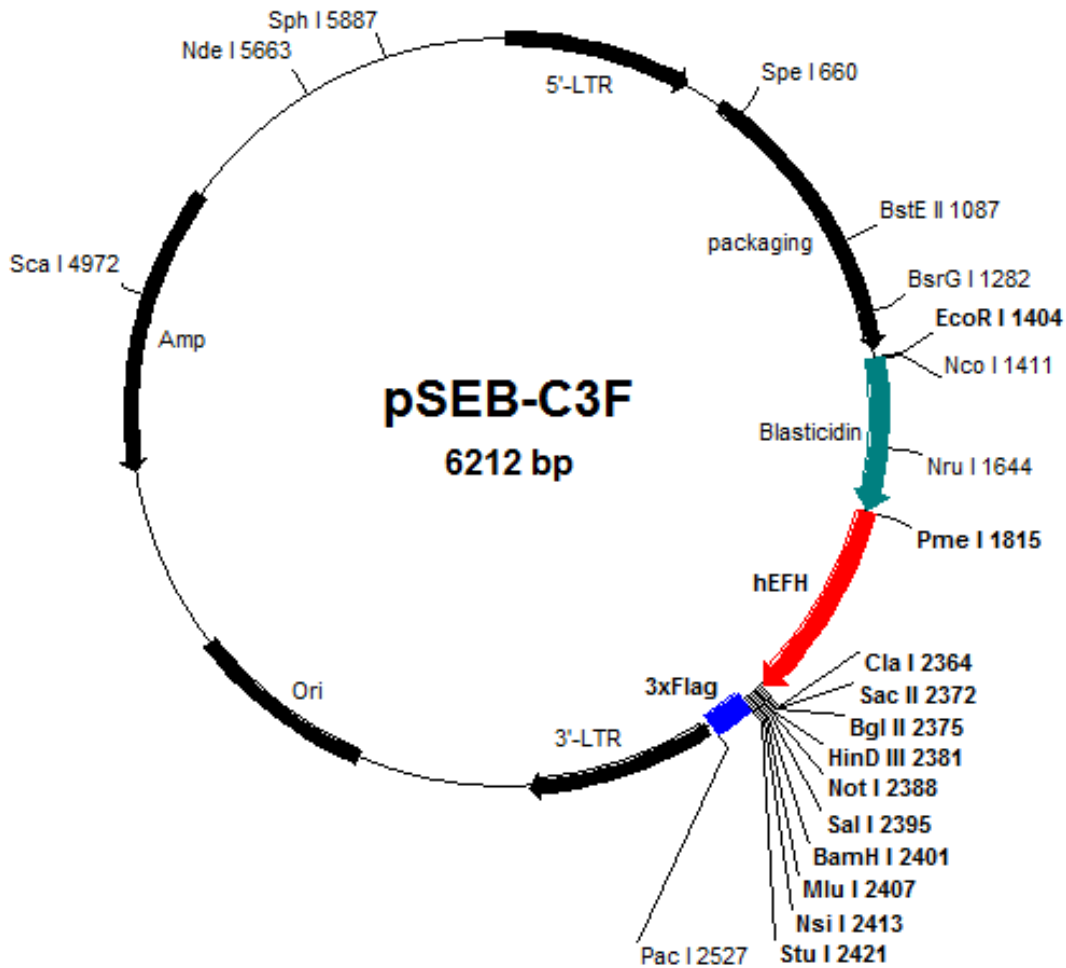


Vector: pSEB-C3F (C-terminal 3xFlag tags)

Antibiotic Selection: Amp

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

Date of Construction: August, 2007



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      Sac II      Bgl II      Hind III      Not I      Sal I      Bam HI      Mlu I      Nsi I      Stu I
tcc gcg gag atc taa gct tgc ggc cgc gtc gac gga tcc acg cgt atg cat agg
S  A  E  I  -  A  C  G  R  V  D  G  S  T  R  M  H  R

      Flag
cct gcaggc gat tac aag gat gac gac gat aag ata ggcgga gat tac aag gat
P  A  G  D  Y  K  D  D  D  D  K  I  G  G  D  Y  K  D

      Flag                                  Flag                                Pac I
gac gac gat aag ata ggcgga gat tac aag gat gac gac gat aag att taa ttaa
D  D  D  K  I  G  G  D  Y  K  D  D  D  D  K  I  -

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pSEB-C3F (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACAC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG TTAGGAACAGAGACGACAGCAGAAATAGGGCCAAACAGGTAATCTGTGGTAAGCAGTTCCTCCCGGCTCAGGGCCAAGAACAGATGGTCCCAGATGCGGTCCCCTTCTCAGCAGTTCTTAGAGAACCATCAGATGTTCCAGGGTGCCTCAAGGACCTGAAATGACCTTGTCCTTATTGAACTAACCAATCAGATTCGCTTCTCGCTTCT GTTCGCGCGTCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCCAGTCTCCGATAGACTGCGTCCCGGGTACCCGATATCCCAAT AAAGCCTCTTG CTGTTTGCAT CGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAG GTTCCACCAG GATTTGGAGACCCCTGCCA GGGACCACCGACCCCCCGC CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGCTTTTGTG CTGTGTTGTGCCGGCATCTAATGTTTGGCCTGCGTCTGCTACTAGTCTAGCTAAGCTCTGTATCTGGCGACCCGTTGGTGAAGTGAAGTCTGAACACCCG GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCCAGGATATGTGGTT CTGGTAGGAGACGAGAACC AAAACGTACT CCGCCTCCGT CTGAATTTTGTCTTCCGGT TGGAACCGAAGCCCGCGCT TTGTCTGCTG CAGCGCTGCA GCATCGTTCT GTGTTGTCTC TGTCTACTGTGTTTCTGTA TTTGCTGAA AATTAGGGCC AGACTGTTAC CACTCCCTAAGTTTGACCTTAGGTCAGT GAAAGATGTGAGCGGATCG CTCACAACCA GTCGGTAGAT TGTCAAGAAGAGACGTTGGGT TACCTTCTGC TCTGCAAAAT GGCCAACTTTAACGTCGGA TGGCCGCGAGACGGCACCT TAACCGAGAC CTCATCACCC AGGTTAAGAT CAAGGTCTTT TCACCTGGCCCGCATGGACA CCCAGACCAGGTCCCCTACA TCGTGACCTG GGAAGCCTTG GCTTTGACCCCTCCCTG GTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT CCCCTTGAACCTCTCGTTTCGACCCCGCTCGATCCTCCCTTATTCACGCCCTCACTCCTTCTTAGGCGCCGGAATTCACCATG GCCAAGCCTTTGTCTCAAGA AGAATCCACCCTCATTGAAAGAGCAACGGCTACAATCAACAGCATCCCATCTCTGAAGACTACAGCTCGCCAGCGCAGCTCTCTTAGCCAGCGCCGATCTTC ACTGGTGTCAATGTATATCATTTTACTGGGGACCTTGTGCAGAACTCGTGTGCTGGGCACTGCTGCTGCGCAGCTGGCAACCTGACTTGTATCGTCGGA TCGGAATGAGAACAGGGCATCTTGGACCCCTGCGGACGGTGCAGAGGTGCTTCTCGATCTGCATCTGGGATCAAAGCCATAGTGAAGACAGTGTAGGACA GCCGACGGCAGTTGGGATTCTGTAATTGCTGCCCTCTGTTTATGTGTGGAGGGCtaaggtttaaactatgagcagcgtccggtgcccgtcagtgggcagagcgccacat CGCCACAGTCCCGAGAAGTTGGGGGAGGGTCCGCAATTGAACCGGTGCTTAGAGAAGGTGGCGGGGTAACCTGGGAAGTATGTCGTGTACTGGTCCG CTTTTTCCCGAGGGTGGGGGAAACCGTATATAAGTGCAGTAGTCCCGTGAACGTTCTTTTCGCAACCGGGTTGGCCGAGAACACAGCAGTAACTAGCTTTCG AGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGCGCCCATCCACCGGGTTGAGTCCGCTTCTGCGCCTCCCGCTGTGGTCCCTCTGAACT GCGTCCGCGCTTAGGTAAGTTAAAGCTCAGGTGCAGACCGGGCTTTGTCCGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGCTCTCCAGCTTTGCCTGA CCTGTCTGCTCACTACGTCAGCTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAAGCTGTGACCCGCGCTAC atcgat ccgagg AGActaagcctt gggg ccg cgt cya cgg atc cA CGC GT atgcAT AGGCCt gcaagg gat tac aag gat gac gac gat aag ata ggggga gat tac aag gat gac gac gat aag ata TAATTA CGATAAAAATAAAGATTTTTATTTAGTCTCCAGAAAAGGGGGAAATGAAAGACCCACCTGTAGTGTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATG GAAAATACATAACTGAGAATAGAGAAAGTTCAGATCAAGTTTAGGAACAGAGACAGCAGAAATATGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTGCCCCGT CACAGGCCAAAGAACAGACATAGTCCCAACTCTCCTGAAATGCTTCAATATGAGCAGCGCAAGAGAAACATCAGATGTTTCCAGGGTTCGCCCAAGGACCTGAACTGTT GCCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGCCGACGTC CTCGATAGACTGCTGCGCCGGGTACCCGTGTATCCAATAAACCCCTTTCGAGTTGCATCCGACTTGTGGTCTCGCTGTTCCCTTGGGAGGGTCTCCTCTGAGTGA TTGACTACCCGTCAGCGGGGCTTTCATGGGTAAAGTTCCTGAAAGTTCTGAAAGTTGGAGAACAACATCTGAGGGTAGGAGTCAATTAAGTAATCTGACTCAATTAG CCACGTGTTTGAATCCACATACTCCCAATACTCCTGAAATGCTTCAATATGAGCAGCGCAAGAGAAATTAATCTGAATCATGGTCAATAGCTAGTTCCTTCC TGTGTGAAATGTTATCCGCTCACAAATCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAAGTAACTCACATTAATTTGCC TTGCCTCACTGCCCGCTTTCAGTTCGGGAAACCTGTCTGTCAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTTCGCTATTGGGG CTCTTCCGCT TCCCTCGTCA CTGACTGCTGCGCTCGGTC GTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAA TCAGGGGATAAACGCAGGAAA GAACATGTGAGCAAAAAGCC AGCAAAAAGC CAGGAACCGT AAAAAAGCCGCTTGTCTGGC GTTTTTCCATAGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCTCAAGTCAGAG GTGGCGAAAC CCGACAGGAC TATAAAGATACCAGGCGTTT CCCCTGGAAGCTCCCTCGT GCGCTCTCCT GTTCCGACCC TGCCGCTTAC CGGATACCTG TCCGCTTTCTCCCTTTCGGG AAGCGTGGCGCTTTTCTCATA GCTCACGCTGTAGTATCTA AGTTCGGTGTAGGTCGTTCC CTCAAGCTGGGCTGTGTGTC ACGAACCCCT CGTTAGCC GACCGTGGCCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGTAAGACACGACTTA TCGCCACTGGCAGCAGCCAC TGTAAACAGG ATTAGCAGG CAGAGTATGT AGGCGGTGCT ACAGAGTCTTGAAGTGGTG GCCTAACTACGGCTACACTA GAAGGACAGT ATTTGGTATC TCGCTCTGCTGAAGCCAGT TACCTTCGAAAAAGAGTTG GTAGCTCTTG ATCCGGCAAA CAAACCACCGCTGTGTAGCGG TGGTTTTTTT GTTTGCAAGC AGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGTT CTGACGCTCA GTGGAACGAA AACTCACGTTAAGGGATTTT GGTCAATGAGATTATCAAAA GGATCTTAC CTAGTACCTT TAAATTAATAAAGTGAAGTTT TAAATCTAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAGTATTAATCAG TGAGGCACCT ATCTCAGCGA TGTGCTATTTCTGTTATCCT CCGAGCTGCTGCAATGATAAC GCGAGACCCACGCTCACCGG ATAGTTGCCCTGACTCCCGT CGTGTAGATA ACTACGATAC GGGAGGGCTT ACCATCTGGC CCCAGTGTGCAATGATAAC GCGAGACCCACGCTCACCGG CGAGCGCAGAAGTGGTCTG CAACTTATC CGCCTCCATC CAGTCTATTAATTGTTGCC GGAAGCTAGA GTAAGTAGTT CGCCAGTTAATAGTTTGGC AACGTTGTTGCCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCTGTTGGTATGGCTTCA TTCAGCTCCGGTTCACCAAG ATCAAGCGGA GTTACATGAT GCATAATTCT CTTACTGTCA TGCCATCCGTAAGATGCTTT TCTGTGACTGGTGAAGTACTC AGTGGCCCG AGTGTATCA CTCATGTTTATGGCAGCACT GCATAATTCT CTTACTGTCA TGCCATCCGTAAGATGCTTT TCTGTGACTGGTGAAGTACTC AACCAAGTCA TTCTGAGAAAT AGTGTATGCG GCGACCGAGT TGCTCTTCCCGCGCTCAAT ACCGGATAAT ACCGCGCCATAGCAGAACTTTAAAAGTT CTCATCATTTGAAAACGTTT TCCGGGGCGAAAACCTCTCAA GGATCTTACC GCTGTTGAGA TCCAGTTCCGATGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTTTACTTTTACC AGCGTTTCTGGGTGAGCAAAA AACAGGAAG CAAAATGCCG CAAAAGAGGG AATAAGGGCG ACACGGAAATGTTGAATACT CATACTCTTCT CTTTTTCAAT ATTATTGAAG CATTATCAG GGTATTGTCTCATGAGCG ATACATATTTGAATGTATTT AGAAAAATAAACAATAAGGG GTTCCGCGCACATTTCCCG AAAAGTGCCA CCTGACGCTT AAGAAACCATTATTATCATG ACATTAACCTATAAAAATAG CCGTATCACG AGGCCCTTTCT GTCTCGCGCG TTTCCGTTGAT GACGGTGA AAAACCTCTGACA CATGCACTC CCGGAGACGG TCACAGCTT TCTGTAAGCGGATCCGGGAGCAGACAAGC CCGTACAGGGCGCTCAGCGG GTGTGGCCG GTGTCGGGGT TGGCTTAACTATGCGGCATC AGAGCAGATT GTACTGAGAG TGCACCATATGCGGTGTGAA ATACCGCACAGATGCGTAAG GAGAAAATAC CGCATCAGGC GCCATTGCGC ATTCAGGCTG CGCAACTGTTGGGAAGGGCG ATCCGGTGGCGCCCTCTTCCG TATTACGCCA GCTGGCGAAA GGGGATGTGCTGCAAGGGC ATTAAGTTGGGTAAACGGCAG GGTTTTCCCA GTCAGCAGT TGTAACGACGGCGCAAG AATGGTGCAT GCAAGGAGAT GCGCCCAACAGTCCCCCGC CCACGGGGCCTGCCACCATA CCCAGCCGA AACAGCGCT CATGAGCCGAAAGTGGCGAG CCCGATCTCCCATCGGTG ATGTCGGCGA TATAGCGCC AGCAACCGCA CTTGTGGCGC CGTGATGCCGGCCAGATG CGTCCGCGTATAGGGCGATT AGTCCAATTT GTTAAAGACA GGAATACAGTGGTCCAGGCT CTAGTTTTCGA CTCAACAATA TCACAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGAA

Unique enzymes in PSEB-C3F.TXT:

Spe I	A`CTAG,T	660	Cla I	AT`CG,AT	2364
BstE II	G`GTNAC,C	1087	Sac II	CC,GC`GG	2372
BsrG I	T`GTAC,A	1282	Bgl II	A`GATC,T	2375
EcoR I	G`AATT,C	1404	HinD III	A`AGCT,T	2381
Nco I	C`CATG,G	1411	Not I	GC`GGCC,GC	2388
Bbv II	GAAGAC 7/11	1497	Sal I	G`TCGA,C	2395
Bbs I	GAAGAC 8/12	1498	Acc I	GT`MK,AC	2396
Nru I	TCG CGA	1644	HinC II	GTY RAC	2397
BsaB I	GATNN NNATC	1711	Hind II	GTY RAC	2397
Pme I	CTTT AAAC	1815	BamH I	G`GATC,C	2401
Mun I	C`AATT,G	1897	Mlu I	A`CGCG,T	2407
Age I	A`CCGG,T	1904	Nsi I	A,TGCA`T	2417
			Stu I	AGG CCT	2421
			Pac I	TTA,AT`TAA	2527

Sca I	AGT ACT	4972			694	733	734	746	
Nde I	CA`TA,TG	5663			747	1167	1236	1245	
Sph I	G,CATG`C	5887			1265	1266	1411	1716	
Number of enzymes = 29					1974	2238	2369	2737	
					2816	2826	2973	3036	
					3338	3759	5833	5911	
					5917				
The following enzymes do not cut in PSEB-C3F.TXT:					BsaW I (5)	1829	1904	3805	3952
Apa I	Avr II	Bcl I	Blp I	BsaA I					
BsiC I	BsiW I	Bsm I	Bsp120 I	Bsp1286 I					
BspM I	BspM II	Bst1107 I	BstB I	BstX I	BseR I (4)	464	1293	1332	3039
Dra III	Eco72 I	Esp I	Fse I	Hpa I	Bsg I (2)	1600	2022		
PaeR7 I	PflM I	Pml I	Rsr II	Sfi I	BsiE I (10)	592	727	1532	1648
SnaB I	Spl I	Srf I	Xca I	Xcm I		2391	3515	3939	4862
						5011	5758		
PSEB-C3F.TXT: sites sorted by name:					BsiHKA I (6)	338	2914	3917	5078
						5163	5660		
Aat II (2)	745	5414			BsmA I (22)	107	475	531	609
Acc I (1)	2396					734	832	949	1073
Acc65 I (2)	401	2977				1132	1150	1328	1431
Aci I (70)	197	203	566	588		2208	2559	2682	3029
	688	727	860	901		3050	4554	5328	5481
	1042	1133	1199	1298	BsmB I (7)	5525	6197		
	1317	1355	1532	1614		733	831	1072	1131
	1681	1926	1963	2043		1329	5482	5524	
	2099	2102	2117	2148	BsmF I (11)	172	185	564	729
	2155	2182	2369	2371		764	1205	1585	1853
	2387	2391	2459	2492		2748	2761	5893	
	2773	2779	3075	3289	BsoF I (41)	727	901	917	920
	3392	3448	3458	3482		925	928	1133	1513
	3525	3532	3553	3644		1532	1606	1609	1612
	3672	3799	3818	3939		1615	1618	1782	1823
	4049	4184	4193	4555		2043	2102	2117	2148
	4646	4837	4883	5004		2388	2391	3424	3505
	5048	5125	5234	5333		3523	3526	3644	3799
	5380	5554	5593	5603		3942	4007	4010	4216
	5629	5667	5680	5706		4544	4883	4910	5005
	5763	6022				5234	5521	5630	5734
Afl II (3)	35	1006	2609			5807			
Afl III (2)	2407	3599			BspH I (4)	4319	5327	5432	5956
Age I (1)	1904				Bsr I (18)	374	1030	1058	1546
Aha II (9)	742	1398	2355	5029		1570	1939	1960	2950
	5411	5715	5898	6012		3400	4006	4019	4133
	6033					4539	4657	4700	4967
Ahd I (4)	1020	3022	3068	4492		5139	5845		
Alu I (33)	30	34	336	580	BsrB I (4)	1042	3291	3532	5333
	668	676	1515	1620	BsrD I (2)	4553	4727		
	2056	2062	2066	2204	BsrG I (1)	1282			
	2345	2383	2604	2608	BssH II (4)	317	368	2893	2944
	2912	3231	3264	3359	BssS I (4)	1587	3772	5156	5463
	3423	3541	3767	3857	BstE II (1)	1087			
	3903	4160	4681	4781	BstN I (17)	241	548	735	748
	4844	5523	5542	5787		1169	1194	1217	1237
	6143					1267	1717	2817	3339
Alw I (16)	453	1051	1357	1727		3627	3748	3761	5834
	2333	2361	2397	2408		6111			
	4161	4247	4247	4344	BstU I (26)	317	319	370	903
	4345	4809	5124	5130		905	1135	1644	1926
AlwN I (2)	2733	4015				2095	2140	2371	2393
ApaL I (3)	3913	5159	5656			2409	2893	2895	2946
Apo I (2)	872	1404				3446	3448	3646	4227
Asc I (2)	368	2944				4557	5050	5382	5482
Ase I (4)	3242	3370	3429	4664		5484	5587		
Asp718 (2)	401	2977			BstY I (9)	2337	2375	2401	4240
Ava I (7)	331	397	498	1871		4251	4337	4349	5117
	1973	2907	2973			5134			
Ava II (13)	186	199	254	551	Bsu36 I (3)	781	1018	2111	
	690	1219	1572	2762	Cac8 I (39)	28	32	319	370
	2775	2830	4630	4852		582	586	631	650
	6107					1199	1508	1622	2064
BamH I (1)	2401					2078	2099	2262	2290
Ban I (17)	244	401	1142	1397		2385	2423	2427	2602
	1687	1832	1907	2163		2606	2895	2946	3392
	2354	2820	2977	3343		3421	3530	3616	3653
	4440	5714	5897	6011		4213	4604	5617	5765
	6032					5785	5789	5885	5926
Ban II (8)	338	351	1677	2078		5974	6016	6046	
	2914	2927	5964	5978	Cfr10 I (8)	629	1904	2128	2260
Bbe I (6)	1401	2358	5718	5901		2351	4572	6035	6044
	6015	6036							
Bbs I (1)	1498				Cla I (1)	2364			
Bbv I (10)	931	939	1524	1629	Csp6 I (8)	402	658	1283	1954
	1834	4018	4021	4227		2978	4971	5647	6158
	4921	5532				75	167	208	476
Bbv II (1)	1497				Dde I (23)	781	1018	1290	1808
Bcn I (15)	164	399	400	571		2111	2205	2256	2379
	724	2219	2740	2975		2649	2743	2784	3053
	2976	3980	4676	5027		3124	3874	4283	4449
	5528	5563	5914			4989	5415	5650	
Bfa I (16)	31	219	661	673	Dpn I (28)	94	459	1046	1178
	1394	1522	1912	2063		1363	1647	1708	1722
	2189	2251	2605	2795		2339	2367	2377	2403
	4094	4347	4682	6117		2669	4167	4242	4253
Bgl I (2)	4612	5730				4261	4339	4351	4456
Bgl II (1)	2375					4797	4815	4861	5119
Bpm I (3)	2542	4562	6180			5136	5172	5757	5981
Bsa I (7)	476	530	1149	2207	DpnII (28)	92	457	1044	1176
	3030	3051	4553			1361	1645	1706	1720
BsaB I (1)	1711					2337	2365	2375	2401
BsaH I (9)	742	1398	2355	5029		2667	4165	4240	4251
	5411	5715	5898	6012		4259	4337	4349	4454
	6033					4795	4813	4859	5117
BsaJ I (33)	161	240	250	397		5134	5170	5755	5979
	461	497	546	547	Dra I (5)	1815	2200	4358	4377
						5069			

Drd I	(3)	1500	3707	5576		Hph I	(13)	1157	1183	1401	4336
Dsa I	(4)	694	1411	2369	5917			4563	4977	5185	5218
Eae I	(11)	582	724	1109	1130			5502	5511	6004	6049
		1414	1529	2388	3438			6130			
Eag I	(3)	724	1529	2388		Kas I	(6)	1397	2354	5714	5897
Ear I	(6)	1070	1311	3221	3483			6011	6032		
		5287	5775			Kpn I	(2)	405	2981		
Eco47 III	(3)	923	1826	5953		Mae I	(16)	31	219	661	673
Eco57 I	(5)	1509	2077	4146	5160			1394	1522	1912	2063
		6164						2189	2251	2605	2795
EcoN I	(4)	784	1392	1915	2110			4094	4347	4682	6117
EcoO109 I	(6)	254	1219	1572	2830	Mae II	(10)	742	1081	1122	2019
		5468	5922					2302	4302	4718	5091
EcoR I	(1)	1404				Mae III	(20)	5411	5853		
EcoR II	(17)	239	546	733	746			39	994	1022	1087
		1167	1192	1215	1235			1231	2331	2347	2613
		1265	1715	2815	3337			3091	3955	4018	4134
		3625	3746	3759	5832			4417	4748	4806	4959
		6109				Mbo I	(28)	5147	5535	5826	5846
EcoR V	(3)	140	2715	6100				92	457	1044	1176
Ehe I	(6)	1399	2356	5716	5899			1361	1645	1706	1720
		6013	6034					2337	2365	2375	2401
Fnu4H I	(41)	727	901	917	920			2667	4165	4240	4251
		925	928	1133	1513			4259	4337	4349	4454
		1532	1606	1609	1612			4795	4813	4859	5117
		1615	1618	1782	1823	Mbo II	(14)	5134	5170	5755	5979
		2043	2102	2117	2148			1086	1299	1445	1502
		2388	2391	3424	3505			1530	3237	3471	4260
		3523	3526	3644	3799			4333	5088	5166	5275
		3942	4007	4010	4216			5763	5975		
		4544	4883	4910	5005	Mlu I	(1)	2407			
		5234	5521	5630	5734	Mme I	(6)	829	1106	3038	3090
		5807						3813	3997		
Fok I	(15)	423	1140	1300	1464	Mnl I	(52)	167	216	368	387
		1699	2107	2452	2485			432	460	484	506
		2518	2998	4458	4639			510	566	776	872
		4926	5569	5813				1168	1271	1304	1310
Fsp I	(2)	4714	5737					1313	1319	1349	1352
Gdi II	(11)	723	725	1129	1528			1367	1374	1390	1454
		1530	2387	2389	3439			1795	1796	1880	1969
		4879	5915	6047				2064	2106	2160	2176
Gsu I	(3)	2543	4563	6181				2792	2944	2963	3008
Hae I	(7)	584	1111	1416	2421			3035	3059	3119	3448
		3614	3625	4077				3497	3707	3780	4031
Hae II	(12)	925	1401	1828	2235			4431	4512	4658	4864
		2358	3477	3847	5718	Msc I	(3)	5459	5517	5777	6061
		5901	5955	6015	6036	Mse I	(26)	36	1007	1119	1149
Hae III	(31)	129	173	584	726			1173	1814	2199	2523
		762	774	987	1111			2527	2610	3144	3242
		1132	1197	1416	1531			3370	3429	4305	4357
		2116	2221	2390	2421			4362	4376	4429	4664
		2704	2749	3440	3614			4703	5068	5440	5621
		3625	3643	4077	4535			5818	6088		
		4615	4882	5469	5767	Msl I	(2)	4744	4903		
		5916	5924	6048		Msp I	(31)	163	398	569	630
Hga I	(12)	381	642	895	1491			723	1401	1830	1905
		2168	2383	2957	3709			2129	2217	2229	2261
		4287	5019	5577	6046			2352	2739	2974	3317
HgiA I	(6)	338	2914	3917	5078			3806	3953	3979	4169
		5163	5660					4573	4607	4674	4784
HgiE II	(2)	4178	5658					5026	5527	5561	5913
Hha I	(43)	319	321	370	372			6036	6045	6060	6060
		648	905	924	1400	MspAl I	(12)	588	1620	2056	2371
		1512	1827	1854	1926			3075	3423	3941	4186
		2097	2234	2329	2357			5127	5593	5787	6143
		2895	2897	2946	2948						
		3223	3383	3448	3476	Mun I	(1)	1897			
		3509	3779	3846	3946	Nae I	(3)	631	2262	6046	
		4120	4229	4622	4715	Nar I	(6)	1398	2355	5715	5898
		5052	5384	5484	5587			6012	6033		
		5717	5738	5871	5900	Nci I	(15)	163	398	399	570
		5954	6014	6035				723	2218	2739	2974
HinC II	(1)	2397						2975	3979	4675	5026
Hind II	(1)	2397						5527	5562	5913	
Hind III	(1)	2381				Nco I	(1)	1411			
Hinf I	(17)	442	450	791	802	Nde I	(1)	5663			
		1437	1769	2135	2254	NgoM I	(3)	629	2260	6044	
		3134	3156	3177	3434	Nhe I	(3)	30	2062	2604	1822
		3499	3574	3970	4487	Nla III	(18)	62	1205	1415	1822
		6125						2636	3090	3257	3603
HinI I	(9)	742	1398	2355	5029			4323	4814	4824	4902
		5411	5715	5898	6012			4938	5331	5436	5520
		6033						5887	5960		
HinP I	(43)	317	319	368	370	Nla IV	(38)	188	201	246	403
		646	903	922	1398			521	552	692	761
		1510	1825	1852	1924			893	1144	1221	1399
		2095	2232	2327	2355			1573	1689	1834	1909
		2893	2895	2944	2946			1961	2165	2244	2356
		3221	3381	3446	3474			2403	2764	2777	2822
		3507	3777	3844	3944			2979	3345	3631	3670
		4118	4227	4620	4713			4442	4536	4577	4788
		5050	5382	5482	5585			5378	5716	5899	5923
		5715	5736	5869	5898			6013	6034		
		5952	6012	6033		Not I	(1)	2388			
Hpa II	(31)	163	398	569	630	Nru I	(1)	1644			
		723	1401	1830	1905	Nsi I	(1)	2417			
		2129	2217	2229	2261	Nsp7524 I	(4)	1818	3599	5516	5883
		2352	2739	2974	3317	NspB II	(12)	588	1620	2056	2371
		3806	3953	3979	4169			3075	3423	3941	4186
		4573	4607	4674	4784			5127	5593	5787	6143
		5026	5527	5561	5913	NspH I	(4)	1822	3603	5520	5887
		6036	6045	6060		Pac I	(1)	2527			
						Pal I	(31)	129	173	584	726

		762	774	987	1111	Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	33
		1132	1197	1416	1531	Alw I	GGATC 8/9	16	AlwN I	CAG,NNN`CTG	2
		2116	2221	2390	2421	Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
		2704	2749	3440	3614	Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
		3625	3643	4077	4535	Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
		4615	4882	5469	5767	Ava I	C`YCGR,G	7	Ava II	G`GWC,C	13
		5916	5924	6048		Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ple I	(4)	799	2143	3142	3978	Ban I	G`GYRC,C	17	Ban II	G,RCGY`C	8
Pme I	(1)	1815				Bbe I	G,CGCG`C	6	Bbs I	GAAGC 8/12	1
PpuM I	(4)	254	1219	1572	2830	Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Psp1406 I	(3)	2019	4718	5091		Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	15
PspA I	(2)	397	2973			Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2
Pst I	(4)	921	929	1105	2427	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Pvu I	(3)	1648	4862	5758		Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
Pvu II	(5)	1620	2056	3423	5787	BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	1
		6143				BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	33
Rsa I	(8)	403	659	1284	1955	BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
		2979	4972	5648	6159	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
Sac I	(2)	338	2914			BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	6
Sac II	(1)	2372				BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
Sal I	(1)	2395				BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
Sap I	(2)	3221	3483			BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	41
Sau3A I	(28)	92	457	1044	1176	Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
		1361	1645	1706	1720	BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
		2337	2365	2375	2401	BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	18
		2667	4165	4240	4251	BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
		4259	4337	4349	4454	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
		4795	4813	4859	5117	BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	1
		5134	5170	5755	5979	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
Sau96 I	(27)	127	171	186	199	BstN I	CC`W,GG	17	BstU I	CG CG	26
		254	551	690	760	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9
		773	985	1196	1219	Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	39
		1572	2219	2702	2747	Cfr10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
		2762	2775	2830	4534	Csp6 I	G`TA,C	8	Dde I	C`TNA,G	23
		4613	4630	4852	5468	Dpn I	GA TC	28	DpnII	`GATC,	28
		5765	5922	6107		Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Sca I	(1)	4972				Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
ScrF I	(32)	163	241	398	399	Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
		548	570	723	735	Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	3
		748	1169	1194	1217	Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
		1237	1267	1717	2218	EcoN I	CCTNN`N,NNAGG	4	Eco0109 I	RG`GNC,CY	6
		2739	2817	2974	2975	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
		3339	3627	3748	3761	EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
		3979	4675	5026	5527	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	41
		5562	5834	5913	6111	Fok I	GGATG 14/18	15	Fse I	GG,CCGG`CC	-
Sec I	(33)	161	240	250	397	Fsp I	TGC GCA	2	Gdi II	`YGGC,CC	11
		461	497	546	547	Gsu I	CTGGAG 21/19	3	Hae I	WGG CGW	7
		694	733	734	746	Hae II	R,CGCG`Y	12	Hae III	GG CC	31
		747	1167	1236	1245	Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	6
		1265	1266	1411	1716	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	43
		1974	2238	2369	2737	HinC II	GTY RAC	1	Hind II	GTY RAC	1
		2816	2826	2973	3036	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	17
		3338	3759	5833	5911	HinI I	GR`CG,YC	9	HinP I	G`CG,C	43
		5917				Hpa I	GTT AAC	-	Hpa II	C`CG,G	31
SfaN I	(21)	185	444	641	938	Hph I	GGTGA 12/11	13	Kas I	G`CGCG,C	6
		1485	1542	1674	1720	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
		2088	2761	3019	3695	Mae II	A`CG,T	10	Mae III	`GTNAC,	20
		4747	4940	5187	5548	Mbo I	`GATC,	28	Mbo II	GAAGA 12/11	14
		5640	5678	5716	6032	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Sfc I	(11)	15	917	925	1101	Mnl I	CCTC 10/10	52	Msc I	TGG CCA	3
		1496	2423	2589	3864	Mse I	T`TA,A	26	Mel I	CAYNN NNRTG	2
		4055	4733	6151		Msp I	C`CG,G	31	MspAl I	CMG CKG	12
Sma I	(2)	399	2975			Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Spe I	(1)	660				Nar I	GG`CG,CC	6	Nci I	CC`S,GG	15
Sph I	(1)	5887				Nco I	C`CATG,G	1	Nde I	CA`TA,TG	1
Ssp I	(2)	3142	5296			NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3
Stu I	(1)	2421				Nla III	,CATG`	18	Nla IV	GGN NCC	38
Sty I	(7)	250	461	1245	1411	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
		2238	2826	3036		Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	4
Taq I	(12)	794	1038	1349	1360	NspB II	CMG CKG	12	NspH I	R,CATG`Y	4
		1705	2069	2211	2364	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
		2396	3137	3699	5143	Pal I	GG CC	31	Pf1M I	CCAN,NNN`NTGG	-
Tfi I	(7)	442	802	1437	1769	Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
		3177	3434	3574		Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Tsp45 I	(7)	1022	1231	2347	4748	Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
		4959	5535	5846		Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Tth111 I	(4)	390	811	1217	2966	Pvu II	CAG CTG	5	Rsa I	GT AC	8
Tth111 II	(9)	146	422	613	632	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
		2278	2721	4188	4197	Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
		4227				Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	28
Vsp I	(4)	3242	3370	3429	4664	Sau96 I	G`GNC,C	27	Sca I	AGT ACT	1
Xba I	(2)	218	2794			ScrF I	CC`N,GG	32	Sec I	C`CNNG,G	33
Xho II	(9)	2337	2375	2401	4240	SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	11
		4251	4337	4349	5117	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
		5134				SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
Xma I	(2)	397	2973			Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
Xma III	(3)	724	1529	2388		Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Xmn I	(3)	3205	3243	5091		Stu I	AGG CCT	1	Sty I	C`CWG,G	7
						Taq I	T`CG,A	12	Tfi I	G`AWT,C	7
						Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Site usage in PSEB-C3F.TXT:						Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	4
Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1	Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	70	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2	Xho II	R`GATC,Y	9	Xma I	C`CCG,G	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	9	Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	3
							GAANN NNTTC	3			