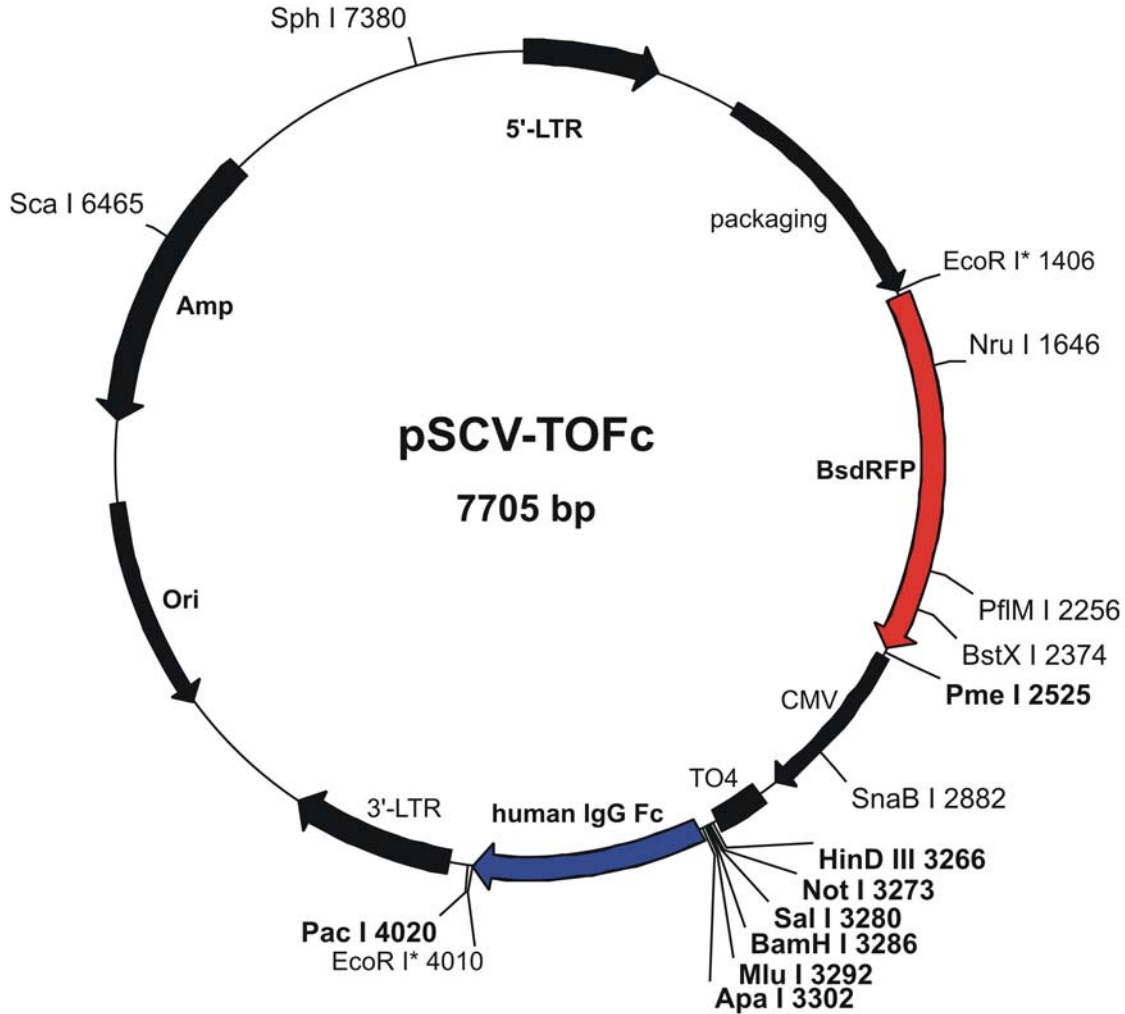


Name of Vector: pSCV-TOFc
 Antibiotic Selection: Amp
 Created by: Hong Yin
 (He Lab @ The University of Chicago)
 Date of Creation: April 2005



Linker Sequence

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  Bgl II (1/4)  Hind III    Not I      Sal I      BamH I    Mlu I      Apa I
  |-----| |-----| |-----| |-----| |-----| |-----| |-----|
  agatc taa gct tgc ggc cgc gtc gac gga tcc acg cgt ggg ccc gga ggc ggc
      -  A  C  G  R  V  D  G  S  T  R  G  P  G  G  G
  gag ccc aaa .....ccg ggt aaa. TGA attcttaattaa
  E  P  K ..... P  G  K
  └────────────────────────────────────────────────────────────────────────────────┘
  Human IgG Fc Tag
  
```

EcoR I (1/2) Pac I

pSCV-TOFc Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA
TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCAGAATATGGGC CAAACAGGAT ATCTGTGGTAAGCAGTTCCCT
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Unique enzymes in pSCV-TOFc:

Nru I	TCG CGA	1646	1959	1983	2058	2136	
PfiI	CCAN,MNN`NTGG	2256	2205	2275	2340	2488	
BstX I	CCAN,MNNN`NTGG	2374	2516	2518	2600	2628	
Pme I	CTTT AAAC	2525	2640	2654	2821	2912	
SnaB I	TAC GTA	2882	2945	3049	3070	3272	
HinD III	A`AGCT,T	3266	3276	3308	3538	3540	
Not I	GC`GGCC,GC	3273	4266	4272	4568	4782	
Sal I	G`TCGA,C	3280	4885	4941	4951	4975	
Acc I	GT`MK,AC	3281	5018	5025	5046	5137	
HinC II	GTY RAC	3282	5165	5292	5311	5432	
Hind II	GTY RAC	3282	5542	5677	5686	6048	
BamH I	G`GATC,C	3286	6139	6330	6376	6497	
Mlu I	A`CGCG,T	3292	6541	6618	6727	6826	
Bsp120 I	G`GGCC,C	3298	6873	7047	7086	7096	
Apa I	G,GGCC`C	3302	7122	7160	7173	7199	
Nsi I	A,TGCA`T	3953	7256	7515			
Pac I	TTA,AT`TAA	4020	Afl II (3)	35	1008	4102	
Sca I	AGT ACT	6465	Afl III (2)	3292	5092		
Sph I	G,CATG`C	7380	Aha II (18)	744	1400	1848	2295
Number of enzymes = 19				2352	2403	2502	2664
				2717	2800	2986	3229
				6522	6904	7208	7391

The following enzymes do not cut in pSCV-TOFc:

Age I	Avr II	Bcl I	Blp I	BsiC I	Ahd I	(6)	7505	7526		
BsiW I	Bsm I	Bsp1286 I	BspM II	Bst1107 I	Alu I	(38)	1022	2011	3382	4515
BstB I	Cla I	Dra III	Eco72 I	Esp I			4561	5985		
Fse I	Hpa I	Mun I	PaeR7 I	Pml I			30	34	338	582
Rsr II	Sfi I	Spl I	Srf I	Xca I			670	678	1517	1622

pSCV-TOFc: sites sorted by name:

Aat II	(7)	747	1851	2667	2720						
Acc I	(1)	3281	2803	2989	6907						
Acc65 I	(2)	403	4470								
Aci I	(82)	199	205	568	590						
		690	729	862	903						
		1044	1135	1201	1300						
		1319	1357	1534	1616						
		1683	1821	1824	1936						
						Alw I	(15)	455	1053	1359	1729
								2517	3282	3293	5654
								5740	5740	5837	5838
								6302	6617	6623	
						AlwN I	(4)	159	3361	4226	5508
						Apa I	(1)	3302			
						ApaL I	(3)	5406	6652	7149	
						Apo I	(3)	874	1406	4010	

Asc I	(2)	370	4437			BspM I	(2)	3772	3902		
Ase I	(5)	2549	4735	4863	4922	Bsr I	(20)	376	1032	1060	1548
		6157						1572	2027	2838	3498
Asp718	(2)	403	4470					3606	4443	4893	5499
Ava I	(9)	333	399	500	2093			5512	5626	6032	6150
		2285	3695	3728	4400			6193	6460	6632	7338
		4466				BsrB I	(5)	1044	2275	4784	5025
Ava II	(15)	188	201	256	553			6826			
		692	1221	1574	3376	BsrD I	(3)	3822	6046	6220	
		3431	4255	4268	4323	BsrG I	(2)	1284	3710		
		6123	6345	7600		BssH II	(5)	319	370	2476	4386
BamH I	(1)	3286						4437			
Ban I	(18)	246	403	1144	1399	BssS I	(5)	1589	1904	5265	6649
		1689	1949	2207	2294			6956			
		2402	2501	4313	4470	BstE II	(3)	1089	1972	2143	
		4836	5933	7207	7390	BstN I	(26)	243	550	737	750
		7504	7525					1171	1196	1219	1239
Ban II	(12)	340	353	1679	1811			1269	1719	2002	2156
		1892	3110	3302	3317			2632	2825	3223	3370
		4407	4420	7457	7471			3598	3751	3769	4310
Bbe I	(8)	1403	2298	2406	2505			4832	5120	5241	5254
		7211	7394	7508	7529			7327	7604		
Bbs I	(5)	1500	2252	3378	3479	BstU I	(28)	319	321	372	905
		3924						907	1137	1646	2115
Bbv I	(13)	933	941	1526	1631			2205	2478	2518	2602
		2404	3702	3834	3930			3278	3294	3540	4386
		5511	5514	5720	6414			4388	4439	4939	4941
		7025						5139	5720	6050	6543
Bbv II	(5)	1499	2251	3379	3478			6875	6975	6977	7080
		3925				BstX I	(1)	2374			
Bcn I	(20)	166	401	402	573	BstY I	(12)	2510	3128	3149	3170
		726	2401	3303	3430			3260	3286	5733	5744
		3730	3731	4002	4233			5830	5842	6610	6627
		4468	4469	5473	6169	Bsu36 I	(5)	783	1020	2506	3437
		6520	7021	7056	7407			3479			
Bfa I	(14)	31	221	663	675	Cac8 I	(37)	28	32	321	372
		1396	1524	1812	2542			584	588	633	652
		4098	4288	5587	5840			1201	1510	1624	2478
		6175	7610					2628	2821	3270	3313
Bgl I	(5)	2632	2754	2825	6105			3892	4095	4099	4388
		7223						4439	4885	4914	5023
Bgl II	(4)	3128	3149	3170	3260			5109	5146	5706	6097
Bpm I	(4)	3244	4035	6055	7673			7110	7258	7278	7282
Bsa I	(7)	478	532	1151	3639			7378	7419	7467	7509
		4523	4544	6046				7539			
BsaA I	(4)	2047	2882	3501	3563	Cfr10 I	(5)	631	2498	6065	7528
BsaB I	(5)	1713	3127	3148	3169			7537			
		3190				Csp6 I	(21)	404	660	1285	2029
BsaH I	(18)	744	1400	1848	2295			2281	2470	2760	2785
		2352	2403	2502	2664			2840	2873	2924	3081
		2717	2800	2986	3229			3498	3552	3564	3621
		6522	6904	7208	7391			3711	4471	6464	7140
		7505	7526					7651			
BsaJ I	(48)	163	242	252	399	Dde I	(23)	75	169	210	478
		463	499	548	549			783	1020	1292	2019
		696	735	736	748			2506	3264	3437	3479
		749	1169	1238	1247			4142	4236	4277	4546
		1267	1268	1413	1718			4617	5367	5776	5942
		1842	1977	2001	2037			6482	6908	7143	
		2094	2154	2250	2286	Dpn I	(35)	95	461	1048	1180
		2355	2481	2516	2902			1365	1649	1710	1724
		3369	3407	3538	3728			1916	2312	2512	3130
		3800	3899	4230	4309			3151	3172	3193	3218
		4319	4466	4529	4831			3262	3288	3424	4162
		5252	7326	7404	7410			5660	5735	5746	5754
BsaW I	(3)	5298	5445	6276				5832	5844	5949	6290
BseR I	(8)	466	1295	1334	1828			6308	6354	6612	6629
		1830	2152	3559	4532			6665	7250	7474	
Bsg I	(4)	1602	2411	3577	3946	DpnII	(35)	93	459	1046	1178
BsiE I	(10)	594	729	1534	1650			1363	1647	1708	1722
		3276	5008	5432	6355			1914	2310	2510	3128
		6504	7251					3149	3170	3191	3216
BsiHKA I	(7)	340	3110	4407	5410			3260	3286	3422	4160
		6571	6656	7153				5658	5733	5744	5752
BsmA I	(25)	108	477	533	611			5830	5842	5947	6288
		736	834	951	1075			6306	6352	6610	6627
		1134	1152	1330	1433			6663	7248	7472	
		2975	3221	3638	4000	Dra I	(4)	2525	5851	5870	6562
		4052	4175	4522	4543	Drd I	(5)	1502	2357	3481	5200
		6047	6821	6974	7018			7069			
		7690				Dsa I	(9)	696	1413	2250	2516
BsmB I	(8)	735	833	1074	1133			2902	3538	3800	3899
		1331	3220	6975	7017			7410			
BsmF I	(16)	174	187	566	731	Eae I	(14)	584	726	1111	1132
		766	1207	1587	1999			1416	1531	1900	2341
		2018	2717	2868	3036			2376	3273	4931	6373
		3389	4241	4254	7386			7407	7539		
BsoF I	(51)	729	903	919	922	Eag I	(3)	726	1531	3273	
		927	930	1135	1515	Ear I	(8)	1072	1313	3397	3976
		1534	1608	1611	1614			4714	4976	6780	7268
		1617	1620	1784	1822	Eco47 III	(2)	925	7446		
		1936	1984	2137	2201	Eco57 I	(8)	1511	1987	2320	2344
		2206	2341	2393	2396			2350	5639	6653	7657
		2488	3273	3276	3309	EcoN I	(3)	786	1394	3595	
		3538	3691	3823	3919	EcoO109 I	(6)	256	1221	1574	4323
		4917	4998	5016	5019			6961	7415		
		5137	5292	5435	5500	EcoR I	(2)	1406	4010		
		5503	5709	6037	6376	EcoR II	(26)	241	548	735	748
		6403	6498	6727	7014			1169	1194	1217	1237
		7123	7227	7300				1267	1717	2000	2154
Bsp120 I	(1)	3298						2630	2823	3221	3368
BspH I	(5)	3419	5812	6820	6925			3596	3749	3767	4308
		7449						4830	5118	5239	5252

		7325	7602						7207	7390	7504	7525
EcoR V	(3)	141	4208	7593				Kpn I	(2)	407	4474	
Ehe I	(8)	1401	2296	2404	2503			Mae I	(14)	31	221	663 675
		7209	7392	7506	7527					1396	1524	1812 2542
Fnu4H I	(51)	729	903	919	922					4098	4288	5587 5840
		927	930	1135	1515					6175	7610	
		1534	1608	1611	1614			Mae II	(20)	744	1083	1124 1848
		1617	1620	1784	1822					2046	2664	2676 2717
		1936	1984	2137	2201					2800	2881	2986 3461
		2206	2341	2393	2396					3500	3562	3929 5795
		2488	3273	3276	3309					6211	6584	6904 7346
		3538	3691	3823	3919			Mae III	(26)	39	996	1024 1089
		4917	4998	5016	5019					1233	1972	2143 2149
		5137	5292	5435	5500					2603	2690	3039 3325
		5503	5709	6037	6376					3441	4106	4584 5448
		6403	6498	6727	7014					5511	5627	5910 6241
		7123	7227	7300						6299	6452	6640 7028
Fok I	(17)	425	1142	1302	1466					7319	7339	
		1701	1994	2051	2290			Mbo I	(35)	93	459	1046 1178
		3219	3711	3745	4491					1363	1647	1708 1722
		5951	6132	6419	7062					1914	2310	2510 3128
		7306								3149	3170	3191 3216
Fsp I	(3)	1880	6207	7230						3260	3286	3422 4160
Gdi II	(13)	725	727	1131	1530					5658	5733	5744 5752
		1532	1901	2342	3272					5830	5842	5947 6288
		3274	4932	6372	7408					6306	6352	6610 6627
		7540						Mbo II	(23)	6663	7248	7472
Gsu I	(4)	3243	4036	6056	7674					1088	1301	1447 1504
Hae I	(10)	586	1113	1418	1835					1532	2253	2256 3269
		2042	2264	2378	5107					3379	3385	3483 3871
		5118	5570							3925	3992	4730 4964
Hae II	(12)	927	1403	2298	2406					5753	5826	6581 6659
		2505	4970	5340	7211					6768	7256	7468
		7394	7448	7508	7529			Mlu I	(1)	3292		
		130	175	586	728			Mme I	(9)	831	1108	2246 3661
Hae III	(41)	764	776	989	1113					3889	4531	4583 5306
		1134	1199	1418	1533					5490		
		1835	1902	1935	1986			Mnl I	(84)	218	370	389 434
		2042	2229	2264	2343					462	486	508 512
		2378	2487	2626	2819					568	778	874 1170
		3275	3300	4197	4242					1273	1306	1312 1315
		4933	5107	5118	5136					1321	1351	1354 1369
		5570	6028	6108	6375					1376	1392	1456 1797
		6962	7260	7409	7417					1798	1808	1811 1820
		7541								1837	1845	1848 1879
Hga I	(15)	383	644	897	1493					1912	1918	1924 1939
		2359	3067	3236	3268					2027	2089	2122 2172
		3568	4450	5202	5780					2229	2254	2274 2281
		6512	7070	7539						2313	2350	2440 2445
HgiA I	(7)	340	3110	4407	5410					2476	3083	3259 3298
		6571	6656	7153						3399	3426	3432 3474
HgiE II	(2)	5671	7151							3507	3537	3591 3657
Hha I	(45)	321	323	372	374					3859	3891	3948 3996
		650	907	926	1402					4285	4437	4456 4501
		1514	1869	1881	2115					4528	4552	4612 4941
		2205	2297	2405	2478					4990	5200	5273 5524
		2480	2504	4388	4390					5924	6005	6151 6357
		4439	4441	4716	4876					6952	7010	7270 7554
		4941	4969	5002	5272			Msc I	(4)	586	1113	1418 2378
		5339	5439	5613	5722			Mse I	(26)	36	1009	1121 1151
		6115	6208	6545	6877					1175	2524	2549 4016
		6977	7080	7210	7231					4020	4103	4637 4735
		7364	7393	7447	7507					4863	4922	5798 5850
		7528								5855	5869	5922 6157
Hinc II	(1)	3282								6196	6561	6933 7114
Hind II	(1)	3282								7311	7581	
Hind III	(1)	3266						Msl I	(4)	2907	3799	6237 6396
Hinf I	(18)	444	452	793	804			Msp I	(31)	165	400	571 632
		1439	1771	2159	2952					725	1403	2400 2499
		3862	4627	4649	4670					3302	3429	3729 3826
		4927	4992	5067	5463					4000	4232	4467 4810
		5980	7618							5299	5446	5472 5662
HinI I	(18)	744	1400	1848	2295					6066	6100	6167 6277
		2352	2403	2502	2664					6519	7020	7054 7406
		2717	2800	2986	3229					7529	7538	7553
		6522	6904	7208	7391			MspAl I	(13)	590	1622	2395 2518
		7505	7526							3540	4568	4916 5434
HinP I	(45)	319	321	370	372					5679	6620	7086 7280
		648	905	924	1400					7636		
		1512	1867	1879	2113			Nae I	(2)	633	7539	
		2203	2295	2403	2476			Nar I	(8)	1400	2295	2403 2502
		2478	2502	4386	4388					7208	7391	7505 7526
		4437	4439	4714	4874						400	401 572
		4939	4967	5000	5270			Nci I	(20)	165	2400	3302 3429
		5337	5437	5611	5720					725	2400	4001 4232
		6113	6206	6543	6875					3729	3730	4467 6168
		6975	7078	7208	7229					4467	4468	5472 6168
		7362	7391	7445	7505					6519	7020	7055 7406
		7526						Nco I	(3)	1413	2250	2902
		165	400	571	632			Nde I	(2)	2776	7156	
Hpa II	(31)	725	1403	2400	2499			NgoM I	(2)	631	7537	
		3302	3429	3729	3826			Nhe I	(2)	30	4097	
		4000	4232	4467	4810			Nla III	(28)	62	1207	1417 1867
		5299	5446	5472	5662					1885	2254	2377 2846
		6066	6100	6167	6277					2906	3344	3423 3449
		6519	7020	7054	7406					3941	3955	4129 4583
		7529	7538	7553						4750	5096	5816 6307
		1159	1185	1403	1983					6317	6395	6431 6824
Hph I	(20)	2154	2205	2426	2917					6929	7013	7380 7453
		3577	3889	5829	6056					190	203	248 405
		6470	6678	6711	6995			Nla IV	(46)	523	554	694 763
		7004	7497	7542	7623					895	1146	1223 1401
Kas I	(8)	1399	2294	2402	2501					1575	1691	1891 1951
										1987	2035	2209 2230

Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1	ScrF I	CC`N,GG	46	Sec I	C`CNNG,G	48
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	5	SfaN I	GCATC 9/13	22	Sfc I	C`TRYA,G	12
NspB II	CMG CKG	13	NspH I	R,CATG`Y	5	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	3
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	2
Pal I	GG CC	41	PflM I	CCAN,NNN`NTGG	1	Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4	Stu I	AGG CCT	2	Sty I	C`CWWG,G	11
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	3	Taq I	T`CG,A	14	Tfi I	G`AWT,C	7
Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3	Tsp45 I	`GTSAC,	11	Tth111 I	GACN`N,NGTC	4
Pvu II	CAG CTG	5	Rsa I	GT AC	21	Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	5
Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	3	Xba I	T`CTAG,A	3	Xca I	GTA TAC	-
Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Sap I	GCTCTC 8/11	3	Sau3A I	`GATC,	35	Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	3
Sau96 I	G`GNC,C	36	Sca I	AGT ACT	1	Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	4