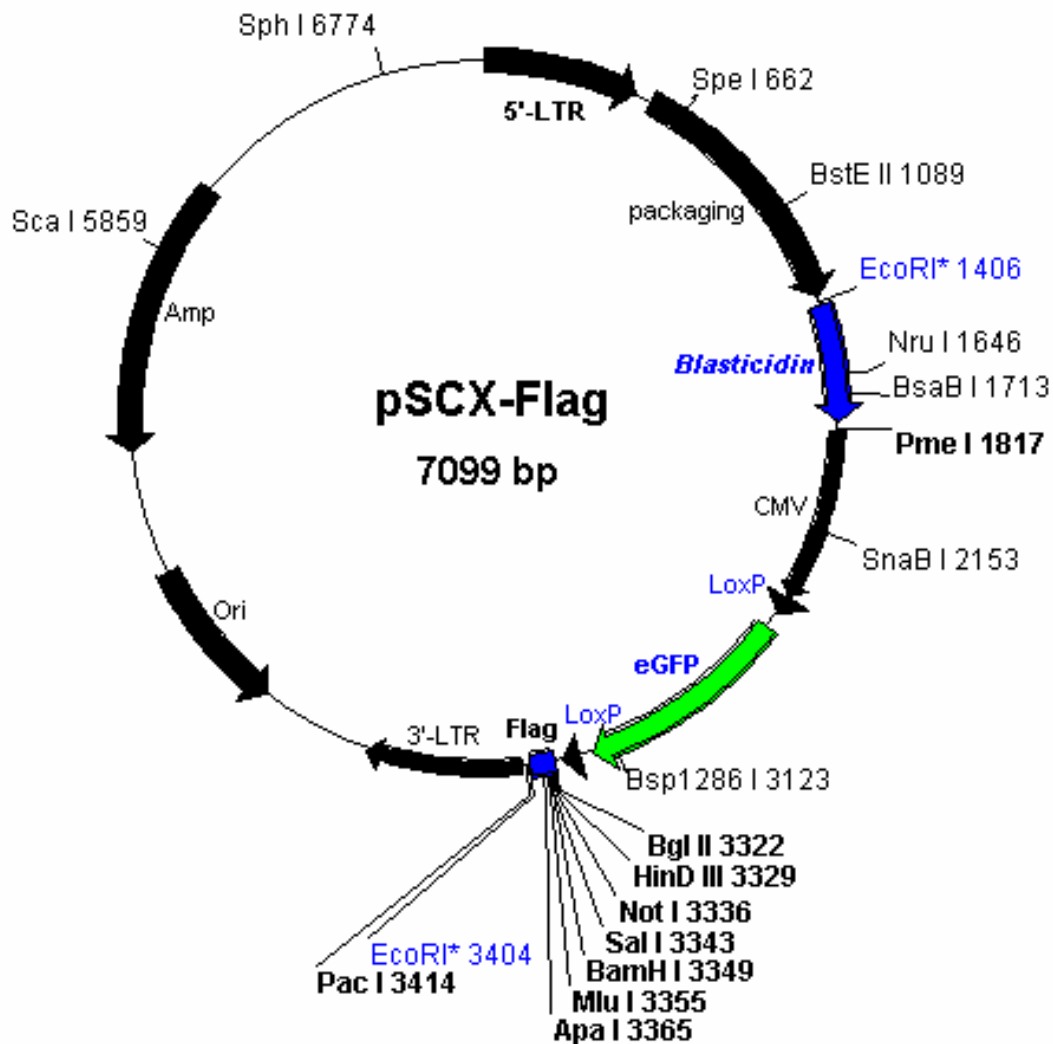


Vector: pSCX-Flag

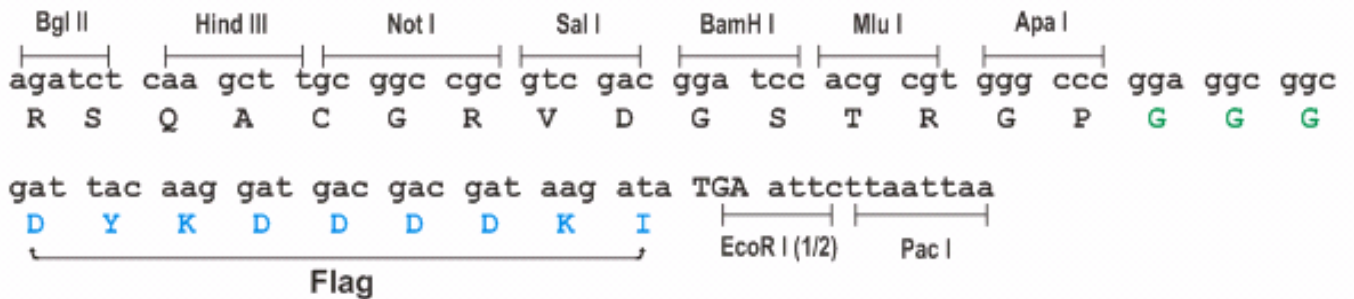
Antibiotic Selection: Amp

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

Date of Construction: June, 2005



Linker Sequence



pSCX-Flag Full-Length Sequence

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CTGCCACCT CGGGGTCTT TCATTTGGAG GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCGACCCCCCGC
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CTGCGTCTGTACTAGTTAG TAAGTAGCTC TGTATCTGGC GGACCCGTGG TGGAACTGAC GAGTTCTGAACACCCGGCCG
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Unique enzymes in pSCX-Flag:

Spe I	A`CTAG,T	662	Acc I	(1)	3344				
BstE II	G`GTNAC,C	1089	Acc65 I	(2)	403	3864			
Bbv II	GAAGAC 7/11	1499	Aci I	(76)	199	205	568	590	
Bbs I	GAAGAC 8/12	1500			690	729	862	903	
Nru I	TCG CGA	1646			1044	1135	1201	1300	
BsaB I	GATNN NNATC	1713			1319	1357	1534	1616	
Pme I	CTTT AAAC	1817			1683	1871	1899	1911	
BsaA I	YAC GTR	2153			1925	2092	2183	2216	
SnaB I	TAC GTA	2153			2320	2341	2402	2732	
Bsp1286 I	G,DGCH`C	3123			2773	2840	2879	3017	
BspM II	T`CCGG,A	3250			3130	3190	3193	3335	
Bgl II	A`GATC,T	3322			3339	3371	3660	3666	
Hind III	A`AGCT,T	3329			3962	4176	4279	4335	
Not I	GC`GGCC,GC	3336			4345	4369	4412	4419	
Sal I	G`TCGA,C	3343			4440	4531	4559	4686	
Acc I	GT`MK,AC	3344			4705	4826	4936	5071	
HinC II	GTY RAC	3345			5080	5442	5533	5724	
Hind II	GTY RAC	3345			5770	5891	5935	6012	
BamH I	G`GATC,C	3349			6121	6220	6267	6441	
Mlu I	A`CGCG,T	3355			6480	6490	6516	6554	
Bsp120 I	G`GGCC,C	3361			6567	6593	6650	6909	
Apa I	G,GGCC`C	3365	Afl II	(3)	35	1008	3496		
Pac I	TTA,AT`TAA	3414	Afl III	(2)	3355	4486			
Sca I	AGT ACT	5859	Aha II	(12)	744	1400	1935	1988	
Sph I	G,CATG`C	6774			2071	2257	5916	6298	
					6602	6785	6899	6920	
			Ahd I	(4)	1022	3909	3955	5379	
			Alu I	(38)	30	34	338	582	
					670	678	1517	1622	
					2379	2500	2534	2567	
					2639	2672	2888	2936	
					3047	3221	3331	3491	
					3495	3799	4118	4151	
					4246	4310	4428	4654	
					4744	4790	5047	5568	
					5668	5731	6410	6429	
					6674	7030			
			Alw I	(18)	455	1053	1359	1729	
					2394	3009	3206	3243	
					3345	3356	5048	5134	
					5134	5231	5232	5696	
					6011	6017			
			AlwN I	(3)	159	3620	4902		
			Apa I	(1)	3365				
			ApaL I	(3)	4800	6046	6543		
			Apo I	(3)	874	1406	3404		
			Asc I	(2)	370	3831			

The following enzymes do not cut in pSCX-Flag:

Age I	Avr II	Bcl I	Blp I	BsiC I				
BsiW I	Bsm I	BspM I	Bst1107 I	BstB I				
BstX I	Cla I	Dra III	Eco72 I	Esp I				
Fse I	Hpa I	Mun I	Nsi I	Paer7 I				
PflM I	Pml I	Rsr II	Sac II	Sfi I	Alw I	(18)		
Spl I	Srf I	Stu I	Xca I	Xcm I				

pSCX-Flag: sites sorted by name:

Aat II	(6)	747	1938	1991	2074		
		2260	6301				

Ase I	(4)	4129	4257	4316	5551		1171	1196	1219	1239
Asp718	(2)	403	3864				1269	1719	1903	2096
Ava I	(5)	333	399	500	3794		2559	2684	2796	2871
		3860					2925	3704	4226	4514
Ava II	(15)	188	201	256	553		4635	4648	6721	6998
		692	1221	1574	3170	BstU I	(26)	319	321	372
		3301	3649	3662	3717		907	1137	1646	1873
		5517	5739	6994			2842	3160	3244	3341
BamH I	(1)	3349					3357	3780	3782	3833
Ban I	(15)	246	403	1144	1399		4333	4335	4533	5114
		1689	2278	2549	3707		5444	5937	6269	6369
		3864	4230	5327	6601		6371	6474		
		6784	6898	6919		BstY I	(10)	2398	3013	3322
Ban II	(8)	340	353	1679	3365		5127	5138	5224	5236
		3801	3814	6851	6865		6004	6021		
Bbe I	(5)	1403	6605	6788	6902	Bsu36 I	(2)	783	1020	
		6923				Cac8 I	(39)	28	32	321
Bbs I	(1)	1500					584	588	633	652
Bbv I	(12)	933	941	1526	1631		1201	1510	1624	1899
		2765	3049	3056	4905		2092	2637	2670	2718
		4908	5114	5808	6419		3042	3049	3333	3489
Bbv II	(1)	1499					3493	3782	3833	4279
Bcn I	(17)	166	401	402	573		4308	4417	4503	4540
		726	2544	3198	3366		5100	5491	6504	6652
		3627	3862	3863	4867		6672	6676	6772	6813
		5563	5914	6415	6450		6861	6903	6933	
		6801				Cfr10 I	(5)	631	2664	5459
Bfa I	(16)	31	221	663	675		6931			6922
		1396	1524	2405	2503	Csp6 I	(15)	404	660	1285
		3238	3320	3492	3682		2056	2111	2144	2195
		4981	5234	5569	7004		2352	2942	3224	3865
Bgl I	(5)	1903	2025	2096	5499		5858	6534	7045	
		6617				Dde I	(21)	75	169	210
Bgl II	(1)	3322					783	1020	1292	1810
Bpm I	(5)	2958	3198	3429	5449		3117	3135	3536	3630
		7067					3671	3940	4011	4761
Bsa I	(6)	478	532	1151	3917		5170	5336	5876	6302
		3938	5440				6537			
BsaA I	(1)	2153				Dpn I	(32)	95	461	1048
BsaB I	(1)	1713					1365	1649	1710	1724
BsaH I	(12)	744	1400	1935	1988		2400	2413	3015	3163
		2071	2257	5916	6298		3201	3249	3324	3351
		6602	6785	6899	6920		3556	5054	5129	5140
BsaJ I	(37)	163	242	252	399		5148	5226	5238	5343
		463	499	548	549		5684	5702	5748	6006
		696	735	736	748		6023	6059	6644	6868
		749	1169	1238	1247	DpnII	(32)	93	459	1046
		1267	1268	1413	1718		1363	1647	1708	1722
		2173	2512	2542	2682		2398	2411	3013	3161
		2845	2869	2924	3624		3199	3247	3322	3349
		3703	3713	3860	3923		3554	5052	5127	5138
		4225	4646	6720	6798		5146	5224	5236	5341
		6804					5682	5700	5746	6004
BsaW I	(4)	3250	4692	4839	5670		6021	6057	6642	6866
BseR I	(6)	466	1295	1334	2494	Dra I	(4)	1817	5245	5264
		2544	3926			Drd I	(3)	1502	4594	6463
Bsg I	(4)	1602	2642	2739	3063	Dsa I	(5)	696	1413	2512
BsiE I	(10)	594	729	1534	1650		6804			
		3339	4402	4826	5749	Eae I	(13)	584	726	1111
		5898	6645				1416	1531	2585	2974
BsiHKA I	(7)	340	3123	3801	4804		3336	4325	5767	6801
		5965	6050	6547			6933			
BsmA I	(22)	108	477	533	611	Eag I	(3)	726	1531	3336
		736	834	951	1075	Ear I	(8)	1072	1313	2471
		1134	1152	1330	1433		4108	4370	6174	6662
		2246	3446	3569	3916	Eco47 III	(2)	925	6840	
		3937	5441	6215	6368	Eco57 I	(8)	1511	2494	2666
		6412	7084				2909	5033	6047	7051
BsmB I	(7)	735	833	1074	1133	EcoN I	(3)	786	1394	3309
		1331	6369	6411		EcoO109 I	(7)	256	1221	1574
BsmF I	(14)	174	187	566	731		3717	6355	6809	3301
		766	1207	1587	1988	EcoR I	(2)	1406	3404	
		2139	2307	3287	3635	EcoR II	(24)	241	548	735
		3648	6780				1169	1194	1217	1237
BsoF I	(45)	729	903	919	922		1267	1717	1901	2094
		927	930	1135	1515		2557	2682	2794	2869
		1534	1608	1611	1614		2923	3702	4224	4512
		1617	1620	1784	2673		4633	4646	6719	6996
		2732	2754	3038	3045	EcoR V	(3)	141	3602	6987
		3096	3099	3193	3336	Ehe I	(5)	1401	6603	6786
		3339	3372	4311	4392		6921			
		4410	4413	4531	4686	Fnu4H I	(45)	729	903	919
		4829	4894	4897	5103		927	930	1135	1515
		5431	5770	5797	5892		1534	1608	1611	1614
		6121	6408	6517	6621		1617	1620	1784	2673
		6694					2732	2754	3038	3045
Bsp120 I	(1)	3361					3096	3099	3193	3336
Bsp1286 I	(1)	3123					3339	3372	4311	4392
BspH I	(4)	5206	6214	6319	6843		4410	4413	4531	4686
BspM II	(1)	3250					4829	4894	4897	5103
Bsr I	(18)	376	1032	1060	1548		5431	5770	5797	5892
		1572	2109	3126	3837		6121	6408	6517	6621
		4287	4893	4906	5020		6694			
		5426	5544	5587	5854	Fok I	(14)	425	1142	1302
		6026	6732				1701	2541	2907	3397
BsrB I	(4)	1044	4178	4419	6220		3885	5345	5526	5813
BsrD I	(2)	5440	5614				6456	6700		
BsrG I	(2)	1284	3223			Fsp I	(2)	5601	6624	
BssH II	(4)	319	370	3780	3831	Gdi II	(13)	725	727	1131
BssS I	(5)	1589	2694	4659	6043		1532	2586	2973	3335
		6350					3337	4326	5766	6802
BstE II	(1)	1089					6934			
BstN I	(24)	243	550	737	750	Gsu I	(5)	2957	3197	3430

		7068						1273	1306	1312	1315
Hae I	(6)	586	1113	1418	4501			1321	1351	1354	1369
		4512	4964					1376	1392	1456	1797
Hae II	(10)	927	1403	2509	4364			1798	2354	2472	2522
		4734	6605	6788	6842			2603	2609	2702	2840
		6902	6923					2852	2903	3023	3305
Hae III	(35)	130	175	586	728			3314	3361	3679	3831
		764	776	989	1113			3850	3895	3922	3946
		1134	1199	1418	1533			4006	4335	4384	4594
		1897	2090	2587	2687			4667	4918	5318	5399
		2976	3088	3338	3363			5545	5751	6346	6404
		3591	3636	4327	4501			6664	6948		
		4512	4530	4964	5422	Msc I	(3)	586	1113	1418	
		5502	5769	6356	6654	Mse I	(27)	36	1009	1121	1151
		6803	6811	6935				1175	1816	2430	3260
Hga I	(12)	383	644	897	1493			3410	3414	3497	4031
		2338	3331	3844	4596			4129	4257	4316	5192
		5174	5906	6464	6933			5244	5249	5263	5316
HgiA I	(7)	340	3123	3801	4804			5551	5590	5955	6327
		5965	6050	6547				6508	6705	6975	
HgiE II	(2)	5065	6545			Msl I	(4)	2178	3000	5631	5790
Hha I	(41)	321	323	372	374	Msp I	(30)	165	400	571	632
		650	907	926	1402			725	1403	2542	2605
		1514	2508	2803	2844			2665	3196	3251	3365
		3160	3244	3782	3784			3626	3861	4204	4693
		3833	3835	4110	4270			4840	4866	5056	5460
		4335	4363	4396	4666			5494	5561	5671	5913
		4733	4833	5007	5116			6414	6448	6800	6923
		5509	5602	5939	6271			6932	6947		
		6371	6474	6604	6625	MspAl I	(10)	590	1622	3962	4310
		6758	6787	6841	6901			4828	5073	6014	6480
		6922						6674	7030		
HinC II	(1)	3345				Nae I	(2)	633	6933		
Hind II	(1)	3345				Nar I	(5)	1400	6602	6785	6899
HinD III	(1)	3329						6920			
Hinf I	(16)	444	452	793	804	Nci I	(17)	165	400	401	572
		1439	1771	2223	4021			725	2543	3197	3365
		4043	4064	4321	4386			3626	3861	3862	4866
		4461	4857	5374	7012			5562	5913	6414	6449
HinI I	(12)	744	1400	1935	1988			6800			
		2071	2257	5916	6298	Nco I	(3)	1413	2173	2512	
		6602	6785	6899	6920	Nde I	(2)	2047	6550		
HinP I	(41)	319	321	370	372	Ngm I	(2)	631	6931		
		648	905	924	1400	Nhe I	(2)	30	3491		
		1512	2506	2801	2842	Nla III	(25)	62	1207	1417	2117
		3158	3242	3780	3782			2177	2516	2750	2780
		3831	3833	4108	4268			2975	3170	3215	3523
		4333	4361	4394	4664			3977	4144	4490	5210
		4731	4831	5005	5114			5701	5711	5789	5825
		5507	5600	5937	6269			6218	6323	6407	6774
		6369	6472	6602	6623			6847			
		6756	6785	6839	6899	Nla IV	(38)	190	203	248	405
		6920						523	554	694	763
Hpa II	(30)	165	400	571	632			895	1146	1223	1401
		725	1403	2542	2605			1575	1691	2280	2551
		2665	3196	3251	3365			3089	3255	3303	3351
		3626	3861	4204	4693			3363	3651	3664	3709
		4840	4866	5056	5460			3866	4232	4518	4557
		5494	5561	5671	5913			5329	5423	5464	5675
		6414	6448	6800	6923			6265	6603	6786	6810
		6932	6947					6900	6921		
Hph I	(19)	1159	1185	1403	2188	Not I	(1)	3336			
		2527	2532	2860	2884	Nru I	(1)	1646			
		3013	5223	5450	5864	Nsp7524 I	(3)	4486	6403	6770	
		6072	6105	6389	6398	NspB II	(10)	590	1622	3962	4310
		6891	6936	7017				4828	5073	6014	6480
Kas I	(5)	1399	6601	6784	6898			6674	7030		
		6919				NspH I	(3)	4490	6407	6774	
Kpn I	(2)	407	3868			Pac I	(1)	3414			
Mae I	(16)	31	221	663	675	Pal I	(35)	130	175	586	728
		1396	1524	2405	2503			764	776	989	1113
		3238	3320	3492	3682			1134	1199	1418	1533
		4981	5234	5569	7004			1897	2090	2587	2687
Mae II	(18)	744	1083	1124	1935			2976	3088	3338	3363
		1947	1988	2071	2152			3591	3636	4327	4501
		2257	2488	2578	2791			4512	4530	4964	5422
		2962	5189	5605	5978			5502	5769	6356	6654
		6298	6740					6803	6811	6935	
Mae III	(24)	39	996	1024	1089	Ple I	(3)	801	4029	4865	
		1233	1874	1961	2310	Pme I	(1)	1817			
		2696	3185	3229	3500	PpuM I	(5)	256	1221	1574	3301
		3978	4842	4905	5021			3717			
		5304	5635	5693	5846	Psp1406 I	(2)	5605	5978		
		6034	6422	6713	6733	PspA I	(2)	399	3860		
Mbo I	(32)	93	459	1046	1178	Pst I	(3)	923	931	1107	
		1363	1647	1708	1722	Pvu I	(3)	1650	5749	6645	
		2398	2411	3013	3161	Pvu II	(4)	1622	4310	6674	7030
		3199	3247	3322	3349	Rea I	(15)	405	661	1286	2032
		3554	5052	5127	5138			2057	2112	2145	2196
		5146	5224	5236	5341			2353	2943	3225	3866
		5682	5700	5746	6004			5859	6535	7046	
		6021	6057	6642	6866	Sac I	(2)	340	3801		
Mbo II	(20)	1088	1301	1447	1504	Sal I	(1)	3343			
		1532	2487	2757	2802	Sap I	(2)	4108	4370		
		2805	2998	3320	4124	Sau3A I	(32)	93	459	1046	1178
		4358	5147	5220	5975			1363	1647	1708	1722
		6053	6162	6650	6862			2398	2411	3013	3161
Mlu I	(1)	3355						3199	3247	3322	3349
Mme I	(6)	831	1108	3925	3977			3554	5052	5127	5138
		4700	4884					5146	5224	5236	5341
Mnl I	(58)	218	370	389	434			5682	5700	5746	6004
		462	486	508	512			6021	6057	6642	6866
		568	778	874	1170	Sau96 I	(34)	128	173	188	201

		256	553	692	762	BstN I	CC`W,GG	24	BstU I	CG CG	26
		775	987	1198	1221	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	10
		1574	1896	2089	2686	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	39
		3087	3170	3301	3361	Cfr10 I	R`CCGG,Y	5	Cla I	AT`CG,AT	-
		3362	3589	3634	3649	Csp6 I	G`TA,C	15	Dde I	C`TNA,G	21
		3662	3717	5421	5500	Dpn I	GA TC	32	DpnII	`GATC,	32
		5517	5739	6355	6652	Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	5
		6809	6994			Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	5
Sca I	(1)	5859				Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	3
ScrF I	(41)	165	243	400	401	Ear I	CTCTTC 7/10	8	Eco47 III	AGC GCT	2
		550	572	725	737	Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	-
		750	1171	1196	1219	EcoN I	CCTNN`N,NNAGG	3	Eco109 I	RG`GNC,CY	7
		1239	1269	1719	1903	EcoR I	G`AATT,C	2	EcoR II	`CCWGG,	24
		2096	2543	2559	2684	EcoR V	GAT ATC	3	Ehe I	GGC GCC	5
		2796	2871	2925	3197	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	45
		3365	3626	3704	3861	Fok I	GGATG 14/18	14	Fse I	GG,CCGG`CC	-
		3862	4226	4514	4635	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	13
		4648	4866	5562	5913	Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	6
		6414	6449	6721	6800	Hae II	R,CGC`Y	10	Hae III	GG CC	35
		6998				Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	7
Sec I	(37)	163	242	252	399	HgiE II	ACNNNNNNNGGT -1/132	-	Hha I	G,CG`C	41
		463	499	548	549	Hinc II	GTY RAC	1	Hind II	GTY RAC	1
		696	735	736	748	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	16
		749	1169	1238	1247	HinI I	GR`CG,YC	12	HinP I	G`CG,C	41
		1267	1268	1413	1718	Hpa I	GTT AAC	-	Hpa II	C`CG,G	30
		2173	2512	2542	2682	Hph I	GGTGA 12/11	19	Kas I	G`GCG,C	5
		2845	2869	2924	3624	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
		3703	3713	3860	3923	Mae II	A`CG,T	18	Mae III	`GTNAC,	24
		4225	4646	6720	6798	Mbo I	`GATC,	32	Mbo II	GAAGA 12/11	20
SfaN I	(25)	187	446	643	940	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
		1487	1544	1676	1722	Mnl I	CCTC 10/10	58	Msc I	TGG CCA	3
		2171	2613	2889	2904	Mse I	T`TA,A	27	Msl I	CAYNN NNRTG	4
		3003	3648	3906	4582	Msp I	C`CG,G	30	MspA I	CMG CKG	10
		5634	5827	6074	6435	Mun I	C`AATT,G	-	Nae I	GCC GGC	2
		6527	6565	6603	6919	Nar I	GG`CG,CC	5	Nci I	CC`s,G	17
		6931				Nco I	C`CATG,G	3	Nde I	CA`TA,TTG	2
Sfc I	(10)	15	919	927	1103	Ngm I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
		1498	3476	4751	4942	Nla III	,CATG`	25	Nla IV	GGN NCC	38
		5620	7038			Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Sma I	(2)	401	3862			Nsi I	A,RGCA`T	-	Nsp7524 I	R`CATG,Y	3
SnaB I	(1)	2153				NspB II	CMG CKG	10	NspH I	R,CATG`Y	3
Spe I	(1)	662				Pac I	TTA,AT`TAA	1	Paer7 I	C`TGA,G	-
Sph I	(1)	6774				Pal I	GG CC	35	Pflm I	CCAN,NNN`NTGG	-
Ssp I	(2)	4029	6183			Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Sty I	(8)	252	463	1247	1413	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	5
		2173	2512	3713	3923	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
Taq I	(15)	796	1040	1351	1362	Pst I	C, TGCA`G	3	Pvu I	CG,AT`CG	3
		1707	2563	2857	2884	Pvu II	CAG CTG	4	Rsa I	GT AC	15
		2899	3028	3307	3344	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
		4024	4586	6030		Sac II	CC,GC`GG	-	Sal I	G`TGA,C	1
Tfi I	(7)	444	804	1439	1771	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	32
		4064	4321	4461		Sau96 I	G`GNC,C	34	Sca I	AGT ACT	1
Tsp45 I	(8)	1024	1233	2696	3185	ScrF I	CC`N,GG	41	Sec I	C`CNNG,G	37
		5635	5846	6422	6733	SfaN I	GCATC 9/13	25	Sfc I	C`TRYA,G	10
Tth111 I	(4)	392	813	1219	3853	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
Tth111 II	(9)	147	424	615	634	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
		2996	3608	5075	5084	Sph I	G, CATG`C	1	Spl I	C`GTAC,G	-
		5114				Srf I	GCCC GGCC	-	Ssp I	AAT ATT	2
Vsp I	(4)	4129	4257	4316	5551	Stu I	AGG CCT	-	Sty I	C`CWGG,G	8
Xba I	(2)	220	3681			Taq I	T`CG,A	15	Tfi I	G`AWT,G	7
Xho II	(10)	2398	3013	3322	3349	Tsp45 I	`GTSAC,	8	Tth111 I	GACN`N,NGTC	4
		5127	5138	5224	5236	Tth111 II	CAARCA 16/14	9	Vsp I	AT`TA,AT	4
		6004	6021			Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xma I	(2)	399	3860			Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TGA,G	-
Xma III	(3)	726	1531	3336		Xho II	R`GATC,Y	10	Xma I	C`CCGG,G	2
Xmn I	(4)	3313	4092	4130	5978	Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	4

Site usage in pSCX-Flag:

Aat II	G,ACGT`C	6	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	76
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	12
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	38
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	5	Ava II	G`GWC,C	15
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	15	Ban II	G,RGYC`C	8
Bbe I	G,CGCC`C	5	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	12	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	5
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	6
BsaA I	YAC GTR	1	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	12	BsaJ I	C`CNNG,G	37
BsaW I	W`CCGG,W	4	BseR I	GAGGAG 16/14	6
Bsg I	GTGCAG 22/20	4	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	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	14	BsoF I	GC`N,GC	45
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	1
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	2	BssH II	G`CGCG,C	4
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1