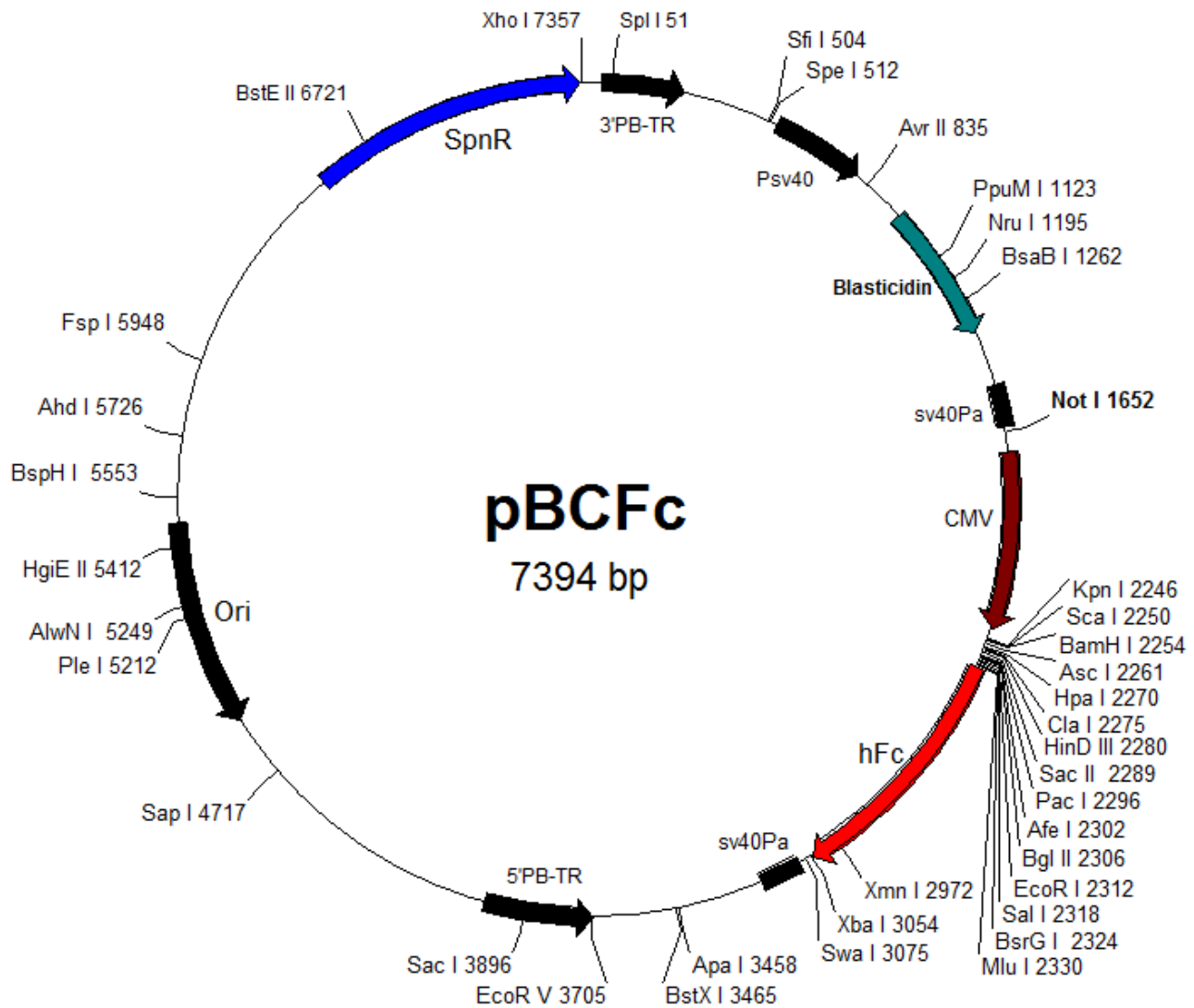


**Vector:** pBCFc (Molab modified PiggyBac vector for CMV-driven hIgG1 Fc fusion)

**Antibiotic Selection:** Spectinomycin or Blasticidin-resistant

**Creator:** Xin Wang, Molecular Oncology Lab of The University of Chicago

**Date of Construction:** January 2015



KpnI ScaI BamHI AscI HpaI ClaI HindIII SacII PacI AfeI  
GGTACCAGTACTGGATCCGGCGCGCCGTTAACATCGATAAGCTTCCGCGGTTAATTAAGCGCT  
- S A

BglIII EcoRI SalI BsrGI MluI  
AGATCTGAATTCGTCGACTGTACAACGCGTGGAGGC GGCGGAGGTGTCGAGCCC AAAATCTTGTG  
K S V I F D C T T R G G G G G V E P K S C

## pBCFc Vector Full-Length Sequence (Spectinomycin or Blasticin-resistant)

CTGCAGAACACGCAGCTAGATTAACCCCTAGAAAAGATAATCATATTGTGACGTACGTTAAAGATAATCATGCGTAAAAATTGACGCATGTGTTTTA  
TCGGTCTGTATATCGAGGTTTATTTATTAATTTGAATAGATATTAAGTTTTATTATATTTACTTACATACTAATAATAAAATCAACAAAACA  
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AAGCCCCCAGGGATGTAATTACGTCCCTCCCCCGCTAGGGGGCAGCAGCGAGCCGCCCGGGGCTCCGCTCCGGTCCGGCCTCCCCCGCATCC  
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AATTTTTTTTATTTATGCAAGGCGAGGCCGCTCTGCTCTGAGCTATTCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCTTAGGCTTTTGC  
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GAGCCCCGCGGACGGTGCAGCAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTT  
GGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAAGCACTTCGTGGCCGAGGAGCAGGACTGACACGTGCTACGAGATTCGAT  
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GGTCGATGTTTGTATGTTATGGAGCAGCAACGATGTTACGCAGCAGGGCAGTCGCCCTAAAACAAAGTTAAACATTATGAGGGAAGCGGTGATCG  
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 AGCTAGACAGGCTTATCTTGACAAGAAGAAGATCGCTTGGCCTCGCGCGCAGATCAGTTGGAAGAATTTGTCCACTACGTGAAAGGCGAGATC  
 ACCAAGGTAGTCGGCAAATAACCCTCGAGCCACCCATGACCAAATCCCTTAACGTGAGTTA

**Unique enzymes in pBCFc:**

			1930	2021	2054	2158
			2179	2286	2288	2340
BsiW I	C`GTAC,G	51	2343	2579	2581	3572
Spl I	C`GTAC,G	51	3595	3617	3629	3650
Sfi I	GGCCN,NNN`NGGCC	504	3834	3867	3901	4109
Spe I	A`CTAG,T	512	4122	4271	4378	4383
Avr II	C`CTAG,G	835	4431	4468	4523	4626
PpuM I	RG`GWC,CY	1123	4682	4692	4716	4759
Nru I	TCG CGA	1195	4766	4787	4878	4906
BsaB I	GATNN NNATC	1262	5033	5052	5173	5283
Not I	GC`GGCC,GC	1652	5418	5427	5789	5880
Acc65 I	G`GTAC,C	2242	6071	6117	6384	6404
Asp718	G`GTAC,C	2242	6572	6669	6681	6748
Kpn I	G,GTAC`C	2246	6811	7007	7010	7088
Sca I	AGT ACT	2250	7135			
BamH I	G`GATC,C	2254				
Asc I	GG`CGCG,CC	2261	Afe I (1)	2302		
Hpa I	GTT AAC	2270	Afl III (4)	894	1390	2330 4833
Cla I	AT`CG,AT	2275	Aha II (6)	1461	1773	1826 1909
HinD III	A`AGCT,T	2280		2095	6615	
Pac I	TTA,AT`TAA	2296	Ahd I (2)	2423	5726	
Afe I	AGC GCT	2302	Alu I (30)	16	799	853 863
Eco47 III	AGC GCT	2302		1066	1171	1535 2217
Bgl II	A`GATC,T	2306		2282	2779	2935 3260
EcoR I	G`AATT,C	2312		3894	4020	4063 4498
Sal I	G`TCGA,C	2318		4593	4657	4775 5001
Acc I	GT`MK,AC	2319		5091	5137	5394 5915
Mlu I	A`CGCG,T	2330		6015	6078	6325 6755
Xmn I	GAANN NNITC	2972		6869	7241	
Xba I	T`CTAG,A	3054	Alw I (18)	434	888	1278 1469
Swa I	ATTT AAAT	3075		1496	2232	2250 2261
Bsp120 I	G`GGCC,C	3454		3532	4036	5395 5481
Apa I	G,GGCC`C	3458		5481	5578	5579 6043
BstX I	CCAN,NNNN`NTGG	3465		7020	7049	
EcoR V	GAT ATC	3705	AlwN I (2)	2402	5249	
Sac I	G,AGCT`C	3896	Apa I (1)	3458		
Ple I	GAGTC 9/10	5212	ApaL I (2)	5147	6836	
HgiE II	ACCNNNNNNGGT -1/135412		Apo I (6)	175	233	1570 2312
Fsp I	TGC GCA	5948		3144	7304	
Psp1406 I	AA`CG,TT	5952	Asc I (1)	2261		
BstE II	G`GTNAC,C	6721	Ase I (6)	122	906	4369 4604
PaeR7 I	C`TCGA,G	7357		4663	5898	
Xho I	C`TCGA,G	7357	Asp718 (1)	2242		
Number of enzymes = 41			Ava I (11)	339	377	403 856
				2736	2769	3560 3586
				3624	6453	7357

**The following enzymes do not cut in pBCFc:**

Afl II	Age I	Bbe I	BsiC I	BsmB I					
Bsp1286 I	Bst1107 I	BstB I	Ehe I	Fse I	Avr II (1)	835			
Kas I	Mun I	Nar I	Nhe I	PflM I	BamH I (1)	2254			
					Ban I (5)	1238	2116	2242	4577
						5674			
					Ban II (6)	347	1228	2358	3458
						3624	3896		
					Ebs I (4)	1049	2419	2520	2965
					Ebv I (21)	25	337	340	398
						1075	1180	1544	2743
						2875	2971	3424	3523
						5252	5255	5461	6155
						6393	6478	6522	6538
						6910			
					Ebv II (4)	1048	2420	2519	2966
Aat II (4)	1776	1829	1912	2098					
Acc I (1)	2319								
Acc65 I (1)	2242								
Aci I (81)	315	336	348	370					
	393	683	695	704					
	716	726	737	783					
	1083	1165	1232	1416					
	1419	1485	1651	1655					
	1709	1737	1749	1763					

pBCFc: sites sorted by name:

Bcl I	(2)	886	6759					2247	2255	2539	2647	
Bcn I	(21)	341	342	405	406			3331	3441	4262	4634	
		858	859	1458	2471			5240	5253	5367	5773	
		2771	2772	3043	3280			5891	5934	6201	6296	
		3429	3562	3563	3626			6361	7099	7195	7217	
		3627	4466	5214	5910		BsrB I	(4)	350	3617	4525	4766
		6257					BsrD I	(5)	2863	5787	5961	6910
Bfa I	(17)	17	28	318	513			7203				
		836	1073	1605	2304		BsrG I	(2)	2324	2751		
		3055	3179	3647	4006		BssH II	(3)	2261	4472	7285	
		4017	5328	5581	5916		BssS I	(2)	1138	5006		
		7242					BstE II	(1)	6721			
Bgl I	(6)	504	1741	1863	1934		BstN I	(24)	291	477	549	604
		5846	7193					621	1268	1741	1934	
Bgl II	(1)	2306						2411	2639	2792	2810	
Blp I	(2)	1359	6870					3359	3417	3489	3675	
Bpm I	(4)	1463	1520	5796	6813			4253	4420	4573	4861	
Bsa I	(3)	2680	3274	5787				4982	4995	6215	6792	
BsaA I	(9)	895	1393	1991	2542		BstU I	(24)	1195	1485	1711	2263
		2604	3062	3743	3801			2288	2332	2581	3834	
		7318						3940	4111	4271	4474	
BsaB I	(1)	1262						4680	4682	4880	5461	
BsaH I	(6)	1461	1773	1826	1909			5791	6475	6748	6813	
		2095	6615					6876	7169	7285	7287	
BsaJ I	(44)	289	290	339	340		BstX I	(1)	3465			
		403	476	502	547		BstY I	(10)	881	1489	2236	2254
		619	742	777	835			2306	5474	5485	5571	
		856	962	1267	1374			5583	7042			
		2011	2286	2410	2448		Bsu36 I	(2)	2478	2520		
		2579	2769	2841	2940		Cac8 I	(40)	333	384	391	467
		3278	3426	3487	3560			562	581	634	653	
		3623	3624	3673	3674			1059	1173	1465	1737	
		4141	4252	4572	4993			1930	2263	2933	3500	
		6246	6269	6452	6483			3576	3583	3634	3881	
		6790	6854	6993	7335			3978	4065	4219	4470	
BsaW I	(9)	352	2239	3611	4279			4474	4626	4655	4764	
		4291	5039	5186	6017			4850	4887	5447	5838	
		7027						6471	6648	6753	6933	
BseR I	(3)	831	1391	2600				7102	7208	7212	7287	
Bsg I	(4)	1151	2618	2987	4383		Cfr10 I	(8)	382	1463	3581	4332
BsiE I	(8)	1083	1199	1655	3838			4356	5806	7157	7210	
		4749	5173	6096	6942		Cla I	(1)	2275			
BsiHKA I	(3)	3896	5151	6840			Csp6 I	(21)	52	1869	1894	1949
BsiW I	(1)	51						1982	2033	2190	2243	
Bsm I	(3)	1600	3174	3978				2249	2325	2539	2593	
BsmA I	(6)	982	2084	2679	3041			2605	2662	2752	3063	
		3273	5788					6207	6440	6653	6661	
BsmF I	(18)	281	291	410	529			7144				
		601	665	1136	1472		Dde I	(9)	795	1359	2478	2520
		1826	1977	2145	2430			3908	5108	5517	5683	
		3296	3379	3553	3672			6870				
		3682	7117				Dpn I	(34)	429	883	888	1198
BsoF I	(62)	14	326	329	336			1259	1273	1475	1491	
		387	454	783	1064			2238	2256	2308	2465	
		1083	1157	1160	1163			3081	3538	4031	5401	
		1166	1169	1333	1419			5476	5487	5495	5573	
		1533	1652	1655	2341			5585	5690	6031	6049	
		2579	2732	2864	2960			6095	6578	6761	6941	
		3413	3512	3579	3630			6951	7026	7044	7272	
		3637	3640	3902	4021			7293	7331			
		4123	4154	4157	4272		DpnII	(34)	427	881	886	1196
		4384	4431	4658	4739			1257	1271	1473	1489	
		4757	4760	4878	5033			2236	2254	2306	2463	
		5176	5241	5244	5450			3079	3536	4029	5399	
		5778	6117	6144	6239			5474	5485	5493	5571	
		6382	6467	6511	6527			5583	5688	6029	6047	
		6682	6749	6899	7008			6093	6576	6759	6939	
		7088	7185					6949	7024	7042	7270	
Bsp120 I	(1)	3454						7291	7329			
BspH I	(2)	2460	5553				Dra I	(4)	3075	3308	5592	5611
BspM I	(3)	2813	2943	6908			Dra III	(4)	1369	6270	6698	7318
BspM II	(2)	4279	4291				Drd I	(4)	1051	2522	3912	4941
Bsr I	(24)	721	1097	1121	1947		Dsa I	(11)	502	742	962	2011

		2286	2579	2841	2940			6815	6876	6903	7057
		6269	6483	6854				7151	7171	7206	7287
Eae I	(9)	505	965	1080	1371						
		1652	4210	4672	6114						
		6648				HinC II	(4)	900	2270	2320	3355
Eag I	(2)	1080	1652			Hind II	(4)	900	2270	2320	3355
Ear I	(3)	2438	3017	4717		HinD III	(1)	2280			
Eco47 III	(1)	2302				Hinf I	(19)	988	1320	1409	1446
Eco57 I	(3)	1060	5380	6706				2061	2903	3051	3229
Eco72 I	(2)	895	1393					3441	3827	3935	4196
EcoN I	(2)	2636	3449					4668	4733	4808	5204
EcoO109 I	(2)	1123	3454					5721	6592	6805	
EcoR I	(1)	2312				HinI I	(6)	1461	1773	1826	1909
EcoR II	(24)	289	475	547	602			2095	6615		
		619	1266	1739	1932	HinP I	(37)	361	1061	1483	2261
		2409	2637	2790	2808			2263	2301	3604	3940
		3357	3415	3487	3673			4067	4310	4386	4472
		4251	4418	4571	4859			4474	4615	4680	4708
		4980	4993	6213	6790			4741	5011	5078	5178
EcoR V	(1)	3705						5352	5461	5854	5947
Esp I	(2)	1359	6870					6346	6396	6473	6625
Fnu4H I	(62)	14	326	329	336			6813	6874	6901	7055
		387	454	783	1064			7149	7169	7204	7285
		1083	1157	1160	1163	Hpa I	(1)	2270			
		1166	1169	1333	1419	Hpa II	(40)	340	353	358	383
		1533	1652	1655	2341			404	857	1456	1464
		2579	2732	2864	2960			2240	2258	2470	2770
		3413	3512	3579	3630			2867	3041	3278	3428
		3637	3640	3902	4021			3561	3582	3607	3612
		4123	4154	4157	4272			3625	4280	4292	4333
		4384	4431	4658	4739			4343	4357	4465	4551
		4757	4760	4878	5033			5040	5187	5213	5403
		5176	5241	5244	5450			5807	5841	5908	6018
		5778	6117	6144	6239			6255	7028	7158	7211
		6382	6467	6511	6527	Hph I	(13)	959	2026	2618	2930
		6682	6749	6899	7008			4241	5570	5797	6211
		7088	7185					6269	6585	6732	6818
Fok I	(21)	307	359	686	1015			7325			
		1250	1483	2752	2786	Kpn I	(1)	2246			
		3277	3604	3656	4158	Mae I	(17)	17	28	318	513
		4307	4439	5692	5873			836	1073	1605	2304
		6160	6292	6445	6689			3055	3179	3647	4006
		7190						4017	5328	5581	5916
Fsp I	(1)	5948						7242			
Gdi II	(9)	506	1079	1081	1370	Mae II	(28)	50	54	304	894
		1651	1653	4673	6113			1392	1773	1785	1826
		6647						1909	1990	2095	2502
Gsu I	(4)	1464	1519	5797	6812			2541	2603	2970	3061
Hae I	(9)	498	834	967	4212			3661	3742	3800	4165
		4248	4848	4859	5311			4182	4399	5536	5952
		7280						6641	7127	7317	7386
Hae II	(10)	364	2304	3607	4070	Mae III	(28)	46	248	1544	1712
		4389	4711	5081	6628			1799	2148	2366	2482
		7058	7207					3118	3796	3856	4459
Hae III	(26)	498	507	776	782			5189	5252	5368	5651
		834	967	1082	1373			5982	6040	6193	6258
		1654	1735	1928	3456			6389	6476	6520	6715
		4212	4248	4674	4848			6721	6823	7153	7391
		4859	4877	5311	5769	Mbo I	(34)	427	881	886	1196
		5849	6116	6650	6684			1257	1271	1473	1489
		7214	7280					2236	2254	2306	2463
Hga I	(11)	89	1042	1468	2176			3079	3536	4029	5399
		2609	3807	3970	4943			5474	5485	5493	5571
		5521	6269	6605				5583	5688	6029	6047
HgiA I	(3)	3896	5151	6840				6093	6576	6759	6939
HgiE II	(1)	5412						6949	7024	7042	7270
Hha I	(37)	363	1063	1485	2263			7291	7329		
		2265	2303	3606	3942	Mbo II	(19)	231	996	1053	1081
		4069	4312	4388	4474			1499	2420	2426	2524
		4476	4617	4682	4710			2912	2966	3033	4100
		4743	5013	5080	5180			4705	5494	5567	6917
		5354	5463	5856	5949			7276	7279	7312	
		6348	6398	6475	6627	Mlu I	(1)	2330			

Mme I	(5)	2702	2930	5047	5231	NspH I	(7)	88	583	655	2385
		7279						2490	3980	4837	
Mnl I	(58)	103	258	318	446	Pac I	(1)	2296			
		508	766	772	795	Paer7 I	(1)	7357			
		801	809	812	824	Pal I	(26)	498	507	776	782
		944	1005	1346	1347			834	967	1082	1373
		1369	1486	2192	2330			1654	1735	1928	3456
		2339	2440	2467	2473			4212	4248	4674	4848
		2515	2548	2578	2632			4859	4877	5311	5769
		2698	2900	2932	2989			5849	6116	6650	6684
		3037	3388	3521	3649			7214	7280		
		3893	4079	4106	4136	Fle I	(1)	5212			
		4400	4682	4731	4941	Fml I	(2)	895	1393		
		5014	5265	5665	5746	PpuM I	(1)	1123			
		5892	6098	6237	6461	Psp1406 I	(1)	5952			
		6558	6598	7006	7045	PspA I	(6)	339	403	856	2769
		7290	7365					3560	3624		
Msc I	(2)	967	4212			Pst I	(3)	6	471	3500	
Mse I	(29)	22	57	122	138	Pvu I	(3)	1199	6096	6942	
		212	906	2269	2292	Pvu II	(2)	1171	4657		
		2296	3074	3300	3307	Rsa I	(21)	53	1870	1895	1950
		3784	3791	4012	4225			1983	2034	2191	2244
		4369	4604	4663	5539			2250	2326	2540	2594
		5591	5596	5610	5663			2606	2663	2753	3064
		5898	5937	6554	7070			6208	6441	6654	6662
		7383						7145			
Msl I	(6)	2016	2840	3463	5978	Rsr II	(2)	355	3609		
		6137	6833			Sac I	(1)	3896			
Msp I	(40)	340	353	358	383	Sac II	(2)	2289	2582		
		404	857	1456	1464	Sal I	(1)	2318			
		2240	2258	2470	2770	Sap I	(2)	3017	4717		
		2867	3041	3278	3428	Sau3A I	(34)	427	881	886	1196
		3561	3582	3607	3612			1257	1271	1473	1489
		3625	4280	4292	4333			2236	2254	2306	2463
		4343	4357	4465	4551			3079	3536	4029	5399
		5040	5187	5213	5403			5474	5485	5493	5571
		5807	5841	5908	6018			5583	5688	6029	6047
		6255	7028	7158	7211			6093	6576	6759	6939
MspAl I	(9)	1171	2288	2581	4378			6949	7024	7042	7270
		4657	5175	5420	6384			7291	7329		
		7007				Sau96 I	(16)	355	1123	1734	1927
Nae I	(4)	384	1465	3583	7212			2417	2472	3454	3455
Nci I	(21)	340	341	404	405			3609	5768	5847	5864
		857	858	1457	2470			6086	6360	7001	7213
		2770	2771	3042	3279	Sca I	(1)	2250			
		3428	3561	3562	3625	ScrF I	(45)	291	340	341	404
		3626	4465	5213	5909			405	477	549	604
		6256						621	857	858	1268
Nco I	(3)	742	962	2011				1457	1741	1934	2411
Nde I	(2)	1885	3067					2470	2639	2770	2771
NgoM I	(4)	382	1463	3581	7210			2792	2810	3042	3279
Nla III	(32)	71	88	583	655			3359	3417	3428	3489
		746	966	1498	1646			3561	3562	3625	3626
		1955	2015	2385	2464			3675	4253	4420	4465
		2490	2982	2996	3220			4573	4861	4982	4995
		3757	3817	3980	4129			5213	5909	6215	6256
		4193	4217	4447	4491			6792			
		4837	5557	6048	6058	Sec I	(44)	289	290	339	340
		6136	6172	6415	7371			403	476	502	547
Nla IV	(22)	346	553	625	1124			619	742	777	835
		1240	2118	2244	2256			856	962	1267	1374
		2418	2474	2914	3456			2011	2286	2410	2448
		3621	4579	4865	4904			2579	2769	2841	2940
		5676	5770	5811	6022			3278	3426	3487	3560
		6667	7032					3623	3624	3673	3674
Not I	(1)	1652						4141	4252	4572	4993
Nru I	(1)	1195						6246	6269	6452	6483
Nsi I	(4)	585	657	2994	3978			6790	6854	6993	7335
Nsp7524 I	(7)	84	579	651	2381	SfaN I	(20)	380	591	663	1036
		2486	3976	4833				1093	1225	1271	1571
NspB II	(9)	1171	2288	2581	4378			2009	2980	3145	3583
		4657	5175	5420	6384			4031	4086	4320	4418
		7007						4929	5981	6174	6466

Sfc I	(9)	2	467	1047	2926	Bsr I	ACT,GG`	24	BsrB I	GAG CGG	4
		3496	5098	5289	5967	BsrD I	GCAATG, 8	5	BsrG I	T`GTAC,A	2
		6816				BssH II	G`CGCG,C	3	BssS I	C`TCGT,G	2
Sfi I	(1)	504				Bst1107 I	GTA TAC	-	BstB I	TT`CG,AA	-
Sma I	(6)	341	405	858	2771	BstE II	G`GTNAC,C	1	BstN I	CC`W,GG	24
		3562	3626			BstU I	CG CG	24	BstX I	CCAN,NNNN`NTGG	1
SnaB I	(2)	1991	3062			BstY I	R`GATC,Y	10	Bsu36 I	CC`TNA,GG	2
Spe I	(1)	512				Cac8 I	GCN NGC	40	Cfr10 I	R`CCGG,Y	8
Sph I	(3)	583	655	3980		Cla I	AT`CG,AT	1	Csp6 I	G`TA,C	21
Spl I	(1)	51				Dde I	C`TNA,G	9	Dpn I	GA TC	34
Srf I	(2)	405	3562			DpnII	`GATC,	34	Dra I	TTT AAA	4
Ssp I	(2)	3304	3964			Dra III	CAC,NNN`GTG	4	Drd I	GACNN,NN`NNGTC	4
Stu I	(2)	498	834			Dsa I	C`CRYG,G	11	Eae I	Y`GGCC,R	9
Sty I	(8)	742	835	962	2011	Eag I	C`GGCC,G	2	Ear I	CTCTTC 7/10	3
		2448	6246	6993	7335	Eco47 III	AGC GCT	1	Eco57 I	CTGAAG 21/19	3
Swa I	(1)	3075				Eco72 I	CAC GTG	2	EcoN I	CCTNN`N,NNAGG	2
Taq I	(16)	108	1256	1407	2275	Eco0109 I	RG`GNC,CY	2	EcoR I	G`AATT,C	1
		2319	2352	2703	4933	EcoR II	`CCWGG,	24	EcoR V	GAT ATC	1
		6230	6490	6590	6621	Ehe I	GGC GCC	-	Esp I	GC`TNA,GC	2
		6633	6927	6942	7358	Fnu4H I	GC`N,GC	62	Fok I	GGATG 14/18	21
Tfi I	(10)	988	1320	1409	1446	Fse I	GG,CCGG`CC	-	Fsp I	TGC GCA	1
		3441	3935	4196	4668	Gdi II	`YGGC,CG	9	Gsu I	CTGGAG 21/19	4
		4808	6805			Hae I	WGG CCW	9	Hae II	R,GCGC`Y	10
Tsp45 I	(10)	46	2366	2482	3796	Hae III	GG CC	26	Hga I	GACGC 9/14	11
		3856	5982	6193	6258	HgiA I	G,WGCW`C	3	HgiE II	ACCNNNNNNGGT	-1/131
		6721	6823			Hha I	G,CG`C	37	HinC II	GTY RAC	4
Tth111 II	(7)	198	3891	5422	5431	Hind II	GTY RAC	4	HinD III	A`AGCT,T	1
		5461	6478	6485		Hinf I	G`ANT,C	19	HinI I	GR`CG,YC	6
Vsp I	(6)	122	906	4369	4604	HinP I	G`CG,C	37	Hpa I	GTT AAC	1
		4663	5898			Hpa II	C`CG,G	40	Hph I	GGTGA 12/11	13
Xba I	(1)	3054				Kas I	G`GCGC,C	-	Kpn I	G,GTAC`C	1
Xho I	(1)	7357				Mae I	C`TA,G	17	Mae II	A`CG,T	28
Xho II	(10)	881	1489	2236	2254	Mae III	`GTNAC,	28	Mbo I	`GATC,	34
		2306	5474	5485	5571	Mbo II	GAAGA 12/11	19	Mlu I	A`CGCG,T	1
		5583	7042			Mme I	TCCRAC 25/23	5	Mnl I	CCTC 10/10	58
Xma I	(6)	339	403	856	2769	Msc I	TGG CCA	2	Mse I	T`TA,A	29
		3560	3624			Msl I	CAYNN NNRTG	6	Msp I	C`CG,G	40
Xma III	(2)	1080	1652			MspA1 I	CMG CKG	9	Mun I	C`AATT,G	-
Xmn I	(1)	2972				Nae I	GCC GGC	4	Nar I	GG`CG,CC	-

### Site usage in pBCFc:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1	Nla IV	GGN NCC	22	Not I	GC`GGCC,GC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	81	Nru I	TCG CGA	1	Nsi I	A,TGCA`T	4
Afe I	AGC GCT	1	Afl II	C`TTAA,G	-	Nsp7524 I	R`CATG,Y	7	NspB II	CMG CKG	9
Afl III	A`CRYG,T	4	Age I	A`CCGG,T	-	NspH I	R,CATG`Y	7	Pac I	TTA,AT`TAA	1
Aha II	GR`CG,YC	6	Ahd I	GACNN,N`NNGTC	2	PaeR7 I	C`TCGA,G	1	Pal I	GG CC	26
Alu I	AG CT	30	Alw I	GGATC 8/9	18	PflM I	CCAN,NNN`NTGG	-	Ple I	GAGTC 9/10	1
AlwN I	CAG,NNN`CTG	2	Apa I	G,GGCC`C	1	Pme I	CTTT AAAC	-	Pml I	CAC GTG	2
ApaL I	G`TGCA,C	2	Apo I	R`AATT,Y	6	PpuM I	RG`GWC,CY	1	Psp1406 I	AA`CG,TT	1
Asc I	GG`CGCG,CC	1	Ase I	AT`TA,AT	6	PspA I	C`CCGG,G	6	Pst I	C,TGCA`G	3
Asp718	G`GTAC,C	1	Ava I	C`YCGR,G	11	Pvu I	CG,AT`CG	3	Pvu II	CAG CTG	2
Ava II	G`GWC,C	9	Avr II	C`CTAG,G	1	Rsa I	GT AC	21	Rsr II	CG`GWC,CG	2
BamH I	G`GATC,C	1	Ban I	G`GYRC,C	5	Sac I	G,AGCT`C	1	Sac II	CC,GC`GG	2
Ban II	G,RCGY`C	6	Bbe I	G,GCC`C	-	Sal I	G`TCGA,C	1	Sap I	GCTCTTC 8/11	2
Bbs I	GAAGAC 8/12	4	Bbv I	GCAGC 13/17	21	Sau3A I	`GATC,	34	Sau96 I	G`GNC,C	16
Bbv II	GAAGAC 7/11	4	Bcl I	T`GATC,A	2	Sca I	AGT ACT	1	ScrF I	CC`N,GG	45
Bcn I	CC,S`GG	21	Bfa I	C`TA,G	17	Sec I	C`CNNG,G	44	SfaN I	GCATC 9/13	20
Bgl I	GCCN,NNN`NGGC	6	Bgl II	A`GATC,T	1	Sfc I	C`TRYA,G	9	Sfi I	GGCCN,NNN`NGGCC	1
Blp I	GC`TNA,GC	2	Bpm I	CTGGAG 22/20	4	Sma I	CCC GGG	6	SnaB I	TAC GTA	2
Bsa I	GGTCTC 7/11	3	BsaA I	YAC GTR	9	Spe I	A`CTAG,T	1	Sph I	G,CATG`C	3
BsaB I	GATNN NNATC	1	BsaH I	GR`CG,YC	6	Spl I	C`GTAC,G	1	Srf I	GCCC GGGC	2
BsaJ I	C`CNNG,G	44	BsaW I	W`CCGG,W	9	Ssp I	AAT ATT	2	Stu I	AGG CCT	2
BseR I	GAGGAG 16/14	3	Bsg I	GTGCAG 22/20	4	Sty I	C`CWVG,G	8	Swa I	ATTT AAAT	1
BsiC I	TT`CG,AA	-	Bsie I	CG,RY`CG	8	Taq I	T`CG,A	16	Tfi I	G`AWT,C	10
BsiHKA I	G,WGCW`C	3	BsiW I	C`GTAC,G	1	Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	-
Bsm I	GAATG,C 7	3	BsmA I	GTCTC`/9	6	Tth111 II	CAARCA 16/14	7	Vsp I	AT`TA,AT	6
BsmB I	CGTCTC 7/11	-	BsmF I	GGGAC 15/19	18	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
BsoF I	GC`N,GC	62	Bsp120 I	G`GGCC,C	1	Xcm I	CCANNNN,N`NNNNTGG-		Xho I	C`TCGA,G	1
Bsp1286 I	G,DGCH`C	-	BspH I	T`CATG,A	2	Xho II	R`GATC,Y	10	Xma I	C`CCGG,G	6
BspM I	ACCTGC 10/14	3	BspM II	T`CCGG,A	2	Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1