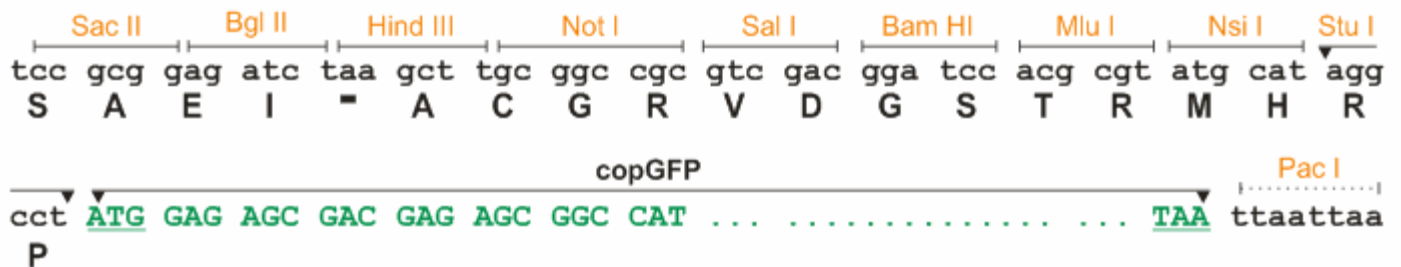
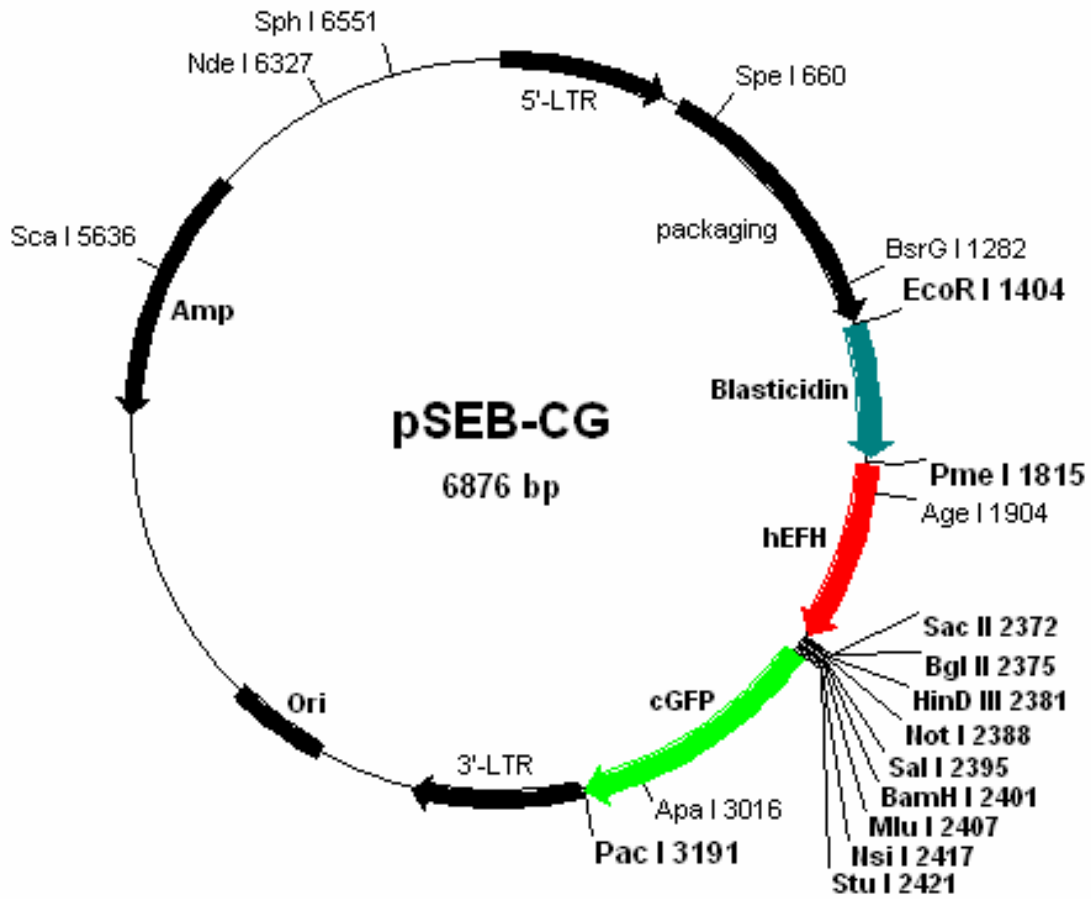


Vector: pSEB-CG (C-terminal copGFP tagged)

Antibiotic Selection: Amp

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

Date of Construction: November, 2007



pSEB-CG (C-terminal copGFP tag) Full-Length Sequence

TGAAAGACCC CACGTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTAGAGAA TAGAGAAAGTT AGATCAAGG
 TTAGGAACACAGACAGCAGATAATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTCCCGGGTCAAGGCAAGAACAGATGGTCCCGACAGATGCGGTCCCGC
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 AGTACGAGCCATAGATAAAA TAAAAGATTT TATTAGTCT CCAGAAAAAG GGGGGAA

Unique enzymes in pSEB-CG:

Spe I A`CTAG,T 660
 BstE II G`GTNAC,C 1087

BsrG I T`GTAC,A 1282
 EcoR I G`AATT,C 1404
 Bbv II GAAGAC 7/11 1497
 Bbs I GAAGAC 8/12 1498
 Nru I TCG|CGA 1644

BsaB I	GATNN NNATC	1711			2638	2800	3151	3484
Pme I	CTTT AAAC	1815			3641	4007	5104	6378
Mun I	C`AATT,G	1897			6561	6675	6696	
Age I	A`CCGG,T	1904	Ban II	(9)	338	351	1677	2078
Cla I	AT`CG,AT	2364			3016	3578	3591	6628
Sac II	CC,GC`GG	2372			6642			
Bgl II	A`GATC,T	2375	Bbe I	(7)	1401	2358	2579	6382
HinD III	A`AGCT,T	2381			6565	6679	6700	
Not I	GC`GGCC,GC	2388	Bbs I	(1)	1498			
Sal I	G`TCGA,C	2395	Bbv I	(12)	931	939	1524	1629
Acc I	GT`MK,AC	2396			1834	2861	2915	4682
HinC II	GTY RAC	2397			4685	4891	5585	6196
Hind II	GTY RAC	2397	Bbv II	(1)	1497			
BamH I	G`GATC,C	2401	Bcn I	(16)	164	399	400	571
Mlu I	A`CGCG,T	2407			724	2219	3165	3404
Nsi I	A,TGCA`T	2417			3639	3640	4644	5340
Stu I	AGG CCT	2421			5691	6192	6227	6578
Blp I	GC`TNA,GC	2602	Bfa I	(16)	31	219	661	673
Esp I	GC`TNA,GC	2602			1394	1522	1912	2063
PflM I	CCAN,NNN`NTGG	2613			2189	2251	3269	3459
Fse I	GG,CCGG`CC	2771			4758	5011	5346	6781
Bsp120 I	G`GGCC,C	3012	Bgl I	(2)	5276	6394		
Apa I	G,GGCC`C	3016	Bgl II	(1)	2375			
Xcm I	CCANNNN,N`NNNTGG3141		Blp I	(1)	2602			
Pac I	TTA,AT`TAA	3191	Bpm I	(3)	3206	5226	6844	
Sca I	AGT ACT	5636	Bsa I	(7)	476	530	1149	2207
Nde I	CA`TA,TG	6327			3694	3715	5217	
Sph I	G,CATG`C	6551	BsaA I	(2)	2610	2742		
Number of enzymes = 35			BsaB I	(1)	1711			
			BsaH I	(10)	742	1398	2355	2576
					5693	6075	6379	6562
					6676	6697		
			BsaJ I	(38)	161	240	250	397
					461	497	546	547
					694	733	734	746
					747	1167	1236	1245
					1265	1266	1411	1716
					1974	2238	2369	2456
					2813	2861	2879	3143
					3401	3480	3490	3637
					3700	4002	4423	6497
					6575	6581		
			BsaW I	(6)	1829	1904	3172	4469
					4616	5447		
			BseR I	(5)	464	1293	1332	3055
					3703			
			Bsg I	(6)	1600	2022	2656	2722
					2857	3031		
			BsiE I	(11)	592	727	1532	1648
					2391	2772	4179	4603
					5526	5675	6422	
			BsiHKA I	(8)	338	2569	2870	3578
					4581	5742	5827	6324
			BsmA I	(22)	107	475	531	609
					734	832	949	1073
					1132	1150	1328	1431
					2208	3223	3346	3693
					3714	5218	5992	6145
					6189	6861		
			BsmB I	(7)	733	831	1072	1131
					1329	6146	6188	
			BsmF I	(11)	172	185	564	729
					764	1205	1585	1853
					3412	3425	6557	
			BsoF I	(55)	727	901	917	920
					925	928	1133	1513
					1532	1606	1609	1612
					1615	1618	1782	1823
					2043	2102	2117	2148
					2388	2391	2442	2472
					2517	2544	2652	2691
					2730	2737	2772	2850
					2904	2937	3033	3046
					4088	4169	4187	4190
					4308	4463	4606	4671
					4674	4880	5208	5547
					5574	5669	5898	6185
					6294	6398	6471	
			Bsp120 I	(1)	3012			
			Bsp1286 I	(2)	2569	2870		
			BspH I	(4)	4983	5991	6096	6620
			BspM I	(2)	2606	2879		
			Bsr I	(18)	374	1030	1058	1546
					1570	1939	1960	3614
					4064	4670	4683	4797
					5203	5321	5364	5631
					5803	6509		
			BsrB I	(5)	1042	2441	3955	4196
					5997			
			BsrD I	(2)	5217	5391		
			BsrG I	(1)	1282			
			BssH II	(4)	317	368	3557	3608
			BssS I	(4)	1587	4436	5820	6127
			BstE II	(1)	1087			
			BstN I	(17)	241	548	735	748
					1169	1194	1217	1237
					1267	1717	3481	4003
					4291	4412	4425	6498
					6775			
			BstU I	(30)	317	319	370	903
					905	1135	1644	1926
					2095	2140	2371	2393
					2409	2774	2930	3035

The following enzymes do not cut in pSEB-CG:

Avr II	Bcl I	BsiC I	BsiW I	Bsm I
BspM II	Bst1107 I	BstB I	BstX I	Dra III
Hpa I	PaeR7 I	Rsr II	Sfi I	SnaB I

pSEB-CG: sites sorted by name:

Aat II	(2)	745	6078					
Acc I	(1)	2396						
Acc65 I	(2)	401	3641					
Aci I	(87)	197	203	566	588			
		688	727	860	901			
		1042	1133	1199	1298			
		1317	1355	1532	1614			
		1681	1926	1963	2043			
		2099	2102	2117	2148			
		2155	2182	2369	2371			
		2387	2391	2441	2453			
		2472	2516	2519	2544			
		2651	2690	2706	2729			
		2757	2772	2847	2913			
		2936	3030	3033	3120			
		3155	3437	3443	3739			
		3953	4056	4112	4122			
		4146	4189	4196	4217			
		4308	4336	4463	4482			
		4603	4713	4848	4857			
		5219	5310	5501	5547			
		5668	5712	5789	5898			
		5997	6044	6218	6257			
		6267	6293	6331	6344			
		6370	6427	6686				
				3273				
Afl II	(3)	35						
Afl III	(2)	2407	4263					
Age I	(1)	1904						
Aha II	(10)	742	1398	2355	2576			
		5693	6075	6379	6562			
		6676	6697					
Ahd I	(4)	1020	3686	3732	5156			
Alu I	(40)	30	34	336	580			
		668	676	1515	1620			
		2056	2062	2066	2204			
		2345	2383	2508	2747			
		2753	2906	2948	3045			
		3063	3268	3272	3576			
		3895	3928	4023	4087			
		4205	4431	4521	4567			
		4824	5345	5445	5508			
		6187	6206	6451	6807			
Alw I	(18)	453	1051	1357	1727			
		2333	2361	2397	2408			
		3111	3182	4825	4911			
		4911	5008	5009	5473			
		5788	5794					
			4679					
AlwN I	(2)	3397						
Apa I	(1)	3016						
ApaL I	(3)	4577	5823	6320				
Apo I	(2)	872	1404					
Asc I	(2)	368	3608					
Ase I	(5)	3187	3906	4034	4093			
		5328						
Asp718	(2)	401	3641					
Ava I	(8)	331	397	498	1871			
		1973	2812	3571	3637			
Ava II	(14)	186	199	254	551			
		690	1219	1572	3160			
		3426	3439	3494	5294			
		5516	6771					
BamH I	(1)	2401						
Ban I	(23)	244	401	1142	1397			
		1687	1832	1907	2163			
		2354	2482	2527	2575			

		3122	3557	3559	3610			6579	6711				
		4110	4112	4310	4891	Gsu I	(3)	3207	5227	6845			
		5221	5714	6046	6146	Hae I	(7)	584	1111	1416	2421		
		6148	6251					4278	4289	4741			
BstY I	(11)	2337	2375	2401	3115	Hae II	(14)	925	1401	1828	2235		
		3175	4904	4915	5001			2358	2579	2984	4141		
Bsu36 I	(3)	5013	5781	5798				4511	6382	6565	6619		
Cac8 I	(44)	781	1018	2111				6679	6700				
		28	32	319	370	Hae III	(36)	129	173	584	726		
		582	586	631	650			762	774	987	1111		
		1199	1508	1622	2064			1132	1197	1416	1531		
		2078	2099	2262	2290			2116	2221	2390	2421		
		2385	2453	2675	2734			2444	2543	2767	2771		
		2769	2913	2926	3086			3014	3368	3413	4104		
		3266	3270	3559	3610			4278	4289	4307	4741		
		4056	4085	4194	4280			5199	5279	5546	6133		
		4317	4877	5268	6281			6431	6580	6588	6712		
		6429	6449	6453	6549	Hga I	(12)	381	642	895	1491		
		6590	6638	6680	6710			2168	2383	3621	4373		
Cfr10 I	(11)	629	1904	2128	2260	HgiA I	(8)	4951	5683	6241	6710		
		2351	2479	2767	2803			338	2569	2870	3578		
		5236	6699	6708				4581	5742	5827	6324		
Cla I	(1)	2364				HgiE II	(2)	4842	6322				
Csp6 I	(10)	402	658	1283	1954	Hha I	(47)	319	321	370	372		
		2718	3078	3642	5635			648	905	924	1400		
		6311	6822					1512	1827	1854	1926		
Dde I	(25)	75	167	208	476			2097	2234	2329	2357		
		781	1018	1290	1808			2578	2930	2983	3124		
		2111	2205	2256	2379			3559	3561	3610	3612		
		2602	3125	3313	3407			3887	4047	4112	4140		
		3448	3717	3788	4538			4173	4443	4510	4610		
		4947	5113	5653	6079			4784	4893	5286	5379		
		6314						5716	6048	6148	6251		
Dpn I	(34)	94	459	1046	1178			6381	6402	6535	6564		
		1363	1647	1708	1722			6618	6678	6699			
		2339	2367	2377	2403	HinC II	(1)	2397					
		2464	2779	2827	2842	Hind II	(1)	2397					
		3117	3177	3333	4831	HinD III	(1)	2381					
		4906	4917	4925	5003	Hinf I	(17)	442	450	791	802		
		5015	5120	5461	5479			1437	1769	2135	2254		
		5525	5783	5800	5836			3798	3820	3841	4098		
		6421	6645					4163	4238	4634	5151		
DpnII	(34)	92	457	1044	1176			6789					
		1361	1645	1706	1720	HinI I	(10)	742	1398	2355	2576		
		2337	2365	2375	2401			5693	6075	6379	6562		
		2462	2777	2825	2840			6676	6697				
		3115	3175	3331	4829			317	319	368	370		
		4904	4915	4923	5001	HinP I	(47)	646	903	922	1398		
		5013	5118	5459	5477			1510	1825	1852	1924		
		5523	5781	5798	5834			2095	2232	2327	2355		
		6419	6643					2576	2928	2981	3122		
Dra I	(5)	1815	2200	5022	5041			3557	3559	3608	3610		
		5733						3885	4045	4110	4138		
Drd I	(3)	1500	4371	6240				4171	4441	4508	4608		
Dsa I	(8)	694	1411	2369	2456			4782	4891	5284	5377		
		2861	2879	3143	6581			5714	6046	6146	6249		
Eae I	(13)	582	724	1109	1130			6379	6400	6533	6562		
		1414	1529	2388	2442			6616	6676	6697			
		2769	4102	5544	6578	Hpa II	(37)	163	398	569	630		
		6710						723	1401	1830	1905		
Eag I	(4)	724	1529	2388	2769			2129	2217	2229	2261		
Ear I	(7)	1070	1311	2557	3885			2352	2480	2768	2804		
		4147	5951	6439				3158	3164	3173	3403		
Eco47 III	(3)	923	1826	6617				3638	3981	4470	4617		
Eco57 I	(8)	1509	2077	2572	2734			4643	4833	5237	5271		
		2905	4810	5824	6828			5338	5448	5690	6191		
Eco72 I	(2)	2610	2742					6225	6577	6700	6709		
EcoN I	(4)	784	1392	1915	2110			6724					
EcoO109 I	(8)	254	1219	1572	3012	Hph I	(15)	1157	1183	1401	2470		
		3013	3494	6132	6586			2824	5000	5227	5641		
EcoR I	(1)	1404						5849	5882	6166	6175		
EcoR II	(17)	239	546	733	746			6668	6713	6794			
		1167	1192	1215	1235	Kas I	(7)	1397	2354	2575	6378		
		1265	1715	3479	4001			6561	6675	6696			
		4289	4410	4423	6496	Kpn I	(2)	405	3645				
		6773				Mae I	(16)	31	219	661	673		
EcoR V	(3)	140	3379	6764				1394	1522	1912	2063		
Ehe I	(7)	1399	2356	2577	6380			2189	2251	3269	3459		
		6563	6677	6698				4758	5011	5346	6781		
Esp I	(1)	2602						742	1081	1122	2019		
Fnu4H I	(55)	727	901	917	920	Mae II	(13)	2302	2609	2741	2891		
		925	928	1133	1513			4966	5382	5755	6075		
		1532	1606	1609	1612			6517					
		1615	1618	1782	1823			39	994	1022	1087		
		2043	2102	2117	2148	Mae III	(20)	1231	2331	2347	3277		
		2388	2391	2442	2472			3755	4619	4682	4798		
		2517	2544	2652	2691			5081	5412	5470	5623		
		2730	2737	2772	2850			5811	6199	6490	6510		
		2904	2937	3033	3046			92	457	1044	1176		
		4088	4169	4187	4190	Mbo I	(34)	1361	1645	1706	1720		
		4308	4463	4606	4671			2337	2365	2375	2401		
		4674	4880	5208	5547			2462	2777	2825	2840		
		5574	5669	5898	6185			3115	3175	3331	4829		
		6294	6398	6471				4904	4915	4923	5001		
Fok I	(15)	423	1140	1300	1464			5013	5118	5459	5477		
		1699	2107	2830	2971			5523	5781	5798	5834		
		2983	3662	5122	5303			6419	6643				
		5590	6233	6477		Mbo II	(16)	1086	1299	1445	1502		
Fse I	(1)	2771						1530	2573	2821	3901		
Fsp I	(2)	5378	6401					4135	4924	4997	5752		
Gdi II	(14)	723	725	1129	1528			5830	5939	6427	6639		
		1530	2387	2389	2443	Mlu I	(1)	2407					
		2768	2770	4103	5543	Mme I	(6)	829	1106	3702	3754		

		4477	4661				2719	3079	3643	5636	
Mnl I	(57)	167	216	368	387		6312	6823			
		432	460	484	506	Sac I	(2)	338	3578		
		510	566	776	872	Sac II	(1)	2372			
		1168	1271	1304	1310	Sal I	(1)	2395			
		1313	1319	1349	1352	Sap I	(3)	2557	3885	4147	
		1367	1374	1390	1454	Sau3A I	(34)	92	457	1044	
		1795	1796	1880	1969			1361	1645	1706	
		2064	2106	2160	2176			2337	2365	2375	
		2517	2715	2757	2808			2462	2777	2825	
		3033	3456	3608	3627			3115	3175	3331	
		3672	3699	3723	3783			4904	4915	4923	
		4112	4161	4371	4444			5013	5118	5459	
		4695	5095	5176	5322			5523	5781	5798	
		5528	6123	6181	6441			6419	6643		
		6725				Sau96 I	(31)	127	171	186	
Msc I	(3)	584	1111	1416				254	551	690	
Mse I	(26)	36	1007	1119	1149			773	985	1196	
		1173	1814	2199	3187			1572	2219	2541	
		3191	3274	3808	3906			3013	3160	3366	
		4034	4093	4969	5021			3426	3439	3494	
		5026	5040	5093	5328			5277	5294	5516	
		5367	5732	6104	6285			6429	6586	6771	
		6482	6752			Sca I	(1)	5636			
Msl I	(2)	5408	5567			ScrF I	(33)	163	241	398	
Msp I	(37)	163	398	569	630			548	570	723	
		723	1401	1830	1905			748	1169	1194	
		2129	2217	2229	2261			1237	1267	1717	
		2352	2480	2768	2804			3164	3403	3481	
		3158	3164	3173	3403			3639	4003	4291	
		3638	3981	4470	4617			4425	4643	5339	
		4643	4833	5237	5271			6191	6226	6498	
		5338	5448	5690	6191			6775			
		6225	6577	6700	6709	Sec I	(38)	161	240	250	
		6724						461	497	546	
MspAl I	(13)	588	1620	2056	2371			694	733	734	
		2651	3739	4087	4605			747	1167	1236	
		4850	5791	6257	6451			1265	1266	1411	
		6807						1974	2238	2369	
Mun I	(1)	1897						2813	2861	2879	
Nae I	(4)	631	2262	2769	6710			3401	3480	3490	
Nar I	(7)	1398	2355	2576	6379			3700	4002	4423	
		6562	6676	6697		SfaN I	(25)	185	444	641	
Nci I	(16)	163	398	399	570			1485	1542	1674	
		723	2218	3164	3403			2088	2482	2716	
		3638	3639	4643	5339			3076	3425	3683	
		5690	6191	6226	6577			5411	5604	5851	
Nco I	(3)	1411	2456	2879				6304	6342	6380	
Nde I	(1)	6327						6708			
NgoM I	(4)	629	2260	2767	6708	Sfc I	(12)	15	917	925	
Nhe I	(3)	30	2062	3268				1496	2943	3001	
Nla III	(24)	62	1205	1415	1822			4528	4719	5397	
		2449	2460	2550	2883			399	3639		
		2970	3021	3300	3754	Sma I	(2)	660			
		3921	4267	4987	5478	Spe I	(1)	6551			
		5488	5566	5602	5995	Sph I	(1)	3806	5960		
		6100	6184	6551	6624	Ssp I	(2)	2421			
Nla IV	(49)	188	201	246	403	Stu I	(1)	250	461	1245	
		521	552	692	761	Sty I	(9)	2238	2456	2879	
		893	1144	1221	1399			3700		3490	
		1573	1689	1834	1909			794	1038	1349	
		1961	2165	2244	2356	Taq I	(15)	1705	2069	2211	
		2403	2484	2529	2577			2396	2465	2504	
		2640	2802	3013	3014			3801	4363	5807	
		3015	3153	3162	3168			442	802	1437	
		3428	3441	3486	3643	Tfi I	(7)	3841	4098	4238	
		4009	4295	4334	5106			1022	1231	2347	
		5200	5241	5452	6042	Tsp45 I	(7)	5623	6199	6510	
		6380	6563	6587	6677			390	811	1217	
		6698				Tth111 I	(4)	146	422	613	
Not I	(1)	2388				Tth111 II	(10)	2278	2550	3385	
Nru I	(1)	1644						4861	4891	4852	
Nsi I	(1)	2417				Vsp I	(5)	3187	3906	4034	
Nsp7524 I	(5)	1818	2966	4263	6180			5328		4093	
		6547				Xba I	(2)	218	3458		
NspB II	(13)	588	1620	2056	2371	Xcm I	(1)	3141			
		2651	3739	4087	4605	Xho II	(11)	2337	2375	2401	
		4850	5791	6257	6451			3175	4904	4915	
		6807						5013	5781	5798	
NspH I	(5)	1822	2970	4267	6184			397	3637		
		6551				Xma I	(2)	724	1529	2388	
Pac I	(1)	3191				Xma III	(4)	2665	3869	3907	
Pal I	(36)	129	173	584	726	Xmn I	(4)				
		762	774	987	1111						
		1132	1197	1416	1531						
		2116	2221	2390	2421						
		2444	2543	2767	2771						
		3014	3368	3413	4104						
		4278	4289	4307	4741						
		5199	5279	5546	6133						
		6431	6580	6588	6712						
PflM I	(1)	2613				Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Ple I	(4)	799	2143	3806	4642	Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	87
Pme I	(1)	1815				Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Pml I	(2)	2610	2742			Age I	A`CCGG,T	1	Aha II	GR`CG,YC	10
PpuM I	(4)	254	1219	1572	3494	Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	40
Psp1406 I	(3)	2019	5382	5755		Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
PspA I	(2)	397	3637			Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Pst I	(4)	921	929	1105	3005	Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Pvu I	(3)	1648	5526	6422		Ase I	AT`TA,AT	5	Asp718	G`GTAC,C	2
Pvu II	(5)	1620	2056	4087	6451	Ava I	C`YCGR,G	8	Ava II	G`GWC,C	14
		6807				Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Rsa I	(10)	403	659	1284	1955	Ban I	G`GYRC,C	23	Ban II	G,RCGY`C	9
						Bbe I	G,CGCG`C	7	Bbs I	GAAAGC 8/12	1
						Bbv I	GCAGC 13/17	12	Bbv II	GAAAGC 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	1

Site usage in pSEB-CG:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	87
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	40
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	5	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	23	Ban II	G,RCGY`C	9
Bbe I	G,CGCG`C	7	Bbs I	GAAAGC 8/12	1
Bbv I	GCAGC 13/17	12	Bbv II	GAAAGC 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	1

Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	2	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	10	BsaJ I	C`CNGG,G	38
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	5
Bsg I	GTGCAG 22/20	6	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	11	BsiHKA I	G,WGCW`C	8
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	55
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	2
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
BssS 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	30
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	11
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	44
Cfr10 I	R`CCGG,Y	11	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	10	Dde I	C`TNA,G	25
Dpn I	GA TC	34	DpnII	`GATC,	34
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	8
Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	4
Ear I	CTCTTC 7/10	7	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	2
EcoN I	CCTNN`N,NNAGG	4	Eco109 I	RG`GNC,CY	8
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	7
Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	55
Fok I	GGATG 14/18	15	Fse I	GG,CCGG`CC	1
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	14
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7
Hae II	R,GC`C`Y	14	Hae III	GG CC	36
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	8
HgiE II	ACCCNNNNNGGT -1/132	-	Hha I	G,CG`C	47
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	10	HinP I	G`CG,C	47
Hpa I	GTT AAC	-	Hpa II	C`CG,G	37
Hph I	GGTGA 12/11	15	Kas I	G`GCGC,C	7
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Mae II	A`CG,T	13	Mae III	`GTNAC,	20
Mbo I	`GATC,	34	Mbo II	GAAGA 12/11	16
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	57	Msc I	TGG CCA	3
Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	2
Msp I	C`CG,G	37	MspAl I	CMG CKG	13
Mun I	C`AATT,G	1	Nae I	GCC GGC	4
Nar I	GG`CG,CC	7	Nci I	CC`S,GG	16
Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1
Ngom I	G`CCGG,C	4	Nhe I	G`CTAG,C	3
Nla III	,CATG`	24	Nla IV	GGN NCC	49
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	5
NspB II	CMG CKG	13	NspH I	R,CATG`Y	5
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-
Pal I	GG CC	36	PflM I	CCAN,NNN`NTGG	1
Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
Pml I	CAC GTG	2	PpuM I	RG`GWC,CY	4
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Pvu II	CAG CTG	5	Rsa I	GT AC	10
Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	34
Sau96 I	G`GNC,C	31	Sca I	AGT ACT	1
ScrF I	CC`N,GG	33	Sec I	C`CNGG,G	38
SfaN I	GCATC 9/13	25	Sfc I	C`TRYA,G	12
Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`CWVG,G	9
Taq I	T`CG,A	15	Tfi I	G`AWT,C	7
Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	5
Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNTGG1	-	Xho I	C`TCGA,G	-
Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	2
Xma III	C`GGCC,G	4	Xmn I	GAANN NNTTC	4