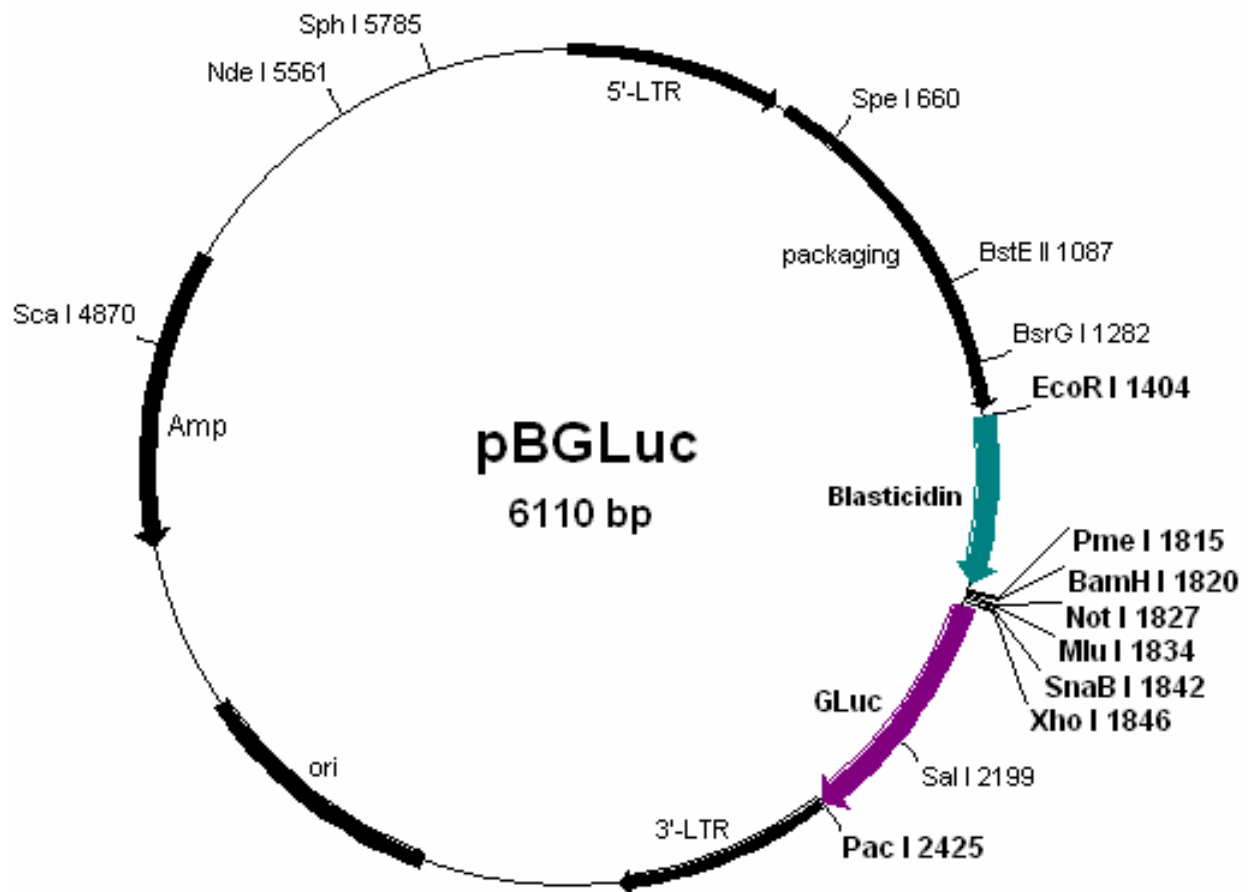


Vector: pBGLuc (SEB based Gaussian Luc Reporter Vector)

Antibiotic Selection: Amp

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

Date of Construction: March 2008



pBGLuc (GLuc Reporter Vector) Full-Length Sequence

TGAAGAACCC CACGTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGCAAGGCATGGAAAATACATAACTGAGAA TAGAGAAGTT AGATCAAGG
 TTAGGAACAGAGACAGCAGAGATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTTCTCCCGGCTCAGGGCCAAAGAACAGATGGTCCCAGATGCGGTCCCGC
 CCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTGCCCAAGGACCTGAAATGACCTGTGCCATTATTGAACTAACCAATGACGTTCGCTTCTCGCTTCT
 GTTCGCGCGCTTCTGCTCCCGAGCTCAATAAAAGAGCCCAACCCCTCACTCGGCGGCCAGTCTCCGATAGACTGCGTCCGCGGGTACCCGATATCCCAAT
 AAAGCCTCTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTGGAG
 GTTCCACCGA GATTTGGAGACCCTGCCA GGGACCACCGACCCCGCG CGGGAGGTAA GCTGGCCAGC GGTCTTTCGTGTCTGTCTC TGCTTTTGTG
 CGTGTGTTGCGCGCATCTAATGTTTGGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCGAAACCCG
 GCCG CAACCCTGGG AGACGTCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTGCATGTGGAATCCGACCCCGTCAAGATATGTGGTT
 CTGGTAGGAGACGAGAACCCT AAAACAGTTC CCGCTCCGT CTGAATTTTGTCTTCCGTT TGAACCCGAAGCCGCGCTC TTGTCTGCTG CAGCGCTGA
 GCATCGTTCT GTGTTGTCTC TGCTGACTGTGTTTCTGTA TTTGTCTGAA AATTAGGGCC AGACTGTAC CACTCCCTAAGTTTACCTTAGTCTACTG
 GAAAGATCTCGAGCGGATGC CTCACAACA GTCGGTAGAT GTCAAGAAAGAGACGTTGGGT TACCCTGTGC TCTGAGAAAT GGCCAACCTTAAACGTCGGA
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 TCGTGACCTG GGAAGCCTTG GCTTTTACCCTCCCTG GGTCAAGCCCTTTGTACACC CTAAGCCTCC GCCTCCTCTT CCTCCATCCGCCCCGTCTCT
 CCCCCTGAACTCCTCGTTTCGACCCCGCTCGATCCTCCTTTATCCAGCCCTCACTCCTTCTCTAGGCGCGGAACTCACATG GCCAAGCCTTTGTCTCAAGA
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 GCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGTTATGTGTGGGAGGGCtaa **gtttaa** ggatcc gcgccgc acgcgt tacgta ctcgag
 tctaga **gtacc** **ATG** GG AGTCAAAGTT CTGTTTGGCC TGATCTGCAT CGCTGTGGCC GAGGCCAAGC CCACCGAGAA CAACGAAGAC TTCAACATCG
 TGGCCGTGGC CAGCAACTTC GCGACCAGG ATCTCGATGC TGACCAGCGG AAGTTGCCCC GCAAGAAGCT GCCCTGGAG GTGCTCAAAG
 AGATGGAAGC CAATGCCCGG AAGCTGGCT GCACCAGGG CTGTCTGATC TGCTGTGCC ACATCAAGTG CACGCCAAG ATGAAGAAGT
 TCATCCAGG ACGTGGCCAC ACCTACGAAG GCGACAAAGA GTCCGACAG GCGCGCATAG GCGAGGCGAT CGTGCACATT CTTGAGATTC
 CTGGGTTCAA GGACTGGAG CCCATGGAGC AGTTCATCGC ACAGGTCGAT CTGTGTGTGG ACTGCACAAC TGCTGCTC AAAGGGCTTG
 CCAAGTGCA GTGTTCTGAC CTGCTCAAGA AGTGGCTGCC GCAACGCTGT GCGACCTTG CCAGCAAGAT CCAGGGCCAG GTGGACAAGA
 TCAAGGGGC CGGTGTT **GAC** **TAA** **ttaattaa**
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TCAGGGATAACGCAGGAAA GAACATGTGAGCAAAAGGCC AGCAAAAGC CAGGAACCGT AAAAAGCCCGCTTGTCTGGC GTTTTTCATAGGCTCCGCC
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ACCCGGTAAGACAGACTTA TGCCACTGGCAGCAGCCAG TGGTAACAG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTCTTGAAGTGGTG
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TTAGCTCCCGTTCCCAACG ATCAAGCGGA GTTACATGAT CCCCCATGTT GTGCAAAAA GCGGTTAGCTCCTTCCGTTCC TCCGATCGTTGTCAGAAGTA
AGTTGGCCCG AGTGTATACA CTACGCTTATGCGAGCAT GGCATAAATT CTTACTGTCA TGCCATCCGTAAGATGCTTT TCTGTGACTGTGTGAGTACT
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AGTCCAATTT GTTAAAGACA GGATATCAGTGGTCCAGGCT CTAGTTTTGA CTCAACAATA TCACCAGCTGAAGCCTATAG AGTACGAGCCATAGATAAAA
TAAAAGATTT TATTAGTCT CCAGAAAAAG GGGGAA

Unique enzymes in pBGLuc:

Spe I	A`CTAG,T	660	PaeR7 I	C`TCGA,G	1846
BstE II	G`GTNAC,C	1087	Xho I	C`TCGA,G	1846
BsrG I	T`GTAC,A	1282	Sal I	G`TCGA,C	2199
EcoR I	G`AATT,C	1404	Acc I	GT`MK,AC	2200
Pme I	CTTT AAAC	1815	HinC II	GTY RAC	2201
BamH I	G`GATC,C	1820	Hind II	GTY RAC	2201
Not I	GC`GGCC,CC	1827	BspM I	ACCTGC 10/14	2335
Mlu I	A`CGCG,T	1834	Pac I	TTA,AT`TAA	2425
BsaA I	YAC GTR	1842	Sca I	AGT ACT	4870
SnaB I	TAC GTA	1842	Nde I	CA`TA,TG	5561
			Sph I	G,CATG`C	5785
			Number of enzymes = 21		

The following enzymes do not cut in pBGLuc:

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

BsaA I	(1)	1842		
BsaB I	(2)	1711	1893	
BsaH I	(8)	742	1398	4927 5309
		5613	5796	5910 5931
BsaJ I	(41)	161	240	250 397
		461	497	546 547
		694	737	734 746
		747	1167	1236 1245
		1265	1266	1411 1716
		1824	1861	1906 1951

pBGLuc: sites sorted by name:

Aat II	(2)	745	5312								
Acc I	(1)	2200									
Acc65 I	(2)	401	2875								
Aci I	(64)	197	203	566	588	BsaW I	(3)	3703	3850	4681	
		688	727	860	901	BseR I	(4)	464	1293	1332	2937
		1042	1133	1199	1298	Bsg I	(4)	1600	2051	2264	2334
		1317	1355	1532	1614	BsiE I	(11)	592	727	1532	1648
		1681	1824	1826	1830			1830	2197	3413	3837
		1991	1993	2019	2170			4760	4909	5656	
		2179	2346	2671	2677	BsiHKA I	(8)	338	2032	2109	2812
		2973	3187	3290	3346			3815	4976	5061	5558
		3356	3380	3423	3430	BsmA I	(21)	107	475	531	609
		3451	3542	3570	3697			734	832	949	1073
		3716	3837	3947	4082			1132	1150	1328	1431
		4091	4453	4544	4735			2457	2580	2927	2948
		4781	4902	4946	5023			4452	5226	5379	5423
		5132	5231	5278	5452			6095			
		5491	5501	5527	5565	BsmB I	(7)	733	831	1072	1131
		5578	5604	5661	5920			1329	5380	5422	
Afl II	(3)	35	1006	2507		BsmF I	(11)	172	185	564	729
Afl III	(2)	1834	3497					764	1205	1585	2078
Aha II	(8)	742	1398	4927	5309			2646	2659	5791	
		5613	5796	5910	5931	BsoF I	(44)	727	901	917	920
Ahd I	(5)	1020	2165	2920	2966			925	928	1133	1513
		4390						1532	1606	1609	1612
Alu I	(29)	30	34	336	580			1615	1618	1782	1827
		668	676	1515	1620			1830	2016	2019	2066
		2015	2061	2502	2506			2141	2180	2291	2343
		2810	3129	3162	3257			2346	3322	3403	3421
		3321	3439	3665	3755			3424	3542	3697	3840
		3801	4058	4579	4679			3905	3908	4114	4442
		4742	5421	5440	5685			4781	4808	4903	5132
		6041						5419	5528	5632	5705
Alw I	(16)	453	1051	1357	1727	BspH I	(4)	4217	5225	5330	5854
		1816	1827	1983	2370	BspM I	(1)	2335			
		4059	4145	4145	4242	Bsr I	(17)	374	1030	1058	1546
		4243	4707	5022	5028			1570	2290	2848	3298
AlwN I	(3)	2077	2631	3913				3904	3917	4031	4437
Apal I	(4)	2105	3811	5057	5554			4555	4598	4865	5037
Apo I	(2)	872	1404					5743			
Asc I	(2)	368	2842			BsrB I	(4)	1042	3189	3430	5231
Ase I	(5)	2421	3140	3268	3327	BsrD I	(2)	4451	4625		
		4562				BsrG I	(1)	1282			
Asp718	(2)	401	2875			BssH II	(4)	317	368	2791	2842
Ava I	(6)	331	397	498	1846	BssS I	(4)	1587	3670	5054	5361
		2805	2871			BstE II	(1)	1087			
Ava II	(13)	186	199	254	551	BstN I	(22)	241	548	735	748
		690	1219	1572	2660			1169	1194	1217	1237
		2673	2728	4528	4750			1267	1717	2072	2134
		6005						2218	2379	2385	2715
BamH I	(1)	1820						3237	3525	3646	3659
Ban I	(13)	244	401	1142	1397			5732	6009		
		1687	2718	2875	3241	BstU I	(24)	317	319	370	903
		4338	5612	5795	5909			905	1135	1644	1826
		5930						1836	1968	1993	2791
Ban II	(8)	338	351	1677	2239			2793	2844	3344	3346
		2812	2825	5862	5876			3544	4125	4455	4948
Bbe I	(5)	1401	5616	5799	5913			5280	5380	5382	5485
		5934				BstY I	(9)	1820	1976	2374	4138
Bbs I	(2)	1498	1939					4149	4235	4247	5015
Bbv I	(9)	931	939	1524	1629			5032			
		3916	3919	4125	4819	Bsu36 I	(2)	781	1018		
		5430				Cac8 I	(37)	28	32	319	370
Bbv II	(2)	1497	1938					582	586	631	650
Bcn I	(16)	164	399	400	571			1199	1508	1622	1834
		724	2006	2055	2638			1958	2063	2109	2305
		2873	2874	3878	4574			2369	2500	2504	2793
		4925	5426	5461	5812			2844	3290	3319	3428
Bfa I	(13)	31	219	661	673			3514	3551	4111	4502
		1394	1522	1853	2503			5515	5663	5683	5687
		2693	3992	4245	4580			5783	5824	5872	5914
		6015						5944			
Bgl I	(2)	4510	5628			Cfr10 I	(5)	629	2406	4470	5933
Bpm I	(4)	2043	2440	4460	6078			5942			
Bsa I	(6)	476	530	1149	2928	Csp6 I	(9)	402	658	1283	1843
		2949	4451					1858	2876	4869	5545

		6056				HgiE II (2)	4076	5556		
Dde I (20)	75	167	208	476		Hha I (36)	319	321	370	372
	781	1018	1290	1808			648	905	924	1400
	2209	2547	2641	2682			1512	2793	2795	2844
	2951	3022	3772	4181			2846	3121	3281	3346
	4347	4887	5313	5548			3374	3407	3677	3744
Dpn I (32)	94	459	1046	1178			3844	4018	4127	4520
	1363	1647	1708	1722			4613	4950	5282	5382
	1822	1890	1978	2085			5485	5615	5636	5769
	2196	2266	2376	2397			5798	5852	5912	5933
	2567	4065	4140	4151		HinC II (1)	2201			
	4159	4237	4249	4354		Hind II (1)	2201			
	4695	4713	4759	5017		Hinf I (19)	442	450	791	802
	5034	5070	5655	5879			1437	1769	1849	1867
DpnII (32)	92	457	1044	1176			2166	2213	3032	3054
	1361	1645	1706	1720			3075	3332	3397	3472
	1820	1888	1976	2083			3868	4385	6023	
	2194	2264	2374	2395		HinI I (8)	742	1398	4927	5309
	2565	4063	4138	4149			5613	5796	5910	5931
	4157	4235	4247	4352		HinP I (36)	317	319	368	370
	4693	4711	4757	5015			646	903	922	1398
	5032	5068	5653	5877			1510	2791	2793	2842
Dra I (4)	1815	4256	4275	4967			2844	3119	3279	3344
Drd I (3)	1500	3605	5474				3372	3405	3675	3742
Dsa I (9)	694	1411	1824	1861			3842	4016	4125	4518
	1951	1972	1991	2239			4611	4948	5280	5380
	5815						5483	5613	5634	5767
Eae I (14)	582	724	1109	1130			5796	5850	5910	5931
	1414	1529	1827	1903		Hpa II (27)	163	398	569	630
	1948	1954	3336	4778			723	1401	2005	2054
	5812	5944					2407	2637	2872	3215
Eag I (3)	724	1529	1827				3704	3851	3877	4067
Ear I (6)	1070	1311	3119	3381			4471	4505	4572	4682
	5185	5673					4924	5425	5459	5811
Eco47 III (2)	923	5851					5934	5943	5958	
Eco57 I (4)	1509	4044	5058	6062		Hph I (14)	1157	1183	1401	2423
EcoN I (2)	784	1392					4234	4461	4875	5083
EcoO109 I (6)	254	1219	1572	2728			5116	5400	5409	5902
	5366	5820					5947	6028		
EcoR I (1)	1404					Kas I (5)	1397		5795	5909
EcoR II (22)	239	546	733	746			5930			
	1167	1192	1215	1235				2879		
	1265	1715	2070	2132		Kpn I (2)	405			
	2216	2377	2383	2713		Mae I (13)	31	219	661	673
	3235	3523	3644	3657			1394	1522	1853	2503
	5730	6007					2693	3992	4245	4580
							6015			
EcoR V (3)	140	2613	5998				742	1081	1122	1841
Ehe I (5)	1399	5614	5797	5911			2311	4200	4616	4989
	5932						5309	5751		
Fnu4H I (44)	727	901	917	920			39	994	1022	1087
	925	928	1133	1513			1231	1837	2412	2511
	1532	1606	1609	1612			2989	3853	3916	4032
	1615	1618	1782	1827			4315	4646	4704	4857
	1830	2016	2019	2066			5045	5433	5724	5744
	2141	2180	2291	2343		Mbo I (32)	92	457	1044	1176
	2346	3322	3403	3421			1361	1645	1706	1720
	3424	3542	3697	3840			1820	1888	1976	2083
	3905	3908	4114	4442			2194	2264	2374	2395
	4781	4808	4903	5132			2565	4063	4138	4149
	5419	5528	5632	5705			4157	4235	4247	4352
Fok I (12)	423	1140	1300	1464			4693	4711	4757	5015
	1699	2115	2896	4356			5032	5068	5653	5877
	4537	4824	5467	5711			1086	1299	1445	1502
						Mbo II (16)	1530	1943	2131	3135
Fsp I (2)	4612	5635					3369	4158	4231	4986
Gdi II (13)	723	725	1129	1528			5064	5173	5661	5873
	1530	1826	1828	1902						
	1947	3337	4777	5813		Mlu I (1)	1834			
	5945					Mme I (6)	829	1106	2936	2988
Gsu I (4)	2042	2441	4461	6079			3711	3895		
Hae I (8)	584	1111	1416	1911		Mnl I (50)	167	216	368	387
	1956	3512	3523	3975			432	460	484	506
Hae II (9)	925	1401	3375	3745			510	566	776	872
	5616	5799	5853	5913			1168	1271	1304	1310
	5934						1313	1319	1349	1352
Hae III (34)	129	173	584	726			1367	1374	1390	1454
	762	774	987	1111			1795	1796	1901	2018
	1132	1197	1416	1531			2183	2303	2690	2842
	1829	1905	1911	1950			2861	2906	2933	2957
	1956	2383	2406	2602			3017	3346	3395	3605
	2647	3338	3512	3523			3678	3929	4329	4410
	3541	3975	4433	4513			4556	4762	5357	5415
	4780	5367	5665	5814			5675	5959		
	5822	5946								
Hga I (11)	381	642	895	1491		Msc I (4)	584	1111	1416	1956
	2145	2855	3607	4185		Mse I (25)	36	1007	1119	1149
	4917	5475	5944				1173	1814	2421	2425
HgiA I (8)	338	2032	2109	2812			2508	3042	3140	3268
	3815	4976	5061	5558			3327	4203	4255	4260
							4274	4327	4562	4601

		4966	5338	5519	5716		5366	5663	5820	6005
		5986				Sca I (1)	4870			
Msl I (3)		1899	4642	4801		ScrF I (38)	163	241	398	399
Msp I (27)		163	398	569	630		548	570	723	735
		723	1401	2005	2054		748	1169	1194	1217
		2407	2637	2872	3215		1237	1267	1717	2005
		3704	3851	3877	4067		2054	2072	2134	2218
		4471	4505	4572	4682		2379	2385	2637	2715
		4924	5425	5459	5811		2872	2873	3237	3525
		5934	5943	5958			3646	3659	3877	4573
MspAl I (13)		588	1620	1826	1993		4924	5425	5460	5732
		2021	2973	3321	3839		5811	6009		
		4084	5025	5491	5685	Sec I (41)	161	240	250	397
		6041					461	497	546	547
Nae I (2)		631	5944				694	733	734	746
Nar I (5)		1398	5613	5796	5910		747	1167	1236	1245
		5931					1265	1266	1411	1716
Nci I (16)		163	398	399	570		1824	1861	1906	1951
		723	2005	2054	2637		1972	1991	2071	2132
		2872	2873	3877	4573		2217	2239	2378	2635
		4924	5425	5460	5811		2714	2724	2871	2934
Nco I (3)		1411	1861	2239			3236	3657	5731	5809
Nde I (1)		5561					5815			
NgoM I (2)		629	5942			SfaN I (22)	185	444	641	938
Nhe I (2)		30	2502				1485	1542	1674	1720
Nla III (19)		62	1205	1415	1865		1902	1974	2659	2917
		2243	2534	2988	3155		3593	4645	4838	5085
		3501	4221	4712	4722		5446	5538	5576	5614
		4800	4836	5229	5334		5930	5942		
		5418	5785	5858		Sfc I (10)	15	917	925	1101
Nla IV (34)		188	201	246	403		1496	2487	3762	3953
		521	552	692	761		4631	6049		
		893	1144	1221	1399	Sma I (2)	399	2873		
		1573	1689	1822	2236	SnaB I (1)	1842			
		2405	2662	2675	2720	Spe I (1)	660			
		2877	3243	3529	3568	Sph I (1)	5785			
		4434	4434	4475	4686	Ssp I (2)	3040	5194		
		5276	5614	5797	5821	Sty I (8)	250	461	1245	1411
		5911	5932				1861	2239	2724	2934
Not I (1)		1827				Taq I (12)	794	1038	1349	1360
Nru I (2)		1644	1968				1705	1847	1981	2200
Nsp7524 I (3)		3497	5414	5781			2263	3035	3597	5041
NspB II (13)		588	1620	1826	1993	Tfi I (8)	442	802	1437	1769
		2021	2973	3321	3839		2213	3075	3332	3472
		4084	5025	5491	5685	Tsp45 I (7)	1022	1231	2412	4646
		6041					4857	5433	5744	
NspH I (3)		3501	5418	5785		Tth111 I (4)	390	811	1217	2864
Pac I (1)		2425				Tth111 II (9)	146	422	613	632
PaeR7 I (1)		1846					1870	2619	4086	4095
Pal I (34)		129	173	584	726		4125			
		762	774	987	1111	Vsp I (5)	2421	3140	3268	3327
		1132	1197	1416	1531		4562			
		1829	1905	1911	1950	Xba I (3)	218	1852	2692	
		1956	2383	2406	2602	Xho I (1)	1846			
		2647	3338	3512	3523	Xho II (9)	1820	1976	2374	4138
		3541	3975	4433	4513		4149	4235	4247	5015
		4780	5367	5665	5814		5032			
		5822	5946			Xma I (2)	397	2871		
Ple I (6)		799	1857	1875	2174	Xma III (3)	724	1529	1827	
		3040	3876			Xmn I (4)	2124	3103	3141	4989
Pme I (1)		1815								
PpuM I (4)		254	1219	1572	2728					
Psp1406 I (2)		4616	4989			Site usage in pBGLuc:				
PspA I (2)		397	2871			Aat II G,ACGT`C	2	Acc I GT`MK,AC		1
Pst I (3)		921	929	1105		Acc65 I G`GTAC,C	2	Acc I C`CG,C		64
Pvu I (4)		1648	2197	4760	5656	Afl II C`TTAA,G	3	Afl III A`CRYG,T		2
Pvu II (4)		1620	3321	5685	6041	Age I A`CCGG,T	-	Aha II GR`CG,YC		8
Rsa I (9)		403	659	1284	1844	Ahd I GACNN,N`NNGTC	5	Alu I AG CT		29
		1859	2877	4870	5546	Alw I GGATC 8/9	16	AlwN I CAG,NNN`CTG		3
		6057				Apa I G,GGCC`C	-	ApaL I G`TGCA,C		4
						Apo I R`AATT,Y	2	Asc I GG`CGCG,CC		2
Sac I (2)		338	2812			Ase I AT`TA,AT	5	Asp718 G`GTAC,C		2
Sac II (2)		1827	1994			Ava I C`YCGR,G	6	Ava II G`GWC,C		13
Sal I (1)		2199				Avr II C`CTAG,G	-	BamH I G`GATC,C		1
Sap I (2)		3119	3381			Ban I G`GYRC,C	13	Ban II G,RCGY`C		8
Sau3A I (32)		92	457	1044	1176	Bbe I G,CGCC`C	5	Bbs I GAAGAC 8/12		2
		1361	1645	1706	1720	Bbv I GCAGC 13/17	9	Bbv II GAAGAC 7/11		2
		1820	1888	1976	2083	Bcl I T`GATC,A	-	Bcn I CC,S`GG		16
		2194	2264	2374	2395	Bfa I C`TA,G	13	Bgl I GCCN,NNN`NGGC		2
		2565	4063	4138	4149	Bgl II A`GATC,T	-	Blp I GC`TNA,GC		-
		4157	4235	4247	4352	Bpm I CTGGAG 22/20	4	Bsa I GGTCTC 7/11		6
		4693	4711	4757	5015	BsaA I YAC GTR	1	BsaB I GATNN NNATC		2
		5032	5068	5653	5877	BsaH I GR`CG,YC	8	BsaJ I C`CNNG,G		41
						BsaW I W`CCGG,W	3	BseE I GAGGAG 16/14		4
						Bsg I GTGCAG 22/20	4	Bsic I TT`CG,AA		-
Sau96 I (28)		127	171	186	199	BsiE I CG,RY`CG	11	BsiHKA I G,WGCW`C		8
		254	551	690	760	BsiW I C`GTAC,G	-	Bsm I GAATG,C 7		-
		773	985	1196	1219	BsmA I GTCTC`/9	21	BsmB I CGTCTC 7/11		7
		1572	2381	2404	2600	BsmF I GGGAC 15/19	11	BsoF I GC`N,GC		44
		2645	2660	2673	2728	Bsp120 I G`GGCC,C	-	Bsp1286 I G,DGCH`C		-
		4432	4511	4528	4750	BspH I T`CATG,A	4	BspM I ACCTGC 10/14		1
						BspM II T`CCGG,A	-	Bsr I ACT,GG`		17
						BsrB I GAG CGG	4	BsrD I GCAATG, 8		2

BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4	Msp I	C`CG,G	27	MspA1 I	CMG CKG	13
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-	Mun I	C`AATT,G	-	Nae I	GCC GGC	2
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1	Nar I	GG`CG,CC	5	Nci I	CC`S,GG	16
BstN I	CC`W,GG	22	BstU I	CG CG	24	Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	9	NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	37	Nla III	,CATG`	19	Nla IV	GGN NCC	34
Cfr10 I	R`CCGG,Y	5	Cla I	AT`CG,AT	-	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	2
Csp6 I	G`TA,C	9	Dde I	C`TNA,G	20	Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	3
Dpn I	GA TC	32	DpnII	`GATC,	32	NspB II	CMG CKG	13	NspH I	R,CATG`Y	3
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	9	Pal I	GG CC	34	Pf1M I	CCAN,NNN`NTGG	-
Eae I	Y`GGCC,R	14	Eag I	C`GGCC,G	3	Ple I	GAGTC 9/10	6	Pme I	CTTT AAAC	1
Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
EcoN I	CCTNN`N,NNAGG	2	EcoO109 I	RG`GNC,CY	6	Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	4
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	22	Pvu II	CAG CTG	4	Rsa I	GT AC	9
EcoR V	GAT ATC	3	Ehe I	GGC GCC	5	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	44	Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
Fok I	GGATG 14/18	12	Fse I	GG,CCGG`CC	-	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	32
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	13	Sau96 I	G`GNC,C	28	Sca I	AGT ACT	1
Gsu I	CTGAG 21/19	4	Hae I	WGG CCW	8	ScrF I	CC`N,GG	38	Sec I	C`CNNG,G	41
Hae II	R,GCGC`Y	9	Hae III	GG CC	34	SfaN I	GCATC 9/13	22	Sfc I	C`TRYA,G	10
Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	8	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	36	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Hinc II	GTY RAC	1	Hind II	GTY RAC	1	Sph I	G,CATG`C	1	Sp1 I	C`GTAC,G	-
Hind III	A`AGCT,T	-	Hinf I	G`ANT,C	19	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
HinI I	GR`CG,YC	8	HinP I	G`CG,C	36	Stu I	AGG CCT	-	Sty I	C`CWWG,G	8
Hpa I	GTT AAC	-	Hpa II	C`CG,G	27	Taq I	T`CG,A	12	Tfi I	G`AWT,C	8
Hph I	GGTGA 12/11	14	Kas I	G`GCGC,C	5	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	4
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	13	Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	5
Mae II	A`CG,T	10	Mae III	`GTNAC,	20	Xba I	T`CTAG,A	3	Xca I	GTA TAC	-
Mbo I	`GATC,	32	Mbo II	GAAGA 12/11	16	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6	Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	2
Mnl I	CCTC 10/10	50	Msc I	TGG CCA	4	Xma III	C`GGCC,G	3	Xmn I	GAANN NNITC	4
Mse I	T`TA,A	25	Msl I	CAYNN NNRTG	3						