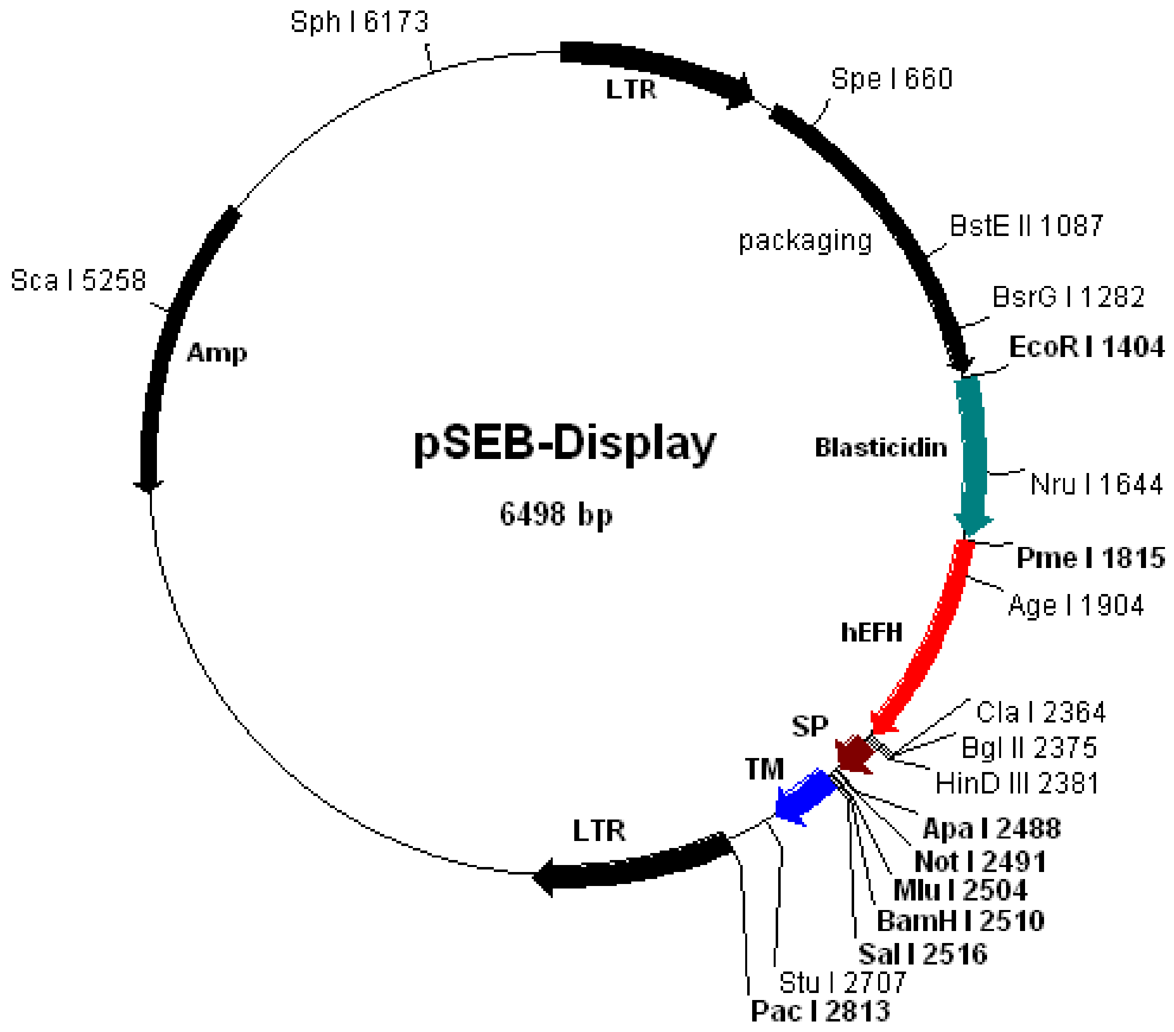
Vector: pSEB-Display (with SP and TM)

Antibiotic Selection: Amp

Creator(s): Qing Luo, Molecular Oncology Lab of The University of Chicago

Date of Construction: October, 2009



Ig κ-chain signal peptide

AGATCTAAGCTT ACCACC **ATG GAG ACA GAC ACA CTC CTG CTA TGG GTA CTG CTG CTC TGG**

HA tag Apa I

GTT CCA GGT TCC ACT GGT GAC TAT CCA TAT GAT GTT CCA GAT TAT GCT GGG GCC CGC

Not I Mlu I BamH I Sal I Myc tag

GGC CGC CCC GGG ACG CGT GGA TCC GTC GAC **GAA CAA AAA CTC ATC TCA GAA GAG GAT**

PDGFR transmembrane domain

CTG AAT GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC TCC TTG CCC

TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG GTG CTC ACC ATC ATC TCC

CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG AAG CCA CGT TAG

pSEB-Display Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGCTAGCTTAAGTAACGCCATTTTGCAAGGCATGGAAAATACATAACTGAGAA
TAGAGAAGTTAGATCAAGGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCTCCCCGG
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ATCATGCTTTGGCAGAAGAAGCC**ACGTTAG AGGCCT** gcaggc gat tac aag gat gac gac gat aag ata
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GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTCAACAATATCACCAGCTGAAGCCTATAGAGTACGAGCCATAGATAAAA
TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAA
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Unique enzymes in pSEB-Display:

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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
Pme I       CTTT|AAAC      1815
Mun I       C`AATT,G       1897
Age I       A`CCGG,T       1904
Cla I       AT`CG,AT       2364
Bgl II      A`GATC,T       2375
HinD III    A`AGCT,T       2381
Bsp120 I    G`GGCC,C       2484
Apa I       G,GGCC`C       2488
Not I       GC`GGCC,GC     2491
Mlu I       A`CGCG,T       2504
BamH I      G`GATC,C       2510
Sal I       G`TCGA,C       2516
Acc I       GT`MK,AC       2517
HinC II     GTY|RAC        2518
Hind II     GTY|RAC        2518
Bsm I       GAATG,C 7      2557
Xcm I       CCANNNN,N`NNNNTGG2635
Stu I       AGG|CCT        2707
Pac I       TTA,AT`TAA     2813
Sca I       AGT|ACT        5258
Sph I       G,CATG`C       6173
Number of enzymes = 29
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The following enzymes do not cut in pSEB-Display:

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Avr II      Bcl I       Blp I       BsaA I      BsiC I
BsiW I      Bsp1286 I   BspM I      BspM II     Bst1107 I
BstB I      BstX I      Dra III     Eco72 I     Esp I
Fse I       Hpa I       Nsi I       PaeR7 I     PflM I
Pml I       Rsr II      Sfi I       SnaB I      Spl I
```

pSEB-Display: sites sorted by name:

```
Aat II      (2)   745      5700
Acc I       (1)   2517
Acc65 I     (2)   401      3263
Aci I       (71)  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
                  2488     2490     2494     2745
                  2778     3059     3065     3361
                  3575     3678     3734     3744
                  3768     3811     3818     3839
                  3930     3958     4085     4104
                  4225     4335     4470     4479
                  4841     4932     5123     5169
                  5290     5334     5411     5520
                  5619     5666     5840     5879
                  5889     5915     5953     5966
                  5992     6049     6308
Afl II      (3)   35       1006     2895
Afl III     (2)   2504     3885
Age I       (1)   1904
Aha II      (9)   742      1398     2355     5315
                  5697     6001     6184     6298
                  6319
Ahd I       (4)   1020     3308     3354     4778
Alu I       (33)  30       34       336      580
                  668      676      1515     1620
                  2056     2062     2066     2204
                  2345     2383     2890     2894
                  3198     3517     3550     3645
                  3709     3827     4053     4143
                  4189     4446     4967     5067
                  5130     5809     5828     6073
                  6429
Alw I       (17)  453      1051     1357     1727
                  2333     2361     2506     2517
                  2552     4447     4533     4533
                  4630     4631     5095     5410
                  5416
AlwN I      (2)   3019     4301
Apa I       (1)   2488
ApaL I      (3)   4199     5445     5942
Apo I       (2)   872      1404
Asc I       (2)   368      3230
Ase I       (4)   3528     3656     3715     4950
Asp718      (2)   401      3263
Ava I       (8)   331      397      498      1871
                  1973     2498     3193     3259
Ava II      (13)  186      199      254      551
                  690      1219     1572     3048
                  3061     3116     4916     5138
                  6393
BamH I      (1)   2510
Ban I       (18)  244      401      1142     1397
                  1687     1832     1907     2163
                  2354     2587     3106     3263
                  3629     4726     6000     6183
                  6297     6318
Ban II      (9)   338      351      1677     2078
                  2488     3200     3213     6250
                  6264
Bbe I       (6)   1401     2358     6004     6187
                  6301     6322
Bbs I       (1)   1498
Bbv I       (10)  931      939      1524     1629
                  1834     4304     4307     4513
                  5207     5818
Bbv II      (1)   1497
Bcn I       (17)  164      399      400      571
                  724      2219     2500     2501
                  3026     3261     3262     4266
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		4962	5313	5814	5849
		6200			
Bfa I	(16)	31	219	661	673
		1394	1522	1912	2063
		2189	2251	2891	3081
		4380	4633	4968	6403
Bgl I	(3)	2633	4898	6016	
Bgl II	(1)	2375			
Bpm I	(3)	2828	4848	6466	
Bsa I	(7)	476	530	1149	2207
		3316	3337	4839	
BsaB I	(1)	1711			
BsaH I	(9)	742	1398	2355	5315
		5697	6001	6184	6298
		6319			
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	2391
		2488	2497	2498	2637
		3023	3102	3112	3259
		3322	3624	4045	6119
		6197	6203		
BsaW I	(5)	1829	1904	4091	4238
		5069			
BseR I	(4)	464	1293	1332	3325
Bsg I	(2)	1600	2022		
BsiE I	(10)	592	727	1532	1648
		2494	3801	4225	5148
		5297	6044		
BsiHKA I	(7)	338	2649	3200	4203
		5364	5449	5946	
Bsm I	(1)	2557			
BsmA I	(23)	107	475	531	609
		734	832	949	1073
		1132	1150	1328	1431
		2208	2391	2845	2968
		3315	3336	4840	5614
		5767	5811	6483	
BsmB I	(7)	733	831	1072	1131
		1329	5768	5810	
BsmF I	(12)	172	185	564	729
		764	1205	1585	1853
		2515	3034	3047	6179
BsoF I	(42)	727	901	917	920
		925	928	1133	1513
		1532	1606	1609	1612
		1615	1618	1782	1823
		2043	2102	2117	2148
		2426	2491	2494	3710
		3791	3809	3812	3930
		4085	4228	4293	4296
		4502	4830	5169	5196
		5291	5520	5807	5916
		6020	6093		
Bsp120 I	(1)	2484			
BspH I	(4)	4605	5613	5718	6242
Bsr I	(19)	374	1030	1058	1546
		1570	1939	1960	2451
		3236	3686	4292	4305
		4419	4825	4943	4986
		5253	5425	6131	
BsrB I	(4)	1042	3577	3818	5619
BsrD I	(2)	4839	5013		
BsrG I	(1)	1282			
BssH II	(4)	317	368	3179	3230
BssS I	(4)	1587	4058	5442	5749
BstE II	(1)	1087			
BstN I	(21)	241	548	735	748
		1169	1194	1217	1237
		1267	1717	2439	2564
		2633	2639	3103	3625
		3913	4034	4047	6120
		6397			
BstU I	(26)	317	319	370	903
		905	1135	1644	1926
		2095	2140	2371	2490
		2506	3179	3181	3232
		3732	3734	3932	4513
		4843	5336	5668	5768
		5770	5873		
BstY I	(10)	2337	2375	2510	2545
		4526	4537	4623	4635
		5403	5420		
Bsu36 I	(3)	781	1018	2111	
Cac8 I	(39)	28	32	319	370
		582	586	631	650
		1199	1508	1622	2064
		2078	2099	2262	2290
		2488	2709	2713	2888
		2892	3181	3232	3678
		3707	3816	3902	3939
		4499	4890	5903	6051
		6071	6075	6171	6212
		6260	6302	6332	
Cfr10 I	(8)	629	1904	2128	2260
		2351	4858	6321	6330
Cla I	(1)	2364			
Csp6 I	(9)	402	658	1283	1954
		2420	3264	5257	5933
		6444			
Dde I	(25)	75	167	208	476
		781	1018	1290	1808
		2111	2205	2256	2379
		2536	2623	2935	3029
		3070	3339	3410	4160
		4569	4735	5275	5701
		5936			
Dpn I	(30)	94	459	1046	1178
		1363	1647	1708	1722
		2339	2367	2377	2512
		2547	2621	2955	4453
		4528	4539	4547	4625
		4637	4742	5083	5101
		5147	5405	5422	5458
		6043	6267		
DpnII	(30)	92	457	1044	1176
		1361	1645	1706	1720
		2337	2365	2375	2510
		2545	2619	2953	4451
		4526	4537	4545	4623
		4635	4740	5081	5099
		5145	5403	5420	5456
		6041	6265		
Dra I	(5)	1815	2200	4644	4663
		5355			
Drd I	(3)	1500	3993	5862	
Dsa I	(6)	694	1411	2369	2391
		2488	6203		
Eae I	(11)	582	724	1109	1130
		1414	1529	2491	3724
		5166	6200	6332	
Eag I	(3)	724	1529	2491	
Ear I	(7)	1070	1311	2535	3507
		3769	5573	6061	
Eco47 III	(3)	923	1826	6239	
Eco57 I	(5)	1509	2077	4432	5446
		6450			
EcoN I	(4)	784	1392	1915	2110
EcoO109 I	(7)	254	1219	1572	2484
		3116	5754	6208	
EcoR I	(1)	1404			
EcoR II	(21)	239	546	733	746
		1167	1192	1215	1235
		1265	1715	2437	2562
		2631	2637	3101	3623
		3911	4032	4045	6118
		6395			
EcoR V	(3)	140	3001	6386	
Ehe I	(6)	1399	2356	6002	6185
		6299	6320		
Fnu4H I	(42)	727	901	917	920
		925	928	1133	1513
		1532	1606	1609	1612
		1615	1618	1782	1823
		2043	2102	2117	2148
		2426	2491	2494	3710
		3791	3809	3812	3930
		4085	4228	4293	4296
		4502	4830	5169	5196
		5291	5520	5807	5916
		6020	6093		
Fok I	(17)	423	1140	1300	1464
		1699	2107	2615	2654
		2738	2771	2804	3284
		4744	4925	5212	5855
		6099			
Fsp I	(2)	5000	6023		
Gdi II	(11)	723	725	1129	1528
		1530	2490	2492	3725
		5165	6201	6333	
Gsu I	(3)	2829	4849	6467	
Hae I	(7)	584	1111	1416	2707
		3900	3911	4363	
Hae II	(12)	925	1401	1828	2235
		2358	3763	4133	6004
		6187	6241	6301	6322
Hae III	(34)	129	173	584	726
		762	774	987	1111
		1132	1197	1416	1531
		2116	2221	2486	2493
		2562	2636	2707	2990
		3035	3726	3900	3911
		3929	4363	4821	4901
		5168	5755	6053	6202
		6210	6334		
Hga I	(12)	381	642	895	1491
		2168	2511	3243	3995
		4573	5305	5863	6332
HgiA I	(7)	338	2649	3200	4203
		5364	5449	5946	
HgiE II	(2)	4464	5944		
Hha I	(43)	319	321	370	372
		648	905	924	1400
		1512	1827	1854	1926
		2097	2234	2329	2357
		3181	3183	3232	3234
		3509	3669	3734	3762
		3795	4065	4132	4232
		4406	4515	4908	5001
		5338	5670	5770	5873
		6003	6024	6157	6186
		6240	6300	6321	
HinC II	(1)	2518			

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Hind II     (1)   2518
HinD III    (1)   2381
Hinf I      (17)  442      450      791      802
                  1437     1769     2135     2254
                  3420     3442     3463     3720
                  3785     3860     4256     4773
                  6411
HinI I      (9)   742      1398     2355     5315
                  5697     6001     6184     6298
                  6319
HinP I      (43)  317      319      368      370
                  646      903      922      1398
                  1510     1825     1852     1924
                  2095     2232     2327     2355
                  3179     3181     3230     3232
                  3507     3667     3732     3760
                  3793     4063     4130     4230
                  4404     4513     4906     4999
                  5336     5668     5768     5871
                  6001     6022     6155     6184
                  6238     6298     6319
Hpa II      (32)  163      398      569      630
                  723      1401     1830     1905
                  2129     2217     2229     2261
                  2352     2499     3025     3260
                  3603     4092     4239     4265
                  4455     4859     4893     4960
                  5070     5312     5813     5847
                  6199     6322     6331     6346
Hph I       (16)  1157     1183     1401     2461
                  2628     2642     4622     4849
                  5263     5471     5504     5788
                  5797     6290     6335     6416
Kas I       (6)   1397     2354     6000     6183
                  6297     6318
Kpn I       (2)   405      3267
Mae I       (16)  31       219      661      673
                  1394     1522     1912     2063
                  2189     2251     2891     3081
                  4380     4633     4968     6403
Mae II      (11)  742      1081     1122     2019
                  2302     2698     4588     5004
                  5377     5697     6139
Mae III     (21)  39       994      1022     1087
                  1231     2331     2347     2450
                  2899     3377     4241     4304
                  4420     4703     5034     5092
                  5245     5433     5821     6112
                  6132
Mbo I       (30)  92       457      1044     1176
                  1361     1645     1706     1720
                  2337     2365     2375     2510
                  2545     2619     2953     4451
                  4526     4537     4545     4623
                  4635     4740     5081     5099
                  5145     5403     5420     5456
                  6041     6265
Mbo II      (16)  1086     1299     1445     1502
                  1530     2551     2700     3523
                  3757     4546     4619     5374
                  5452     5561     6049     6261
Mlu I       (1)   2504
Mme I       (6)   829      1106     3324     3376
                  4099     4283
Mnl I       (56)  167      216      368      387
                  432      460      484      506
                  510      566      776      872
                  1168     1271     1304     1310
                  1313     1319     1349     1352
                  1367     1374     1390     1454
                  1795     1796     1880     1969
                  2064     2106     2160     2176
                  2536     2569     2680     2697
                  3078     3230     3249     3294
                  3321     3345     3405     3734
                  3783     3993     4066     4317
                  4717     4798     4944     5150
                  5745     5803     6063     6347
Msc I       (3)   584      1111     1416
Mse I       (27)  36       1007     1119     1149
                  1173     1814     2199     2607
                  2809     2813     2896     3430
                  3528     3656     3715     4591
                  4643     4648     4662     4715
                  4950     4989     5354     5726
                  5907     6104     6374
Msl I       (3)   2585     5030     5189
Msp I       (32)  163      398      569      630
                  723      1401     1830     1905
                  2129     2217     2229     2261
                  2352     2499     3025     3260
                  3603     4092     4239     4265
                  4455     4859     4893     4960
                  5070     5312     5813     5847
                  6199     6322     6331     6346
MspA1 I     (13)  588      1620     2056     2371
                  2490     3361     3709     4227
                  4472     5413     5879     6073
                  6429
Mun I       (1)   1897
Nae I       (3)   631      2262     6332
Nar I       (6)   1398     2355     6001     6184
                  6298     6319
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Nci I       (17)  163      398      399      570
                  723      2218     2499     2500
                  3025     3260     3261     4265
                  4961     5312     5813     5848
                  6199
Nco I       (2)   1411     2391
Nde I       (2)   2461     5949
NgoM I      (3)   629      2260     6330
Nhe I       (3)   30       2062     2890
Nla III     (20)  62       1205     1415     1822
                  2395     2680     2922     3376
                  3543     3889     4609     5100
                  5110     5188     5224     5617
                  5722     5806     6173     6246
Nla IV      (43)  188      201      246      403
                  521      552      692      761
                  893      1144     1221     1399
                  1573     1689     1834     1909
                  1961     2165     2244     2356
                  2436     2443     2485     2486
                  2512     2589     3050     3063
                  3108     3265     3631     3917
                  3956     4728     4822     4863
                  5074     5664     6002     6185
                  6209     6299     6320
Not I       (1)   2491
Nru I       (1)   1644
Nsp7524 I   (4)   1818     3885     5802     6169
NspB II     (13)  588      1620     2056     2371
                  2490     3361     3709     4227
                  4472     5413     5879     6073
                  6429
NspH I      (4)   1822     3889     5806     6173
Pac I       (1)   2813
Pal I       (34)  129      173      584      726
                  762      774      987      1111
                  1132     1197     1416     1531
                  2116     2221     2486     2493
                  2562     2636     2707     2990
                  3035     3726     3900     3911
                  3929     4363     4821     4901
                  5168     5755     6053     6202
                  6210     6334
Ple I       (4)   799      2143     3428     4264
Pme I       (1)   1815
PpuM I      (4)   254      1219     1572     3116
Psp1406 I   (3)   2019     5004     5377
PspA I      (3)   397      2498     3259
Pst I       (4)   921      929      1105     2713
Pvu I       (3)   1648     5148     6044
Pvu II      (5)   1620     2056     3709     6073
                  6429
Rsa I       (9)   403      659      1284     1955
                  2421     3265     5258     5934
                  6445
Sac I       (2)   338      3200
Sac II      (2)   2372     2491
Sal I       (1)   2516
Sap I       (2)   3507     3769
Sau3A I     (30)  92       457      1044     1176
                  1361     1645     1706     1720
                  2337     2365     2375     2510
                  2545     2619     2953     4451
                  4526     4537     4545     4623
                  4635     4740     5081     5099
                  5145     5403     5420     5456
                  6041     6265
Sau96 I     (31)  127      171      186      199
                  254      551      690      760
                  773      985      1196     1219
                  1572     2219     2484     2485
                  2560     2635     2988     3033
                  3048     3061     3116     4820
                  4899     4916     5138     5754
                  6051     6208     6393
Sca I       (1)   5258
ScrF I      (38)  163      241      398      399
                  548      570      723      735
                  748      1169     1194     1217
                  1237     1267     1717     2218
                  2439     2499     2500     2564
                  2633     2639     3025     3103
                  3260     3261     3625     3913
                  4034     4047     4265     4961
                  5312     5813     5848     6120
                  6199     6397
Sec 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     2391
                  2488     2497     2498     2637
                  3023     3102     3112     3259
                  3322     3624     4045     6119
                  6197     6203
SfaN I      (21)  185      444      641      938
                  1485     1542     1674     1720
                  2088     3047     3305     3981
                  5033     5226     5473     5834
                  5926     5964     6002     6318
                  6330
Sfc I       (11)  15       917      925      1101
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		1496	2709	2875	4150
		4341	5019	6437	
Sma I	(3)	399	2500	3261	
Spe I	(1)	660			
Sph I	(1)	6173			
Ssp I	(2)	3428	5582		
Stu I	(1)	2707			
Sty I	(8)	250	461	1245	1411
		2238	2391	3112	3322
Taq I	(12)	794	1038	1349	1360
		1705	2069	2211	2364
		2517	3423	3985	5429
Tfi I	(7)	442	802	1437	1769
		3463	3720	3860	
Tsp45 I	(8)	1022	1231	2347	2450
		5034	5245	5821	6132
Tth111 I	(4)	390	811	1217	3252
Tth111 II	(9)	146	422	613	632
		2278	3007	4474	4483
		4513			
Vsp I	(4)	3528	3656	3715	4950
Xba I	(2)	218	3080		
Xcm I	(1)	2635			
Xho II	(10)	2337	2375	2510	2545
		4526	4537	4623	4635
		5403	5420		
Xma I	(3)	397	2498	3259	
Xma III	(3)	724	1529	2491	
Xmn I	(3)	3491	3529	5377	

Site usage in pSEB-Display:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	71
Afl II	C`TTAA,G	3	Afl 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	17	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	4	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	18	Ban II	G,RGCY`C	9
Bbe I	G,GCGC`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	17
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	3
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC|GTR	-	BsaB I	GATNN|NNATC	1
BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	38
BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	7
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	1
BsmA I	GTCTC`/9	23	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	12	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`	19
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
BstN I	CC`W,GG	21	BstU I	CG|CG	26
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	10
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN|NGC	39
Cfr10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	25
Dpn I	GA|TC	30	DpnII	`GATC,	30
Dra I	TTT|AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	6
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
Ear I	CTCTTC 7/10	7	Eco47 III	AGC|GCT	3
Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC|GTG	-
EcoN I	CCTNN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	7
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	21
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	17	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	7
Hae II	R,GCGC`Y	12	Hae III	GG|CC	34
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	7
HgiE II	ACCNNNNNNGGT -1/1	32	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	-	Hpa II	C`CG,G	32
Hph I	GGTGA 12/11	16	Kas I	G`GCGC,C	6
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Mae II	A`CG,T	11	Mae III	`GTNAC,	21
Mbo I	`GATC,	30	Mbo II	GAAGA 12/11	16
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	56	Msc I	TGG|CCA	3
Mse I	T`TA,A	27	Msl I	CAYNN|NNRTG	3
Msp I	C`CG,G	32	MspA1 I	CMG|CKG	13
Mun I	C`AATT,G	1	Nae I	GCC|GGC	3
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	17
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3
Nla III	,CATG`	20	Nla IV	GGN|NCC	43
Not I	GC`GGCC,GC	1	Nru I	TCG|CGA	1
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	4
NspB II	CMG|CKG	13	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-
Pal I	GG|CC	34	PflM I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	4	Pme I	CTTT|AAAC	1
Pml I	CAC|GTG	-	PpuM I	RG`GWC,CY	4
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	3
Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Pvu II	CAG|CTG	5	Rsa I	GT|AC	9
Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	30
Sau96 I	G`GNC,C	31	Sca I	AGT|ACT	1
ScrF I	CC`N,GG	38	Sec I	C`CNNG,G	38
SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	11
Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC|GGG	3
SnaB I	TAC|GTA	-	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
Srf I	GCCC|GGGC	-	Ssp I	AAT|ATT	2
Stu I	AGG|CCT	1	Sty I	C`CWWG,G	8
Taq I	T`CG,A	12	Tfi I	G`AWT,C	7
Tsp45 I	`GTSAC,	8	Tth111 I	GACN`N,NGTC	4
Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	4
Xba I	T`CTAG,A	2	Xca I	GTA|TAC	-
Xcm I	CCANNNNN,N`NNNNTGG	1	Xho I	C`TCGA,G	-
Xho II	R`GATC,Y	10	Xma I	C`CCGG,G	3
Xma III	C`GGCC,G	3	Xmn I	GAANN|NNTTC	3