	TCG CGA	1646
BsaB I	GATNN NNATC	1713
Pme I	CTTT AAAC	1817
Mun I	C ⁺ AATT,G	1899
Age I	A ⁺ CGG,T	1906
Cla I	AT ⁺ CG,AT	2366
Sac II	CC,GC ⁺ GG	2374
Egl III	A ⁺ GATC,T	2377
Hind III	A ⁺ AGCT,T	2383
Not I	GC ⁺ GGCC,GC	2390

Sal I	G ⁺ TCGA,C	2397
Acc I	GT ⁺ MK,AC	2398
HinC II	GTY RAC	2399
Hind II	GTY RAC	2399
BamH I	G ⁺ GATC,C	2403
Mlu I	A ⁺ CGCG,T	2409
Bsp120 I	G ⁺ GGCC,C	2415
Apa I	G,GGCC ⁺ C	2419
Pac I	TTA,AT ⁺ TAA	2468
Sca I	AGT ACT	4913
Nde I	CA ⁺ TA,TG	5604
Sph I	G,CATG ⁺ C	5828
Number of enzymes = 28		

The following enzymes do not cut in pSEB-Flag:

Avr II	Bcl I	Blp I	BsaA I	BsiC I
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BsiW I	Bsm I	Bsp1286 I	BspM I	BspM II	766	1207	1587	1855
Bst1107 I	BstB I	BstX I	Dra III	Eco72 I	2689	2702	5834	
Esp I	Fse I	Hpa I	Nsi I	PaeR7 I	729	903	919	922
PflM I	Pml I	Rsr II	Sfi I	SnaB I	927	930	1135	1515
Spl I	Srf I	Stu I	Xca I	Xcm I	1534	1608	1611	1614
					1617	1620	1784	1825
					2045	2104	2119	2150
					2390	2393	2426	3365
					3446	3464	3467	3585
					3740	3883	3948	3951
					4157	4485	4824	4851
					4946	5175	5462	5571
					5675	5748		
					2415			
				BspL20 I (1)	2415			
				BspH I (4)	4260	5268	5373	5897
				Bsr I (18)	376	1032	1060	1548
					1572	1941	1962	2891
					3341	3947	3960	4074
					4480	4598	4641	4908
					5080	5786		
				BsrB I (4)	1044	3232	3473	5274
				BsrD I (2)	4494	4668		
				BsrG I (1)	1284			
				BssH II (4)	319	370	2834	2885
				BssS I (4)	1589	3713	5097	5404
				BstE II (1)	1089			
				BstN I (17)	243	550	737	750
					1171	1196	1219	1239
					1269	1719	2758	3280
					3568	3689	3702	5775
					6052			
				BstU I (26)	319	321	372	905
					907	1137	1646	1928
					2097	2142	2373	2395
					2411	2834	2836	2887
					3387	3389	3587	4168
					4498	4991	5323	5423
					5425	5528		
				BstY I (9)	2339	2377	2403	4181
					4192	4278	4290	5058
					5075			
				Bsu36 I (3)	783	1020	2113	
				Cac8 I (37)	28	32	321	372
					584	588	633	652
					1201	1510	1624	2066
					2080	2101	2264	2292
					2387	2543	2547	2836
					2887	3333	3362	3471
					3557	3594	4154	4545
					5558	5706	5726	5730
					5826	5867	5915	5957
					5987			
				Cfr10 I (8)	631	1906	2130	2262
					2353	4513	5976	5985
				Cla I (1)	2366			
				Csp6 I (8)	404	660	1285	1956
					2919	4912	5588	6099
				Dde I (23)	75	169	210	478
					783	1020	1292	1810
					2113	2207	2258	2381
					2590	2684	2725	2994
					3065	3815	4224	4390
					4930	5356	5591	
				Dpn I (28)	95	461	1048	1180
					1365	1649	1710	1724
					2341	2369	2379	2405
					2610	4108	4183	4194
					4202	4280	4292	4397
					4738	4756	4802	5060
					5077	5113	5698	5922
				DpnII (28)	93	459	1046	1178
					1363	1647	1708	1722
					2339	2367	2377	2403
					2608	4106	4181	4192
					4200	4278	4290	4395
					4736	4754	4800	5058
					5075	5111	5696	5920
				Dra I (5)	1817	2202	4299	4318
					5010			
				Drd I (3)	1502	3648	5517	
				Dsa I (4)	696	1413	2371	5858
				Eae I (11)	584	726	1111	1132
					1416	1531	2390	3379
					4821	5855	5987	
				Eag I (3)	726	1531	2390	
				Ear I (6)	1072	1313	3162	3424
					5228	5716		
				Eco47 III (3)	925	1828	5894	
				Eco57 I (5)	1511	2079	4087	5101
					6105			
				EcoN I (4)	786	1394	1917	2112
				EcoO109 I (6)	256	1221	1574	2771
					5409	5863		
				EcoR I (2)	1406	2458		
				EcoR II (17)	241	548	735	748
					1169	1194	1217	1237
					1267	1717	2756	3278
					3566	3687	3700	5773
					6050			
				EcoR V (3)	141	2656	6041	
				Ehe I (6)	1401	2358	5657	5840
					5954	5975		
				Fnu4H I (42)	729	903	919	922
					927	930	1135	1515
					1534	1608	1611	1614
					1617	1620	1784	1825
					2045	2104	2119	2150
					2390	2393	2426	3365
					3446	3464	3467	3585
					3740	3883	3948	3951
					4157	4485	4824	4851
					4946	5175	5462	5571
					5675	5748		
				Fok I (13)	425	1142	1302	1466
					1701	2109	2451	2939
					4399	4580	4867	5510
					5754			
				Fsp I (2)	4655	5678		
				Gdi II (11)	725	727	1131	1530
					1532	2389	2391	3380
					4820	5856	5988	
				Gsu I (3)	2484	4504	6122	
				Hae I (6)	586	1113	1418	3555
					3566	4018		

pSEB-Flag: sites sorted by name:

Aat II (2)	747	5355		
Acc I (1)	2398			
Acc65 I (2)	403	2918		
Aci I (69)	199	205	568	590
	690	729	862	903
	1044	1135	1201	1300
	1319	1357	1534	1616
	1683	1928	1965	2045
	2101	2104	2119	2150
	2157	2184	2371	2373
	2389	2393	2425	2714
	2720	3016	3230	3333
	3389	3399	3423	3466
	3473	3494	3585	3613
	3740	3759	3880	3990
	4125	4134	4496	4587
	4778	4824	4945	4989
	5066	5175	5274	5321
	5495	5534	5544	5570
	5608	5621	5647	5704
	5963			
Afl II (3)	35	1008	2550	
Afl III (2)	2409	3540		
Age I (1)	1906			
Aha II (9)	744	1400	2357	4970
	5352	5656	5839	5953
	5974			
Ahd I (4)	1022	2963	3009	4433
Alu I (33)	30	34	338	582
	670	678	1517	1622
	2058	2064	2068	2206
	2347	2385	2545	2549
	2853	3172	3205	3300
	3364	3482	3708	3798
	3844	4101	4622	4722
	4785	5464	5483	5728
	6084			
Alw I (16)	455	1053	1359	1729
	2335	2363	2399	2410
	4102	4188	4188	4285
	4286	4750	5065	5071
AlwN I (3)	159	2674	3956	
Apa I (1)	2419			
Apal I (3)	3854	5100	5597	
Apo I (3)	874	1406	2458	
Asc I (2)	370	2885		
Ase I (4)	3183	3311	3370	4605
Asp718 (2)	403	2918		
Ava I (7)	333	399	500	1873
	1975	2848	2914	
Ava II (13)	188	201	256	553
	692	1221	1574	2703
	2716	2771	4571	4793
	6048			
BamH I (1)	2403			
Ban I (17)	246	403	1144	1399
	1689	1834	1909	2165
	2356	2761	2918	3284
	4381	5655	5838	5952
	5973			
Ban II (9)	340	353	1679	2080
	2419	2855	2868	5905
	5919			
Bbe I (6)	1403	2360	5659	5842
	5956	5977		
Bbs I (1)	1500			
Bbv I (10)	933	941	1526	1631
	1836	3959	3962	4168
	4862	5473		
Bbv II (1)	1499			
Bcn I (16)	166	401	402	573
	726	2221	2420	2681
	2916	2917	3921	4617
	4968	5469	5504	5855
Bfa I (16)	31	221	663	675
	1396	1524	1914	2065
	2191	2253	2546	2736
	4035	4288	4623	6058
Bgl I (2)	4553	5671		
Bgl II (1)	2377			
Bpm I (3)	2483	4503	6121	
Bsa I (7)	478	532	1151	2209
	2971	2992	4494	
BsaB I (1)	1713			
BsaH I (9)	744	1400	2357	4970
	5352	5656	5839	5953
	5974			
BsaJ I (33)	163	242	252	399
	463	499	548	549
	696	735	736	748
	749	1169	1238	1247
	1267	1268	1413	1718
	1976	2240	2371	2678
	2757	2767	2914	2977
	3279	3700	5774	5852
	5858			
BsaW I (5)	1831	1906	3746	3893
	4724			
BseR I (4)	466	1295	1334	2980
Bsg I (2)	1602	2024		
BsiE I (10)	594	729	1534	1650
	2393	3456	3880	4803
	4952	5699		
BsiHKA I (6)	340	2855	3858	5019
	5104	5601		
BsmA I (22)	108	477	533	611
	736	834	951	1075
	1134	1152	1330	1433
	2210	2500	2623	2970
	2991	4495	5269	5422
	5466	6138		
BsmB I				

Hae II	(12)	927	1403	1830	2237	Mun I	(1)	1899					
		2360	3418	3788	5659	Nae I	(3)	633	2264	5987			
		5842	5896	5956	5977	Nar I	(6)	1400	2357	5656	5839		
Hae III	(31)	130	175	586	728			5953	5974				
		764	776	989	1113	Nci I	(16)	165	400	401	572		
		1134	1199	1418	1533			725	2220	2419	2680		
		2118	2223	2392	2417			2915	2916	3920	4616		
		2645	2690	3381	3555			4967	5468	5503	5854		
		3566	3584	4018	4476	Nco I	(1)	1413					
		4556	4823	5410	5708	Nde I	(1)	5604					
		5857	5865	5989		NgoM I	(3)	631	2262	5985			
Hga I	(12)	383	644	897	1493	Nhe I	(3)	30	2064	2545			
		2170	2385	2898	3650	Nla III	(18)	62	1207	1417	1824		
		4228	4960	5518	5987			2577	3031	3198	3544		
HgiA I	(6)	340	2855	3858	5019			4264	4755	4765	4843		
		5104	5601					4879	5272	5377	5461		
HgiE II	(2)	4119	5599					5828	5901				
Hha I	(43)	321	323	372	374	Nla IV	(39)	190	203	248	405		
		650	907	926	1402			523	554	694	763		
		1514	1829	1856	1928			895	1146	1223	1401		
		2099	2236	2331	2359			1575	1691	1836	1911		
		2836	2838	2887	2889			1963	2167	2246	2358		
		3164	3324	3389	3417			2405	2417	2705	2718		
		3450	3720	3787	3887			2763	2920	3286	3572		
		4061	4170	4563	4656			3611	4383	4477	4518		
		4993	5325	5425	5528			4729	5319	5657	5840		
		5658	5679	5812	5841			5864	5954	5975			
		5895	5955	5976		Not I	(1)	2390					
HinC II	(1)	2399				Nru I	(1)	1646					
HinD II	(1)	2399				Nsp7524 I	(4)	1820	3540	5457	5824		
HinD III	(1)	2383				NspB II	(12)	590	1622	2058	2373		
Hinf I	(17)	444	452	793	804			3016	3364	3882	4127		
		1439	1771	2137	2256			5068	5534	5728	6084		
		3075	3097	3118	3375			1824	3544	5461	5828		
		3440	3515	3911	4428	NspH I	(4)	1824	3544	5461	5828		
		6066				Pac I	(1)	2468					
HinI I	(9)	744	1400	2357	4970	Pal I	(31)	130	175	586	728		
		5352	5656	5839	5953			764	776	989	1113		
		5974						1134	1199	1418	1533		
HinP I	(43)	319	321	370	372			2118	2223	2392	2417		
		648	905	924	1400			2645	2690	3381	3555		
		1512	1827	1854	1926			3566	3584	4018	4476		
		2097	2234	2329	2357			4556	4823	5410	5708		
		2834	2836	2885	2887	Ple I	(4)	801	2145	3083	3919		
		3162	3322	3387	3415	Pme I	(1)	1817					
		3448	3718	3785	3885	PpuM I	(4)	256	1221	1574	2771		
		4059	4168	4561	4654	PspI406 I	(3)	2021	4659	5032			
		4991	5323	5423	5526	PspA I	(2)	399	2914				
		5656	5677	5810	5839	Pst I	(3)	923	931	1107			
		5893	5953	5974		Pvu I	(3)	1650	4803	5699			
Hpa II	(32)	165	400	571	632	Pvu II	(5)	1622	2058	3364	5728		
		725	1403	1832	1907			6084					
		2131	2219	2231	2263	Rsa I	(8)	405	661	1286	1957		
		2354	2419	2680	2915			2920	4913	5589	6100		
		3258	3747	3894	3920				2855				
		4110	4514	4548	4615	Sac I	(2)	340					
		4725	4967	5468	5502	Sac II	(1)	2374					
		5854	5977	5986	6001	Sal I	(1)	2397					
Hph I	(13)	1159	1185	1403	4277	Sap I	(2)	3162	3424				
		4504	4918	5126	5159	Sau3A I	(28)	93	459	1046	1178		
		5443	5452	5945	5990			1363	1647	1708	1722		
		6071						2339	2367	2377	2403		
Kas I	(6)	1399	2356	5655	5838			2608	4106	4181	4192		
		5952	5973					4200	4278	4290	4395		
Kpn I	(2)	407	2922					4736	4754	4800	5058		
Mae I	(16)	31	221	663	675	Sau96 I	(29)	5075	5111	5696	5920		
		1396	1524	1914	2065			128	173	188	201		
		2191	2253	2546	2736			256	553	692	762		
		4035	4288	4623	6058			775	987	1198	1221		
Mae II	(10)	744	1083	1124	2021			1574	2221	2415	2416		
		2304	4243	4659	5032			2643	2688	2703	2716		
		5352	5794					2771	4475	4554	4571		
Mae III	(20)	39	996	1024	1089			4793	5409	5706	5863		
		1233	2333	2349	2554	Sca I	(1)	4913					
		3032	3896	3959	4075	ScrF I	(33)	165	243	400	401		
		4358	4689	4747	4900			550	572	725	737		
Mbo I	(28)	93	459	1046	1178			750	1171	1196	1219		
		1363	1647	1708	1722			1239	1269	1719	2220		
		2339	2367	2377	2403			2419	2680	2758	2915		
		2608	4106	4181	4192			2916	3280	3568	3689		
		4200	4278	4290	4395			3702	3920	4616	4967		
		4736	4754	4800	5058			5468	5503	5775	5854		
		5075	5111	5696	5920			6052					
Mbo II	(14)	1088	1301	1447	1504	Sec I	(33)	163	242	252	399		
		1532	3178	3412	4201			463	499	548	549		
		4274	5029	5107	5216			696	735	736	748		
		5704	5916					749	1169	1238	1247		
Mlu I	(1)	2409						1267	1268	1413	1718		
Mme I	(6)	831	1108	2979	3031			1976	2240	2371	2678		
		3754	3938					2757	2767	2914	2977		
Mnl I	(52)	218	370	389	434			3279	3700	5774	5852		
		462	486	508	512	SfaN I	(21)	187	446	643	940		
		568	778	874	1170			1487	1544	1676	1722		
		1273	1306	1312	1315			2090	2702	2960	3636		
		1321	1351	1354	1369			4688	4881	5128	5489		
		1376	1392	1456	1797			5581	5619	5657	5973		
		1798	1882	1971	2066			5985					
		2108	2162	2178	2415	Sfc I	(10)	15	919	927	1103		
		2733	2885	2904	2949			1498	2530	3805	3996		
		2976	3000	3060	3389			4674	6092				
		3438	3648	3721	3972	Sma I	(2)	401	2916				
		4372	4453	4599	4805	Spe I	(1)	662					
		5400	5458	5718	6002	Sph I	(1)	5828					
Msc I	(3)	586	1113	1418		Ssp I	(2)	3083	5237				
Mse I	(26)	36	1009	1121	1151	Sty I	(7)	252	463	1247	1413		
		1175	1816	2201	2464			2240	2767	2977			
		2468	2551	3085	3183	Taq I	(12)	796	1040	1351	1362		
		3311	3370	4246	4298			1707	2071	2213	2366		
		4303	4317	4370	4605			2398	3078	3640	5084		
		4644	5009	5381	5562	Tfi I	(7)	444	804	1439	1771		
		5759	6029					3118	3375	3515			
Msl I	(2)	4685	4844			Tsp45 I	(7)	1024	1233	2349	4689		
Msp I	(32)	165	400	571	632			4900	5476	5787			
		725	1403	1832	1907	TthI11 I	(4)	392	813	1219	2907		
		2131	2219	2231	2263	TthI11 II	(9)	147	424	615	634		
		2354	2419	2680	2915			2280	2662	4129	4138		
		3258	3747	3894	3920			4168					
		4110	4514	4548	4615	Vsp I	(4)	3183	3311	3370	4605		
		4725	4967	5468	5502	Xba I	(2)	220	2735				
		5854	5977	5986	6001	Xho II	(9)	2339	2377	2403	4181		
MspAl I	(12)	590	1622	2058	2373			4192	4278	4290	5058		
		3016	3364	3882	4127			5075					
		5068	5534	5728	6084	Xma I	(2)	399	2914				

Xma III (3) 726 1531 2390
 Xmn I (3) 3146 3184 5032

Site usage in pSEB-Flag:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Acc II	C`CG,C	69
Ael II	C`TTAA,G	3	Ael III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	9
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	33
Alw I	GGATC 8/9	16	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	3
Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp178	G`GTAC,C	2
Ava I	C`YCGR,G	7	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	9
Bbe I	G,GGC`C	6	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	16
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GTCCTC 7/11	7
BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	33
BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	6
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	-
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	7
BsmA I	GTCCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	42
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BSSH II	G`CGCG,C	4
BSS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	17	BstU I	CG CG	26
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	37
Cer10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	8	Dde I	C`TNA,G	23
Dpn I	GA TC	28	DpnII	`GATC,	28
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,C	3
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	4	Eco109 I	RG`GNC,CY	6
EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	42

Fok I	GGATG 14/18	13	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	6
Hae II	R,CGCG`Y	12	Hae III	GG CC	31
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	6
HgiE II	ACCNNNNNGGT -1/132	-	Hha I	G,CG`C	43
Hinc II	GTY RAC	1	Hind II	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	17
HinI I	GR`CG,YC	9	HinP I	G`CG,C	43
Hpa I	GTT AAC	1	Hpa II	C`CG,G	32
Hph I	GGTGA 12/11	13	Kas I	G`GGCC,C	6
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Mae II	A`CG,T	10	Mae III	`GTNAC,	20
Mbo I	`GATC,	28	Mbo II	GAAGA 12/11	14
Mlu I	A`CGCG,T	1	Mme I	TCCRC 25/23	6
Mnl I	CCTC 10/10	52	Msc I	TGG CCA	3
Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	2
Nar I	GG`CG,CC	6	MspA I	CMG CKG	12
Nco I	C`CATG,G	1	Nae I	GCC GGC	3
NgoM I	G`CCGG,C	3	Nci I	CC`S,GG	16
Nla III	,CATG`	18	Nde I	CA`TA,TG	3
Not I	GC`GGCC,GC	1	Nhe I	G`CTAG,C	1
Nsi I	A,TGCA`T	-	Nla IV	GGN NCC	39
NspB II	CMG CKG	12	Nru I	TCG CGA	1
Pac I	TTA,AT TAA	1	Nsp7524 I	R`CATG,Y	4
Pal I	GG CC	31	NspH I	R,CATG`Y	4
Ple I	GAGTC 9/10	4	PaeR7 I	C`TCGA,G	-
Pml I	CAC GTG	-	Pf1M I	CCAN,NNN`NTGG	-
Psp1406 I	AA`CG,TT	3	Pme I	CTTT AAAC	1
Pst I	C,TGCA`G	3	PpuM I	RG`GWC,CY	4
Pvu II	CAG CTG	5	PspA I	C`CCGG,G	2
Rsr II	CG`GWC,CG	-	Pvu I	CG,AT`CG	3
Sac II	CC,GC`GG	1	Rsa I	GT AC	8
Sap I	GCTCTTC 8/11	2	Sac I	G,AGCT`C	2
Sau96 I	G`GNC,C	29	Sal I	G`TCGA,C	1
ScrF I	CC`N,GG	33	Sau3A I	`GATC,	28
SfaN I	GCATC 9/13	21	Sca I	AGT ACT	1
Sfi I	GGCCN,NNN`NGGCC	-	Sec I	C`CNNG,G	33
SnaB I	TAC GTA	1	Sfc I	C`TRYA,G	10
Sph I	G,CATG`C	1	Sma I	CCC GGG	2
Srf I	GCCC GGGC	-	Spe I	A`CTAG,T	1
Stu I	AGG CCT	-	Spl I	C`GTAC,G	2
Taq I	T`CG,A	12	Ssp I	AAT ATT	-
Tsp45 I	`GTSAC,	7	Sty I	C`CWMG,G	7
Tth111 II	CAARGA 16/14	9	Tfi I	G`AWT,C	7
Xba I	T`CTAG,A	2	Tth111 I	GACN`N,NGTC	4
Xho I	CCANNRN,N`NNNTGG-	9	Vsp I	AT`TA,AT	4
Xma I	R`GATC,Y	9	Xca I	GTA TAC	-
Xma III	C`GGCC,G	3	Xho I	C`TCGA,G	2
			Xma I	C`CCGG,G	2
			Xmn I	GAANN NNNTTC	3