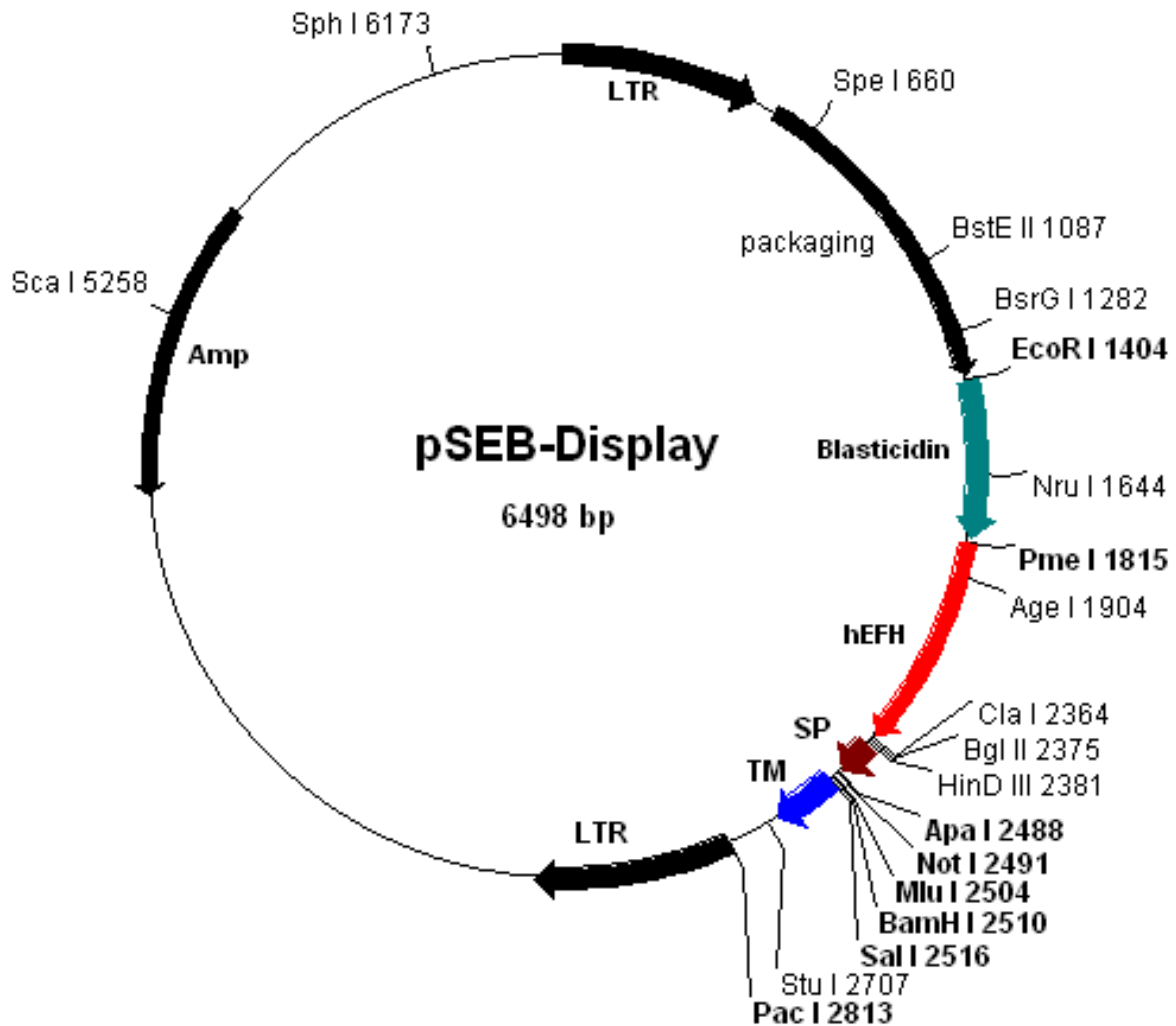


**Vector:** pSEB-Display (with SP and TM)

**Antibiotic Selection:** Amp

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

**Date of Construction:** October, 2009



**Ig  $\kappa$ -chain signal peptide**

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

**HA tag**

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

**Apa I**

**Not I**

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

**Mlu I**

**BamH I**

**Sal I**

**Myc tag**

**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 TTTGGCAAGCTAGCTTAAAGTAACGCCATTTTGCAAGGCATGGAAAATACATAACTGAGAA  
TAGAGAAGTTAGATCAAGGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTTCTCCCCGG  
CTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCC  
AAGGACCTGAAAATGACCCTGTGCCCTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCTCCCCGAG  
CTCAATAAAAAGAGCCCACAACCCCTCACTCGGCGCGCCAGTCTCAGATAGACTGCGTTCGCCCCGGGTACCCGTATTCCCAATAAA  
GCCTCTTGCTGTTTGCATCCGAATCGTGGACTCGCTGATCCTTGGGAGGGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGT  
CTTTTCATTTGGAGGTTCCACCGAGATTTGGAGACCCCTGCCAGGGACCACCGACCCCCCGCCGGGAGGTAAGCTGGCCAGCGG  
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CTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCCTGGGAGACGTCCAGGGACTTTGGGG  
GCCGTTTTTTGTGGCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGATATGTGGTTCTGGTAGGAGACGAGAA  
CCTAAAACAGTTCCCGCCTCCGTCTGAATTTTGTCTTTTCGGTTTGGAAACCGAAGCCGCGCGTC TTGTCTGCTG  
CAGCGCTGCAGCATCGTTCT GTGTTGTCTC TGCTGACTGTGTTTCTGTATTTGTCTGAA AATTAGGGCC AGACTGTTAC  
CACTCCCTTAAAGTTTGACCTTAGGTCAGTGGAAAAGATGTCGAGCGGATCGCTCACAAACA  
GTCGGTAGATGTCAAGAAGAGACGTTGGGTTACCTTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGC  
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TCGTGACCTGGGAAGCCTTGGCTTTTGAACCCCTCCCTGGGTCAAGCCCTTTGTACACCCTAAGCCTCCGCTCCTCTTCTCTCC  
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CCTAGACTCAGCGGCTCCACGCTTTGCTGACCTTGTCTCAACTTACGCTTCTGCTTCTTGTCTTCTGTTCTGCTGCGCCGCTT  
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CGTGTAGATA ACTACGATAC GGGAGGGCTTACCATCTGGCCCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCGG



		4962	5313	5814	5849	Dde I	(25)	75	167	208	476
		6200						781	1018	1290	1808
Bfa I	(16)	31	219	661	673			2111	2205	2256	2379
		1394	1522	1912	2063			2536	2623	2935	3029
		2189	2251	2891	3081			3070	3339	3410	4160
		4380	4633	4968	6403			4569	4735	5275	5701
Bgl I	(3)	2633	4898	6016				5936			
Bgl II	(1)	2375				Dpn I	(30)	94	459	1046	1178
Bpm I	(3)	2828	4848	6466				1363	1647	1708	1722
Bsa I	(7)	476	530	1149	2207			2339	2367	2377	2512
		3316	3337	4839				2547	2621	2955	4453
BsaB I	(1)	1711						4528	4539	4547	4625
BsaH I	(9)	742	1398	2355	5315			4637	4742	5083	5101
		5697	6001	6184	6298			5147	5405	5422	5458
		6319						6043	6267		
BsaJ I	(38)	161	240	250	397	DpnII	(30)	92	457	1044	1176
		461	497	546	547			1361	1645	1706	1720
		694	733	734	746			2337	2365	2375	2510
		747	1167	1236	1245			2545	2619	2953	4451
		1265	1266	1411	1716			4526	4537	4545	4623
		1974	2238	2369	2391			4635	4740	5081	5099
		2488	2497	2498	2637			5145	5403	5420	5456
		3023	3102	3112	3259			6041	6265		
		3322	3624	4045	6119	Dra I	(5)	1815	2200	4644	4663
		6197	6203					5355			
BsaW I	(5)	1829	1904	4091	4238	Drd I	(3)	1500	3993	5862	
		5069				Dsa I	(6)	694	1411	2369	2391
BseR I	(4)	464	1293	1332	3325			2488	6203		
Bsg I	(2)	1600	2022			Eae I	(11)	582	724	1109	1130
BsiE I	(10)	592	727	1532	1648			1414	1529	2491	3724
		2494	3801	4225	5148			5166	6200	6332	
		5297	6044			Eag I	(3)	724	1529	2491	
BsiHKA I	(7)	338	2649	3200	4203	Ear I	(7)	1070	1311	2535	3507
		5364	5449	5946				3769	5573	6061	
Bsm I	(1)	2557				Eco47 III	(3)	923	1826	6239	
BsmA I	(23)	107	475	531	609	Eco57 I	(5)	1509	2077	4432	5446
		734	832	949	1073			6450			
		1132	1150	1328	1431	EcoN I	(4)	784	1392	1915	2110
		2208	2391	2845	2968	EcoO109 I	(7)	254	1219	1572	2484
		3315	3336	4840	5614			3116	5754	6208	
		5767	5811	6483		EcoR I	(1)	1404			
BsmB I	(7)	733	831	1072	1131	EcoR II	(21)	239	546	733	746
		1329	5768	5810				1167	1192	1215	1235
BsmF I	(12)	172	185	564	729			1265	1715	2437	2562
		764	1205	1585	1853			2631	2637	3101	3623
		2515	3034	3047	6179			3911	4032	4045	6118
BsoF I	(42)	727	901	917	920			6395			
		925	928	1133	1513	EcoR V	(3)	140	3001	6386	
		1532	1606	1609	1612	Ehe I	(6)	1399	2356	6002	6185
		1615	1618	1782	1823			6299	6320		
		2043	2102	2117	2148	Fnu4H I	(42)	727	901	917	920
		2426	2491	2494	3710			925	928	1133	1513
		3791	3809	3812	3930			1532	1606	1609	1612
		4085	4228	4293	4296			1615	1618	1782	1823
		4502	4830	5169	5196			2043	2102	2117	2148
		5291	5520	5807	5916			2426	2491	2494	3710
		6020	6093					3791	3809	3812	3930
Bsp120 I	(1)	2484						4085	4228	4293	4296
BspH I	(4)	4605	5613	5718	6242			4502	4830	5169	5196
Bsr I	(19)	374	1030	1058	1546			5291	5520	5807	5916
		1570	1939	1960	2451			6020	6093		
		3236	3686	4292	4305	Fok I	(17)	423	1140	1300	1464
		4419	4825	4943	4986			1699	2107	2615	2654
		5253	5425	6131				2738	2771	2804	3284
BsrB I	(4)	1042	3577	3818	5619			4744	4925	5212	5855
BsrD I	(2)	4839	5013					6099			
BsrG I	(1)	1282				Fsp I	(2)	5000	6023		
BssH II	(4)	317	368	3179	3230	Gdi II	(11)	723	725	1129	1528
BssS I	(4)	1587	4058	5442	5749			1530	2490	2492	3725
BstE II	(1)	1087						5165	6201	6333	
BstN I	(21)	241	548	735	748	Gsu I	(3)	2829	4849	6467	
		1169	1194	1217	1237	Hae I	(7)	584	1111	1416	2707
		1267	1717	2439	2564			3900	3911	4363	
		2633	2639	3103	3625	Hae II	(12)	925	1401	1828	2235
		3913	4034	4047	6120			2358	3763	4133	6004
		6397						6187	6241	6301	6322
BstU I	(26)	317	319	370	903	Hae III	(34)	129	173	584	726
		905	1135	1644	1926			762	774	987	1111
		2095	2140	2371	2490			1132	1197	1416	1531
		2506	3179	3181	3232			2116	2221	2486	2493
		3732	3734	3932	4513			2562	2636	2707	2990
		4843	5336	5668	5768			3035	3726	3900	3911
		5770	5873					3929	4363	4821	4901
BstY I	(10)	2337	2375	2510	2545			5168	5755	6053	6202
		4526	4537	4623	4635			6210	6334		
		5403	5420			Hga I	(12)	381	642	895	1491
Bsu36 I	(3)	781	1018	2111				2168	2511	3243	3995
Cac8 I	(39)	28	32	319	370			4573	5305	5863	6332
		582	586	631	650	HgiA I	(7)	338	2649	3200	4203
		1199	1508	1622	2064			5364	5449	5946	
		2078	2099	2262	2290	HgiE II	(2)	4464	5944		
		2488	2709	2713	2888	Hha I	(43)	319	321	370	372
		2892	3181	3232	3678			648	905	924	1400
		3707	3816	3902	3939			1512	1827	1854	1926
		4499	4890	5903	6051			2097	2234	2329	2357
		6071	6075	6171	6212			3181	3183	3232	3234
		6260	6302	6332				3509	3669	3734	3762
Cfr10 I	(8)	629	1904	2128	2260			3795	4065	4132	4232
		2351	4858	6321	6330			4406	4515	4908	5001
Cla I	(1)	2364						5338	5670	5770	5873
Csp6 I	(9)	402	658	1283	1954			6003	6024	6157	6186
		2420	3264	5257	5933			6240	6300	6321	
		6444				HinC II	(1)	2518			

Hind II	(1)	2518				Nci I	(17)	163	398	399	570
HinD III	(1)	2381						723	2218	2499	2500
Hinf I	(17)	442	450	791	802			3025	3260	3261	4265
		1437	1769	2135	2254			4961	5312	5813	5848
		3420	3442	3463	3720			6199			
		3785	3860	4256	4773	Nco I	(2)		1411	2391	
		6411				Nde I	(2)		2461	5949	
HinI I	(9)	742	1398	2355	5315	Ngm I	(3)	629	2260	6330	
		5697	6001	6184	6298	Nhe I	(3)	30	2062	2890	
		6319				Nla III	(20)	62	1205	1415	1822
HinP I	(43)	317	319	368	370			2395	2680	2922	3376
		646	903	922	1398			3543	3889	4609	5100
		1510	1825	1852	1924			5110	5188	5224	5617
		2095	2232	2327	2355			5722	5806	6173	6246
		3179	3181	3230	3232	Nla IV	(43)	188	201	246	403
		3507	3667	3732	3760			521	552	692	761
		3793	4063	4130	4230			893	1144	1221	1399
		4404	4513	4906	4999			1573	1689	1834	1909
		5336	5668	5768	5871			1961	2165	2244	2356
		6001	6022	6155	6184			2436	2443	2485	2486
		6238	6298	6319				2512	2589	3050	3063
Hpa II	(32)	163	398	569	630			3108	3265	3631	3917
		723	1401	1830	1905			3956	4728	4822	4863
		2129	2217	2229	2261			5074	5664	6002	6185
		2352	2499	3025	3260			6209	6299	6320	
		3603	4092	4239	4265	Not I	(1)	2491			
		4455	4859	4893	4960	Nru I	(1)	1644			
		5070	5312	5813	5847	Nsp7524 I	(4)	1818	3885	5802	6169
		6199	6322	6331	6346	NspB II	(13)	588	1620	2056	2371
Hph I	(16)	1157	1183	1401	2461			2490	3361	3709	4227
		2628	2642	4622	4849			4472	5413	5879	6073
		5263	5471	5504	5788			6429			
		5797	6290	6335	6416	NspH I	(4)	1822	3889	5806	6173
Kas I	(6)	1397	2354	6000	6183	Pac I	(1)	2813			
		6297	6318			Pal I	(34)	129	173	584	726
Kpn I	(2)	405	3267					762	774	987	1111
Mae I	(16)	31	219	661	673			1132	1197	1416	1531
		1394	1522	1912	2063			2116	2221	2486	2493
		2189	2251	2891	3081			2562	2636	2707	2990
		4380	4633	4968	6403			3035	3726	3900	3911
Mae II	(11)	742	1081	1122	2019			3929	4363	4821	4901
		2302	2698	4588	5004			5168	5755	6053	6202
		5377	5697	6139				6210	6334		
Mae III	(21)	39	994	1022	1087	Ple I	(4)	799	2143	3428	4264
		1231	2331	2347	2450	Pme I	(1)	1815			
		2899	3377	4241	4304	PpuM I	(4)	254	1219	1572	3116
		4420	4703	5034	5092	Psp1406 I	(3)	2019	5004	5377	
		5245	5433	5821	6112	PspA I	(3)	397	2498	3259	
		6132				Pst I	(4)	921	929	1105	2713
Mbo I	(30)	92	457	1044	1176	Pvu I	(3)	1648	5148	6044	
		1361	1645	1706	1720	Pvu II	(5)	1620	2056	3709	6073
		2337	2365	2375	2510			6429			
		2545	2619	2953	4451	Rsa I	(9)	403	659	1284	1955
		4526	4537	4545	4623			2421	3265	5258	5934
		4635	4740	5081	5099			6445			
		5145	5403	5420	5456	Sac I	(2)	338	3200		
		6041	6265			Sac II	(2)	2372	2491		
Mbo II	(16)	1086	1299	1445	1502	Sal I	(1)	2516			
		1530	2551	2700	3523	Sap I	(2)	3507	3769		
		3757	4546	4619	5374	Sau3A I	(30)	92	457	1044	1176
		5452	5561	6049	6261			1361	1645	1706	1720
Mlu I	(1)	2504						2337	2365	2375	2510
Mme I	(6)	829	1106	3324	3376			2545	2619	2953	4451
		4099	4283					4526	4537	4545	4623
Mnl I	(56)	167	216	368	387			4635	4740	5081	5099
		432	460	484	506			5145	5403	5420	5456
		510	566	776	872			6041	6265		
		1168	1271	1304	1310	Sau96 I	(31)	127	171	186	199
		1313	1319	1349	1352			254	551	690	760
		1367	1374	1390	1454			773	985	1196	1219
		1795	1796	1880	1969			1572	2219	2484	2485
		2064	2106	2160	2176			2560	2635	2988	3033
		2536	2569	2680	2697			3048	3061	3116	4820
		3078	3230	3249	3294			4899	4916	5138	5754
		3321	3345	3405	3734			6051	6208	6393	
		3783	3993	4066	4317						
		4717	4798	4944	5150	Sca I	(1)	5258			
		5745	5803	6063	6347	ScrF I	(38)	163	241	398	399
Msc I	(3)	584	1111	1416				548	570	723	735
Mse I	(27)	36	1007	1119	1149			748	1169	1194	1217
		1173	1814	2199	2607			1237	1267	1717	2218
		2809	2813	2896	3430			2439	2499	2500	2564
		3528	3656	3715	4591			2633	2639	3025	3103
		4643	4648	4662	4715			3260	3261	3625	3913
		4950	4989	5354	5726			4034	4047	4265	4961
		5907	6104	6374				5312	5813	5848	6120
Msl I	(3)	2585	5030	5189				6199	6397		
Msp I	(32)	163	398	569	630	Sec I	(38)	161	240	250	397
		723	1401	1830	1905			461	497	546	547
		2129	2217	2229	2261			694	733	734	746
		2352	2499	3025	3260			747	1167	1236	1245
		3603	4092	4239	4265			1265	1266	1411	1716
		4455	4859	4893	4960			1974	2238	2369	2391
		5070	5312	5813	5847			2488	2497	2498	2637
		6199	6322	6331	6346			3023	3102	3112	3259
MspAl I	(13)	588	1620	2056	2371			3322	3624	4045	6119
		2490	3361	3709	4227			6197	6203		
		4472	5413	5879	6073	SfaN I	(21)	185	444	641	938
		6429						1485	1542	1674	1720
Mun I	(1)	1897						2088	3047	3305	3981
Nae I	(3)	631	2262	6332				5033	5226	5473	5834
Nar I	(6)	1398	2355	6001	6184			5926	5964	6002	6318
		6298	6319			Sfc I	(11)	6330			
								15	917	925	1101

		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	Acc 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	Alw I	CMG,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	Asp178	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,GGCC`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	GTGCG 22/20	2	BsiC I	TT`CG,AA	-
BsiE I	CG,R `CG	10	BsiHKA I	G,WGCW`C	7
BsiW I	C`GTAC,G	-	Bsm I	GATC,C 7	1
BsmA I	GTCTC`/9	23	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	12	BsoF I	G`C`N,GC	42
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DCGC`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	Cae8 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
Eae I	CTCTTC 7/10	7	Eco47 III	AGC GCT	3
Eco57 I	CTGGAG 21/19	5	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	4	Eco109 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,GGC`Y	12	Hae III	GG CC	34
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	7
HgiE II	ACCNNNNNNGGT -1/132	1	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`GGCG,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	MspAl 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,C	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	Pf1M 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	GCTCTC 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`CWGG,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`GTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNN`N`NNNTGG1	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 NNNTTC	3