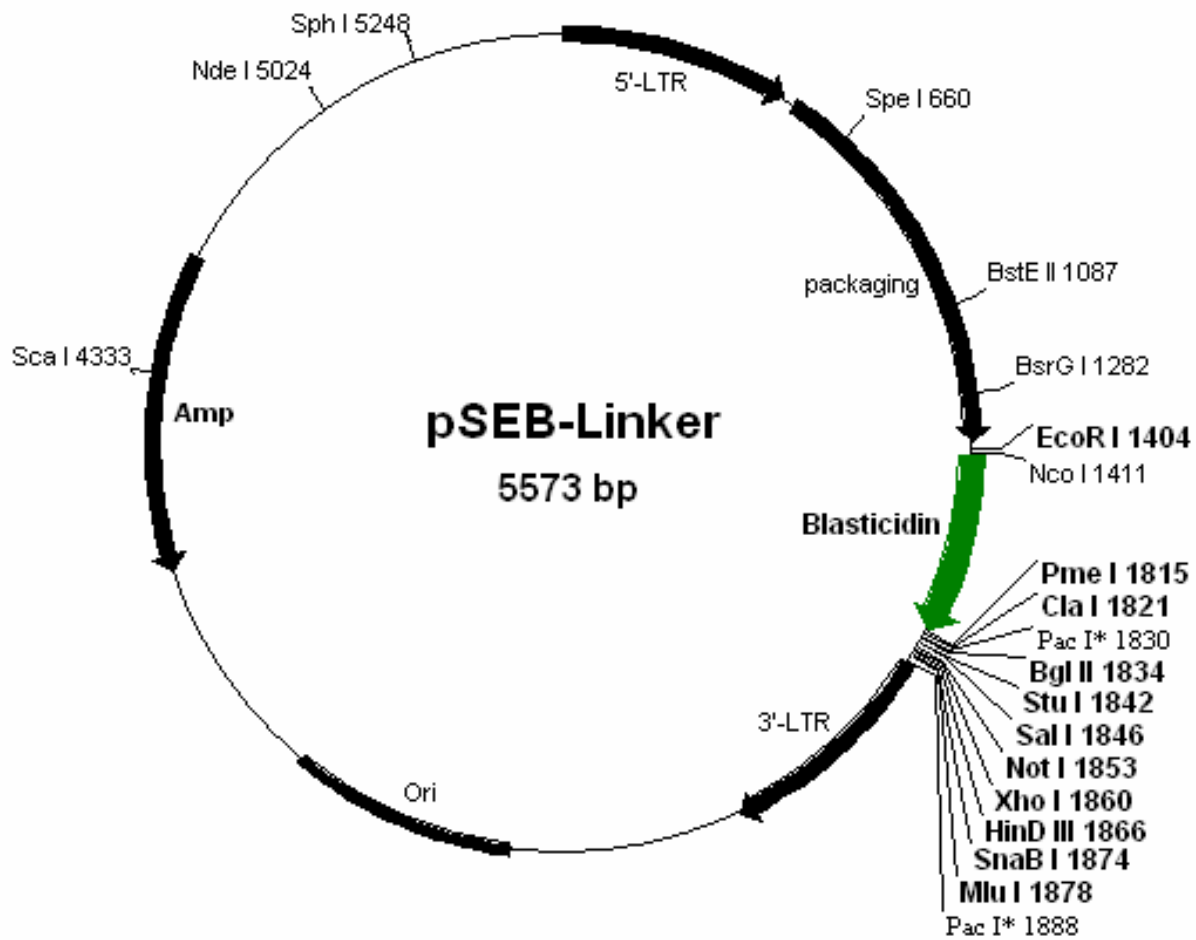


Vector: pSEB-Linker

Antibiotic Selection: Amp

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

Date of Construction: Dec, 2005



pSEB-Linker Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGAAGACAGAGACAGCAGATAATGGGCCAACAGCAGGATATCTGTGTAAGCAGTTCCTCCCGGCTCAGGGCCAAAGAACAGATGGTCCCAGATGCGGTCCC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCTCAGGACCTGAAATGACCTTGCCCTATTGAACTAACCAATCAGTTCGCTTCTCGCTTCT
 GTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATTTCCCAAT
 AAAGCCTCTTG CTGTTTGCAT CGGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG
 GTTCCACCAG GATTGGAGACCCCTGCCA GGGACCACCGACCCCGCG CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGTCTTTGTG
 CGTGTTTGTGCCGGCATCTAAGTTTGCCTGCGCTGCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGAAGTGAAGTGAACACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAGGATATGTGGTT
 CTGGTAGGAGACGAGAACCCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTCGGTT TGAACCCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGCA
 GCATCGTTCT GTGTTGTCTC TGTCTGACTGTGTTTCTGTA TTTGCTGAA AATTAGGGCC AGACTGTTC CACTCCCTTAAGTTTACCTTAGGTCACTG
 GAAAGATGTCGAGCGGATCG CTCACAACA GTCGGTAGA GTCAAGAAAGAGACGTTGGGT TACCTTCTGC TCTGCAGAAAT GGCCAACCTTAAACGTCGGA
 TGGCCGCGAGACGGCACCT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACTGGCCCGCATGGACA CCCAGACCAGGTCCCCTACA
 TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTAGACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT
 CCCCCTTGAACCTCCTCGTTTCGACCCCGCTCGATCCTCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCCGGAATTCACCAATG
 AGAATCCACCCTCATTGAAAGACCAACGGTACAATCAACAGCATCCCATCTCTGAAGACTACAGCTCGCCAGCGCAGCTCTCTTAGCCAGCGCCGATCTCTC
 ACTGGTGTCAATGTATATCATTTTACTGGGGACCTTGTGCAGAATCTGTGTGCTGGGCACTGCTGCTGCGCAGCTGGCAACCTGATTTGATCTCGTCGGA
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 GCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTaa**gtttaaac** at cga ttt aat taa aga tct agg cct gtc
gacgcgccgctcgagaagcttaagtaagcgtttaataaCGATAAAATAAAGATTTTATTAGTCTCCAGAAAAGGGGGGAATGAAAGACCCCACTGTA
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 TCGGCAACG CGCGGGAGA GCGGTTTTGCGTATTGGGCG CTCTTCCGCT TCTCCGCTCA CTGACTCGCTGCGCTCGGT GTTCCGCTGCGCGCCGCGGT
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 TATAAAGATACAGGCGCTTT CCCCCTGGAAGCTCCCTCGT CGCTCTCT GTTCCGACC TTCCGCTTAC CGGATACCTG TCCGCTTTCTCCCTCCGG
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 GACCGCTGCGCTTATCCGG TAACTATCGT CTGAGTCCA ACCCGGTAAGACAGACTTA TCGCCACTGGCAGCAGCCAC TGGTAACAGG ATTAGCAGAG
 CGAGGTATGT AGGCGGTGCT ACAGAGTCTTGAAGTGTG GCCTAATACGCTACACTA GAAGGACAGT ATTTGGTATC TCGCTCTGCTGAAGCCAGT
 TACCTTCGGAAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCGCTGGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTACGCGCAGAAAA
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 GGATCTTAC CTAGATCCTT TTAATTAATAAATGAAGTTT TAAATCAATCTAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAATGCTTAATCAG
 TGAGGACACCT ATCTCAGGCA TCTGCTATTTCTGTTTATCC ATAGTTCGCTGACTCCCGT CGTGTAGATA ACTACGATAC GGGAGGGAATACCATTCTGC
 CCCAGTGTGCAATGATACC GCGAGACCCAGCTCACCGG CTCCAGATTT ATCAGCAATA AACACCCAGCCGGAAGGC CGAGCGCAGAAGTGGTCTGC
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 AGGCATCGTG GTGTCACGCT CGTCTGTTGGTATGGCTTCA TTCAGCTCCGGTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCATGTTGTGCAAAAA
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 TGCCATCCGTAAGATGCTTT TCTGTGACTGTTGAGTACT AACCAAGTCA TTCTGAGAAT AGTGTATGCG GCGACCCAGT TGCTTTGCCCCGCTCAAT
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 GTTTTTCCCA GTACAGCGT TGTAAAACGACGGCGCAAG AATGGTGCAT GCAAGGAGAT GGGCCCAACGATCCCGCG CCACGGGGCTGCCACATA
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 CGGTGATGCCGGCCAGGAT CGTCCGGCTAGAGGCGATT AGTCCAATTT GTTAAAGACA GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTCAACAATA
 TCACCAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA TAAAGATTT TATTTACTCT CCAGAAAAAG GGGGGA

Unique enzymes in pSEB-Linker:

Spe I	A`CTAG,T	660
BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
EcoR I	G`AATT,C	1404
Nco I	C`CATG,G	1411
Bbv II	GAAGAC 7/11	1497
Bbs I	GAAGAC 8/12	1498
Bsg I	GTGCG 22/20	1600
Nru I	TCG CGA	1644
BsaB I	GATNN NNATC	1711
Pme I	CTTT AAAC	1815
Cla I	AT`CG,AT	1821
Bgl II	A`GATC,T	1834
Stu I	AGG CCT	1842
Sal I	G`TCGA,C	1846
Acc I	GT`MK,AC	1847
HinC II	GTY CAC	1848
Hind II	GTY CAC	1848
Not I	GC`GGCC,GC	1853
PaeR7 I	C`TCGA,G	1860
Xho I	C`TCGA,G	1860
Hind III	A`AGCT,T	1866

BsaA I	YAC GTR	1874
SnaB I	TAC GTA	1874
Mlu I	A`CGCG,T	1878
Sca I	AGT ACT	4333
Nde I	CA`TA,TG	5024
Sph I	G,CATG`C	5248
Number of enzymes = 28		

The following enzymes do not cut in pSEB-Linker:

Age I	Apa I	Avr II	BamH I	Bcl I
Blp I	BsiC I	BsiW I	Bsm I	Bsp120 I
Bsp1286 I	BspM I	BspM II	Bst1107 I	BstB I
BstX I	Dra III	Eco72 I	Esp I	Fse I
Hpa I	Mun I	Nsi I	PflM I	Pml I
Rsr II	Sac II	Sfi I	Spl I	Srf I

pSEB-Linker: sites sorted by name:

Aat II	(2)	745	4775
Acc I	(1)	1847	
Acc65 I	(2)	401	2338
Aci I	(57)	197	203 566 588

		688	727	860	901			2887	3005	3160	3303
		1042	1133	1199	1298			3368	3371	3577	3905
		1317	1355	1532	1614			4244	4271	4366	4595
		1681	1852	1856	2134			4882	4991	5095	5168
		2140	2436	2650	2753					4793	5317
		2809	2819	2843	2886	BspH I	(4)	3680	4688	4793	5317
		2893	2914	3005	3033	Bsr I	(16)	374	1030	1058	1546
		3160	3179	3300	3410			1570	2311	2761	3367
		3545	3554	3916	4007			3380	3494	3900	4018
		4198	4244	4365	4409			4061	4328	4500	5206
		4486	4595	4694	4741	BsrB I	(4)	1042	2652	2893	4694
		4915	4954	4964	4990	BsrD I	(2)	3914	4088		
		5028	5041	5067	5124	BsrG I	(1)	1282			
		5383				BssH II	(4)	317	368	2254	2305
Afl II	(3)	35	1006	1970		BssS I	(4)	1587	3133	4517	4824
Afl III	(2)	1878	2960			BstE II	(1)	1087			
Aha II	(8)	742	1398	4390	4772	BstN I	(17)	241	548	735	748
Ahd I	(4)	1020	2383	2429	3853			1169	1194	1217	1237
Alu I	(28)	30	34	336	580			1267	1717	2178	2700
		668	676	1515	1620			2988	3109	3122	5195
		1868	1965	1969	2273	BstU I	(22)	317	319	370	903
		2592	2625	2720	2784			905	1135	1644	1852
		2902	3128	3218	3264			1880	2254	2256	2307
		3521	4042	4142	4205			2807	2809	3007	3588
		4884	4903	5148	5504			3918	4411	4743	4843
Alw I	(12)	453	1051	1357	1727	BstY I	(7)	4845	4948		
		3522	3608	3608	3705			1834	3601	3612	3698
		3706	4170	4485	4491			3710	4478	4495	
AlwN I	(2)	2094	3376			Bsu36 I	(2)	781	1018		
ApaL I	(3)	3274	4520	5017		Cac8 I	(31)	28	32	319	370
Apo I	(2)	872	1404					582	586	631	650
Asc I	(2)	368	2305					1199	1508	1622	1963
Ase I	(4)	2603	2731	2790	4025			1967	2256	2307	2753
Asp718	(2)	401	2338					2782	2891	2977	3014
Ava I	(6)	331	397	498	1860			3574	3965	4978	5126
		2268	2334					5146	5150	5246	5287
Ava II	(13)	186	199	254	551	Cfr10 I	(4)	5335	5377	5407	
		690	1219	1572	2123			629	3933	5396	5405
		2136	2191	3991	4213	Cla I	(1)	1821			
		5468				Csp6 I	(7)	402	658	1283	2339
Ban I	(13)	244	401	1142	1397			4332	5008	5519	
		1687	2181	2338	2704	Dde I	(19)	75	167	208	476
		3801	5075	5258	5372			781	1018	1290	1808
		5393						2010	2104	2145	2414
Ban II	(7)	338	351	1677	2275			2485	3235	3644	3810
Bbe I	(5)	1401	5079	5262	5376	Dpn I	(25)	4350	4776	5011	
		5397						94	459	1046	1178
Bbs I	(1)	1498						1363	1647	1708	1722
Bbv I	(9)	931	939	1524	1629			1836	2030	3528	3603
		3379	3382	3588	4282			3614	3622	3700	3712
		4893						3817	4158	4176	4222
Bbv II	(1)	1497						4480	4497	4533	5118
Bcn I	(14)	164	399	400	571	DpnII	(25)	5342			
		724	2101	2336	2337			92	457	1044	1176
		3341	4037	4388	4889			1361	1645	1706	1720
		4924	5275					1834	2028	3526	3601
Bfa I	(13)	31	219	661	673			3612	3620	3698	3710
		1394	1522	1838	1966			3815	4156	4174	4220
		2156	3455	3708	4043			4478	4495	4531	5116
		5478						5340			
Bgl I	(2)	3973	5091			Dra I	(4)	1815	3719	3738	4430
Bgl II	(1)	1834				Drd I	(3)	1500	3068	4937	
Bpm I	(3)	1903	3923	5541		Dsa I	(3)	694	1411	5278	
Bsa I	(6)	476	530	1149	2391	Eae I	(11)	582	724	1109	1130
		2412	3914					1414	1529	1853	2799
BsaA I	(1)	1874						4241	5275	5407	
BsaB I	(1)	1711				Eag I	(3)	724	1529	1853	
BsaH I	(8)	742	1398	4390	4772	Ear I	(6)	1070	1311	2582	2844
		5076	5259	5373	5394			4648	5136		
BsaJ I	(30)	161	240	250	397	Eco47 III	(2)	923	5314		
		461	497	546	547	Eco57 I	(4)	1509	3507	4521	5525
		694	733	734	746	EcoN I	(2)	784	1392		
		747	1167	1236	1245	EcoO109 I	(6)	254	1219	1572	2191
		1265	1266	1411	1716			4829	5283		
		2098	2177	2187	2334	EcoR I	(1)	1404			
		2397	2699	3120	5194	EcoR II	(17)	239	546	733	746
		5272	5278					1167	1192	1215	1235
BsaW I	(3)	3166	3313	4144				1265	1715	2176	2698
BseR I	(4)	464	1293	1332	2400			2986	3107	3120	5193
Beg I	(1)	1600				EcoR V	(3)	5470			
BsiE I	(10)	592	727	1532	1648	Ehe I	(5)	140	2076	5461	
		1856	2876	3300	4223			1399	5077	5260	5374
		4372	5119					5395			
BsiHKA I	(6)	338	2275	3278	4439	Fnu4H I	(36)	727	901	917	920
		4524	5021					925	928	1133	1513
BsmA I	(21)	107	475	531	609			1532	1606	1609	1612
		734	832	949	1073			1615	1618	1782	1853
		1132	1150	1328	1431			1856	2785	2866	2884
		1920	2043	2390	2411			2887	3005	3160	3303
		3915	4689	4842	4886			3368	3371	3577	3905
		5558						4244	4271	4366	4595
BsmB I	(7)	733	831	1072	1131			4882	4991	5095	5168
		1329	4843	4885				4882	4991	5095	5168
BsmF I	(10)	172	185	564	729			4882	4991	5095	5168
		764	1205	1585	2109			423	1140	1300	1464
		2122	5254					1699	2359	3819	4000
BsoF I	(36)	727	901	917	920			4287	4930	5174	
		925	928	1133	1513	Fsp I	(2)	4075	5098		
		1532	1606	1609	1612	Gdi II	(11)	723	725	1129	1528
		1615	1618	1782	1853			1530	1852	1854	2800
		1856	2785	2866	2884			4240	5276	5408	
						Gsu I	(3)	1904	3924	5542	
						Hae I	(7)	584	1111	1416	1842
								2975	2986	3438	
						Hae II	(9)	925	1401	2838	3208

		5079	5262	5316	5376	Msp I	(24)	163	398	569	630
		5397						723	1401	2100	2335
Hae III	(29)	129	173	584	726			2678	3167	3314	3340
		762	774	987	1111			3530	3934	3968	4035
		1132	1197	1416	1531			4145	4387	4888	4922
		1842	1855	2065	2110			5274	5397	5406	5421
		2801	2975	2986	3004	MspAl I	(10)	588	1620	2436	2784
		3438	3896	3976	4243			3302	3547	4488	4954
		4830	5128	5277	5285			5148	5504		
		5409				Nae I	(2)	631	5407		
Hga I	(11)	381	642	895	1491	Nar I	(5)	1398	5076	5259	5373
		1857	2318	3070	3648			5394			
		4380	4938	5407		Nci I	(14)	163	398	399	570
HgiA I	(6)	338	2275	3278	4439			723	2100	2335	2336
		4524	5021					3340	4036	4387	4888
HgiE II	(2)	3539	5019					4923	5274		
Hha I	(36)	319	321	370	372	Nco I	(1)	1411			
		648	905	924	1400	Nde I	(1)	5024			
		1512	2256	2258	2307	NgoM I	(2)	629	5405		
		2309	2584	2744	2809	Nhe I	(2)	30	1965		
		2837	2870	3140	3207	Nla III	(17)	62	1205	1415	1997
		3307	3481	3590	3983			2451	2618	2964	3684
		4076	4413	4745	4845			4175	4185	4263	4299
		4948	5078	5099	5232			4692	4797	4881	5248
		5261	5315	5375	5396			5321			
HinC II	(1)	1848				Nla IV	(31)	188	201	246	403
Hind II	(1)	1848						521	552	692	761
HinD III	(1)	1866						893	1144	1221	1399
Hinf I	(15)	442	450	791	802			1573	1689	2125	2138
		1437	1769	2495	2517			2183	2340	2706	2992
		2538	2795	2860	2935			3031	3803	3897	3938
		3331	3848	5486				4149	4739	5077	5260
HinI I	(8)	742	1398	4390	4772			5284	5374	5395	
		5076	5259	5373	5394	Not I	(1)	1853			
HinP I	(36)	317	319	368	370	Nru I	(1)	1644			
		646	903	922	1398	Nsp7524 I	(3)	2960	4877	5244	
		1510	2254	2256	2305	NspB II	(10)	588	1620	2436	2784
		2307	2582	2742	2807			3302	3547	4488	4954
		2835	2868	3138	3205			5148	5504		
		3305	3479	3588	3981	NspH I	(3)	2964	4881	5248	
		4074	4411	4743	4843	Pac I	(2)	1830	1888		
		4946	5076	5097	5230	PaeR7 I	(1)	1860			
		5259	5313	5373	5394	Pal I	(29)	129	173	584	726
Hpa II	(24)	163	398	569	630			762	774	987	1111
		723	1401	2100	2335			1132	1197	1416	1531
		2678	3167	3314	3340			1842	1855	2065	2110
		3530	3934	3968	4035			2801	2975	2986	3004
		4145	4387	4888	4922			3438	3896	3976	4243
		5274	5397	5406	5421			4830	5128	5277	5285
Hph I	(13)	1157	1183	1401	3697			5409			
		3924	4338	4546	4579	Ple I	(3)	799	2503	3339	
		4863	4872	5365	5410	Pme I	(1)	1815			
		5491				PpuM I	(4)	254	1219	1572	2191
Kas I	(5)	1397	5075	5258	5372	Psp1406 I	(2)	4079	4452		
		5393				PspA I	(2)	397	2334		
Kpn I	(2)	405	2342			Pst I	(3)	921	929	1105	
Mae I	(13)	31	219	661	673	Pvu I	(3)	1648	4223	5119	
		1394	1522	1838	1966	Pvu II	(4)	1620	2784	5148	5504
		2156	3455	3708	4043	Rsa I	(7)	403	659	1284	2340
		5478						4333	5009	5520	
Mae II	(9)	742	1081	1122	1873	Sac I	(2)	338	2275		
		3663	4079	4452	4772	Sal I	(1)	1846			
		5214				Sap I	(2)	2582	2844		
Mae III	(19)	39	994	1022	1087	Sau3A I	(25)	92	457	1044	1176
		1231	1874	1974	2452			1361	1645	1706	1720
		3316	3379	3495	3778			1834	2028	3526	3601
		4109	4167	4320	4508			3612	3620	3698	3710
		4896	5187	5207				3815	4156	4174	4220
Mbo I	(25)	92	457	1044	1176			4478	4495	4531	5116
		1361	1645	1706	1720			5340			
		1834	2028	3526	3601	Sau96 I	(26)	127	171	186	199
		3612	3620	3698	3710			254	551	690	760
		3815	4156	4174	4220			773	985	1196	1219
		4478	4495	4531	5116			1572	2063	2108	2123
		5340						2136	2191	3895	3974
Mbo II	(14)	1086	1299	1445	1502			3991	4213	4829	5126
		1530	2598	2832	3621			5283	5468		
		3694	4449	4527	4636	Sca I	(1)	4333			
		5124	5336			ScrF I	(31)	163	241	398	399
Mlu I	(1)	1878						548	570	723	735
Mme I	(6)	829	1106	2399	2451			748	1169	1194	1217
		3174	3358					1237	1267	1717	2100
Mnl I	(47)	167	216	368	387			2178	2335	2336	2700
		432	460	484	506			2988	3109	3122	3340
		510	566	776	872			4036	4387	4888	4923
		1168	1271	1304	1310			5195	5274	5472	
		1313	1319	1349	1352	Sec I	(30)	161	240	250	397
		1367	1374	1390	1454			461	497	546	547
		1795	1796	1868	2153			694	733	734	746
		2305	2324	2369	2396			747	1167	1236	1245
		2420	2480	2809	2858			1265	1266	1411	1716
		3068	3141	3392	3792			2098	2177	2187	2334
		3873	4019	4225	4820			2397	2699	3120	5194
		4878	5138	5422				5272	5278		
Msc I	(3)	584	1111	1416		SfaN I	(20)	185	444	641	938
Mse I	(27)	36	1007	1119	1149			1485	1542	1674	1720
		1173	1814	1826	1830			2122	2380	3056	4108
		1884	1888	1971	2505			4301	4548	4909	5001
		2603	2731	2790	3666			5039	5077	5393	5405
		3718	3723	3737	3790	Sfc I	(10)	15	917	925	1101
		4025	4064	4429	4801			1496	1950	3225	3416
		4982	5179	5449				4094	5512		
Msl I	(2)	4105	4264			Sma I	(2)	399	2336		

SnaB I	(1)	1874				BstN I	CC`W,GG	17	BstU I	CG CG	22
Spe I	(1)	660				BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	7
Sph I	(1)	5248				Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	31
Ssp I	(2)	2503	4657			Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1
Stu I	(1)	1842				Csp6 I	G`TA,C	7	Dde I	C`TNA,G	19
Sty I	(6)	250	461	1245	1411	Dpn I	GA TC	25	DpnII	`GATC,	25
		2187	2397			Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-
Taq I	(11)	794	1038	1349	1360	Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3
		1705	1821	1847	1861	Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
		2498	3060	4504		Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2
Tfi I	(7)	442	802	1437	1769	Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-
		2538	2795	2935		EcoN I	CTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	6
Tsp45 I	(6)	1022	1231	4109	4320	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
		4896	5207			EcoR V	GAT ATC	3	Ehe I	GCC GCC	5
Tth111 I	(4)	390	811	1217	2327	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	36
Tth111 II	(8)	146	422	613	632	Fok I	GGATG 14/18	11	Fse I	GG,CCGG`CC	-
		2082	3549	3558	3588	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
Vsp I	(4)	2603	2731	2790	4025	Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7
Xba I	(2)	218	2155			Hae II	R,GC`G`Y	9	Hae III	GG CC	29
Xho I	(1)	1860				Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	6
Xho II	(7)	1834	3601	3612	3698	HgiE II	ACCNNNNNNGGT -1/132	132	Hha I	G,CG`C	36
		3710	4478	4495		Hinc II	GTY RAC	1	Hind II	GTY RAC	1
Xma I	(2)	397	2334			Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	15
Xma III	(3)	724	1529	1853		HinI I	GR`CG,YC	8	HinP I	G`CG,C	36
Xmn I	(3)	2566	2604	4452		Hpa I	GTT AAC	-	Hpa II	C`CG,G	24
						Hph I	GGTGA 12/11	13	Kas I	G`GGCC,C	5
						Kpn I	G,GTAC`C	2	Mae I	C`TA,G	13
						Mae II	A`CG,T	9	Mae III	`GTNAC,	19
						Mbo I	`GATC,	25	Mbo II	GAAGA 12/11	14
						Mlu I	A`GGCG,T	1	Mme I	TCCGAC 25/23	6
						Mnl I	CCTC 10/10	47	Msc I	TGG CCA	3
						Mse I	T`TA,A	27	Msl I	CAYN NNRTG	2
						Msp I	C`CG,G	24	MspAl I	CMG CKG	10
						Mun I	C`AATT,G	-	Nae I	GCC GGC	2
						Nar I	GG`CG,CC	5	Nci I	CC`S,GG	14
						Nco I	C`CATG,G	1	Nde I	CA`TA,TG	2
						NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	1
						Nla III	,CATG`	17	Nla IV	GGN NGC	31
						Not I	GC`GGCC,GC	1	Nru I	TCG CCA	1
						Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	3
						NspB II	CMG CKG	10	NspH I	R,CATG`Y	3
						Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	1
						Pal I	GG CC	29	Pf1M I	CCAN,NNN`NTGG	-
						Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
						Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
						Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
						Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	3
						Pvu II	CAG CTG	4	Rsa I	GT AC	7
						Rar II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
						Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
						Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	25
						Sau96 I	G`GNC,C	26	Sca I	AGT ACT	1
						ScrF I	CC`N,GG	31	Sec I	C`CNNG,G	30
						SfaN I	GCATC 9/13	20	Sfc I	C`TRYA,G	10
						Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
						SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
						Sph I	G,CATG`C	1	Spl I	C`GTAC,G	2
						Srf I	GC`CC GGGC	-	Ssp I	AAT ATT	-
						Stu I	AGG CCT	1	Sty I	C`CWG,G	6
						Taq I	T`CG,A	11	Tfi I	G`AWT,C	7
						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,N`NNNNTGG-	1	Xho I	C`TCGA,G	1
						Xho II	R`GATC,Y	7	Xma I	C`CCGG,G	2
						Xma III	C`GGCC,G	3	Xmn I	GAANN NNVTC	3

Site usage in pSEB-Linker:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	57
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	28
Alw I	GGATC 8/9	12	AlwN I	CMG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	6	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	-
Ban I	G`GYRC,C	13	Ban II	G,RGCY`C	7
Bbe I	G,GGCC`C	5	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	14
Bfa I	C`TA,G	13	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	GGTCTC 7/11	6
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	30
BsaW I	W`CCCG,W	3	BseR I	GAGGAG 16/14	4
Bsg I	GTGCG 22/20	1	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	21	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	36
Bsp120 I	G`GGCC,C	-	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`	16
BsrB I	GAG CGG	4	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