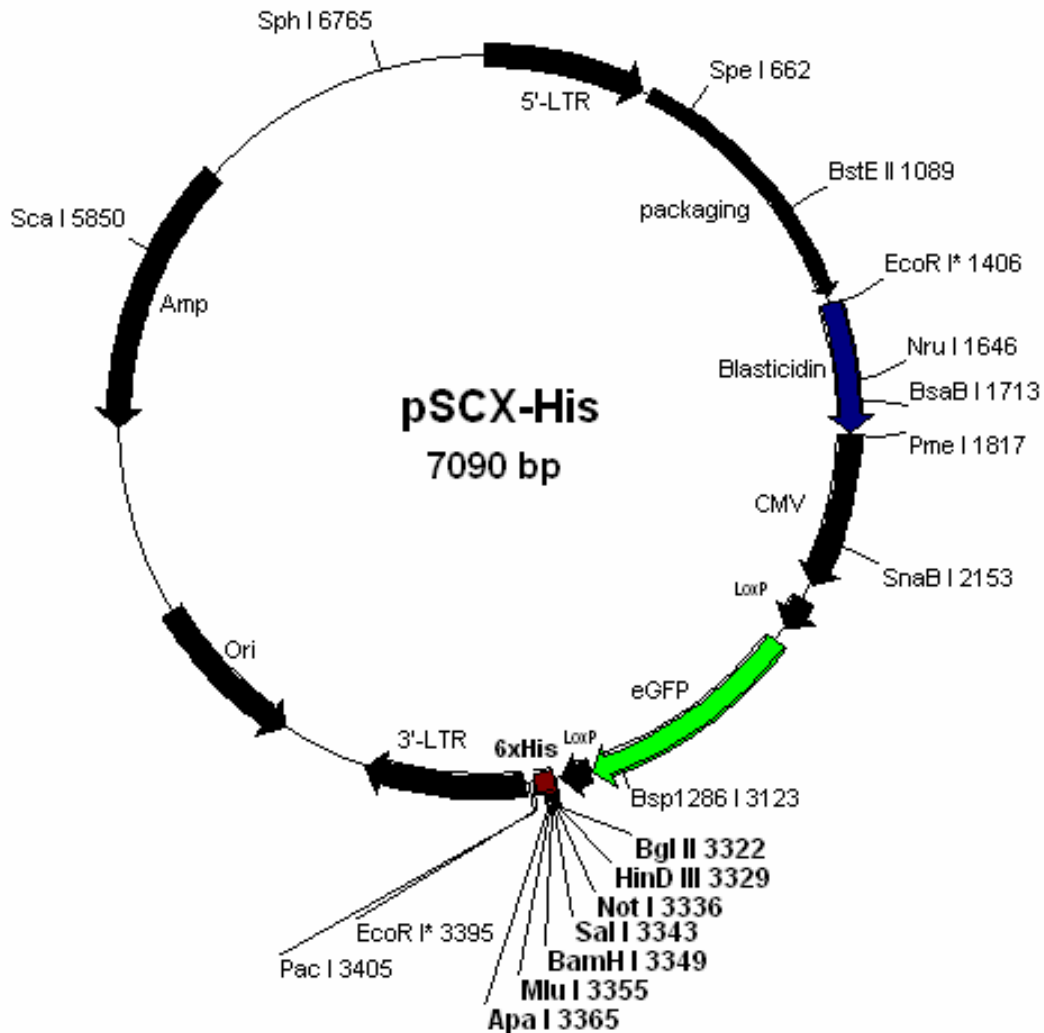


Vector: pSCX-His

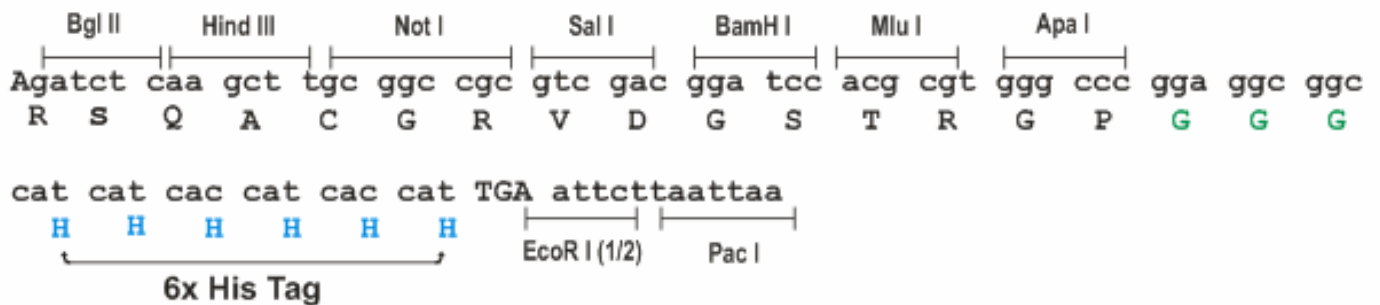
Antibiotic Selection: Amp

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

Date of Construction: July, 2005



Linker Sequence



pSCX-His Full-Length Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACATAACTGAGAA
TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCAGAATATGGGC CAAACAGGAT ATCTGTGGTAAGCAGTTCCCT
GCCCCGGCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTTCCAGG
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CTGCCACCT CGGGGTCTT TCATTTGGAG GTTCCACCGA GATTTGGAGACCCTGCCA GGGACCACCGACCCCCCGC
CGGGAGGTAA GCTGGCCAGC GGTCGTTTCGTGTCTGTCTC TGTCTTTGTG CGTGTTTGTG CCGCATCTAATGTTTGC
CTGCGTCTGTACTAGTTAG TAACTAGCTC TGTATCTGGC GGACCCGTGG TGAAGTGA GAGTTCTGAACACCCGGCCG
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 CCAGAAAAAG GGGGAA

Unique enzymes in pSCX-His:

Spe I	A`CTAG,T	662			1683	1871	1899	1911
BstE II	G`GTNAC,C	1089			1925	2092	2183	2216
Bbv II	GAAGAC 7/11	1499			2320	2341	2402	2732
Bbs I	GAAGAC 8/12	1500			2773	2840	2879	3017
Nru I	TCG CGA	1646			3130	3190	3193	3335
BsaB I	GATNN NNATC	1713			3339	3371	3651	3657
Pme I	CTT AAAC	1817			3953	4167	4270	4326
BsaA I	YAC GTR	2153			4336	4360	4403	4410
SnaB I	TAC GTA	2153			4431	4522	4550	4677
Bsp1286 I	G,DGCH`C	3123			4696	4817	4927	5062
BspM II	T`CCGG,A	3250			5071	5433	5524	5715
Bgl II	A`GATC,T	3322			5761	5882	5926	6003
Hind III	A`AGCT,T	3329	Afl II	(3)	6112	6211	6258	6432
Not I	GC`GGCC,GC	3336	Afl III	(2)	6471	6481	6507	6545
Sal I	G`TCGA,C	3343	Aha II	(12)	6558	6584	6641	6900
Acc I	GT`MK,AC	3344			35	1008	3487	
HinC II	GTY RAC	3345			744	1400	1935	1988
Hind II	GTY CAC	3345	Ahd I	(4)	2071	2257	5907	6289
BamH I	G`GATC,C	3349	Alu I	(38)	6593	6776	6890	6911
Mlu I	A`CGCG,T	3355			1022	3900	3946	5370
Bsp120 I	G`GGCC,C	3361			30	34	338	582
Apa I	G,GGCC`C	3365			670	678	1517	1622
Sca I	AGT ACT	5850			2379	2500	2534	2567
Sph I	G,CATG`C	6765			2639	2672	2888	2936
Number of enzymes = 24					3047	3221	3331	3482
					3486	3790	4109	4142
					4237	4301	4419	4645
					4735	4781	5038	5559
					5659	5722	6401	6420
					6665	7021		

The following enzymes do not cut in pSCX-His:

Age I	Avr II	Bcl I	Blp I	BsiC I	Alw I	(18)	455	1053	1359	1729
BsiW I	Bsm I	BspM I	Bst1107 I	BstB I			2394	3009	3206	3243
BstX I	Cla I	Dra III	Eco72 I	Esp I			3345	3356	5039	5125
Fse I	Hpa I	Mun I	Nsi I	PaeR7 I			5125	5222	5223	5687
PflM I	Pml I	Rsr II	Sac II	Sfi I			6002	6008		
Spl I	Srf I	Stu I	Xca I	Xcm I	AlwN I	(3)	159	3611	4893	
					Apa I	(1)	3365			
					ApaL I	(3)	4791	6037	6534	
					Apo I	(3)	874	1406	3395	
					Asc I	(2)	370	3822		
					Ase I	(4)	4120	4248	4307	5542
					Asp718	(2)	403	3855		
					Ava I	(5)	333	399	500	3785
							3851			
					Ava II	(15)	188	201	256	553
							692	1221	1574	3170
							3301	3640	3653	3708
							5508	5730	6985	
					BamH I	(1)	3349			

pSCX-His: sites sorted by name:

Aat II	(6)	747	1938	1991	2074					
		2260	6292							
Acc I	(1)	3344								
Acc65 I	(2)	403	3855							
Aci I	(76)	199	205	568	590					
		690	729	862	903					
		1044	1135	1201	1300					
		1319	1357	1534	1616					

Ban I	(15)	246	403	1144	1399			4324	4326	4524	5105
		1689	2278	2549	3698			5435	5928	6260	6360
		3855	4221	5318	6592			6362	6465		
		6775	6889	6910		BstY I	(10)	2398	3013	3322	3349
Ban II	(8)	340	353	1679	3365			5118	5129	5215	5227
		3792	3805	6842	6856			5995	6012		
Bbe I	(5)	1403	6596	6779	6893	Bsu36 I	(2)	783	1020		
		6914				Cac8 I	(39)	28	32	321	372
Bbs I	(1)	1500						584	588	633	652
Bbv I	(12)	933	941	1526	1631			1201	1510	1624	1899
		2765	3049	3056	4896			2092	2637	2670	2718
		4899	5105	5799	6410			3042	3049	3333	3480
Bbv II	(1)	1499						3484	3773	3824	4270
Bcn I	(17)	166	401	402	573			4299	4408	4494	4531
		726	2544	3198	3366			5091	5482	6495	6643
		3618	3853	3854	4858			6663	6667	6763	6804
		5554	5905	6406	6441			6852	6894	6924	
		6792				Cfr10 I	(5)	631	2664	5450	6913
Bfa I	(16)	31	221	663	675			6922			
		1396	1524	2405	2503	Csp6 I	(15)	404	660	1285	2031
		3238	3320	3483	3673			2056	2111	2144	2195
		4972	5225	5560	6995			2352	2942	3224	3856
Bgl I	(5)	1903	2025	2096	5490			5849	6525	7036	
		6608				Dde I	(21)	75	169	210	478
Bgl II	(1)	3322						783	1020	1292	1810
Bpm I	(5)	2958	3198	3420	5440			3117	3135	3527	3621
		7058						3662	3931	4002	4752
Bsa I	(6)	478	532	1151	3908			5161	5327	5867	6293
		3929	5431					6528			
BsaA I	(1)	2153				Dpn I	(32)	95	461	1048	1180
BsaB I	(1)	1713						1365	1649	1710	1724
BsaH I	(12)	744	1400	1935	1988			2400	2413	3015	3163
		2071	2257	5907	6289			3201	3249	3324	3351
		6593	6776	6890	6911			3547	5045	5120	5131
BsaJ I	(37)	163	242	252	399			5139	5217	5229	5334
		463	499	548	549			5675	5693	5739	5997
		696	735	736	748			6014	6050	6635	6859
		749	1169	1238	1247	DpnII	(32)	93	459	1046	1178
		1267	1268	1413	1718			1363	1647	1708	1722
		2173	2512	2542	2682			2398	2411	3013	3161
		2845	2869	2924	3615			3199	3247	3322	3349
		3694	3704	3851	3914			3545	5043	5118	5129
		4216	4637	6711	6789			5137	5215	5227	5332
		6795						5673	5691	5737	5995
BsaW I	(4)	3250	4683	4830	5661			6012	6048	6633	6857
BseR I	(6)	466	1295	1334	2494	Dra I	(4)	1817	5236	5255	5947
		2544	3917			Drd I	(3)	1502	4585	6454	
Bsg I	(4)	1602	2642	2739	3063	Dsa I	(5)	696	1413	2173	2512
BsiE I	(10)	594	729	1534	1650			6795			
		3339	4393	4817	5740	Eae I	(14)	584	726	1111	1132
		5889	6636					1416	1531	2585	2974
BsiHKA I	(7)	340	3123	3792	4795			3336	3372	4316	5758
		5956	6041	6538				6792	6924		
BsmA I	(22)	108	477	533	611	Eag I	(3)	726	1531	3336	
		736	834	951	1075	Ear I	(8)	1072	1313	2471	3304
		1134	1152	1330	1433			4099	4361	6165	6653
		2246	3437	3560	3907	Eco47 III	(2)	925	6831		
		3928	5432	6206	6359	Eco57 I	(8)	1511	2494	2666	2712
		6403	7075					2909	5024	6038	7042
BsmB I	(7)	735	833	1074	1133	EcoN I	(3)	786	1394	3309	
		1331	6360	6402		EcoO109 I	(7)	256	1221	1574	3301
BsmF I	(14)	174	187	566	731			3708	6346	6800	
		766	1207	1587	1988	EcoR I	(2)	1406	3395		
		2139	2307	3287	3626	EcoR II	(24)	241	548	735	748
		3639	6771					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	3693	4215	4503
		1617	1620	1784	2673			4624	4637	6710	6987
		2732	2754	3038	3045	EcoR V	(3)	141	3593	6978	
		3096	3099	3193	3336	Ehe I	(5)	1401	6594	6777	6891
		3339	3372	4302	4383			6912			
		4401	4404	4522	4677	Fnu4H I	(45)	729	903	919	922
		4820	4885	4888	5094			927	930	1135	1515
		5422	5761	5788	5883			1534	1608	1611	1614
		6112	6399	6508	6612			1617	1620	1784	2673
		6685						2732	2754	3038	3045
								3096	3099	3193	3336
Bsp120 I	(1)	3361						3339	3372	4302	4383
Bsp1286 I	(1)	3123						4401	4404	4522	4677
BspH I	(4)	5197	6205	6310	6834			4820	4885	4888	5094
BspM II	(1)	3250						5422	5761	5788	5883
Bsr I	(18)	376	1032	1060	1548			6112	6399	6508	6612
		1572	2109	3126	3828			6685			
		4278	4884	4897	5011						
		5417	5535	5578	5845	Fok I	(13)	425	1142	1302	1466
		6017	6723					1701	2541	2907	3876
BsrB I	(4)	1044	4169	4410	6211			5336	5517	5804	6447
BsrD I	(2)	5431	5605					6691			
BsrG I	(2)	1284	3223			Fsp I	(2)	5592	6615		
BssH II	(4)	319	370	3771	3822	Gdi II	(14)	725	727	1131	1530
BssS I	(5)	1589	2694	4650	6034			1532	2586	2973	3335
		6341						3337	3373	4317	5757
BstE II	(1)	1089						6793	6925		
BstN I	(24)	243	550	737	750	Gsu I	(5)	2957	3197	3421	5441
		1171	1196	1219	1239			7059			
		1269	1719	1903	2096	Hae I	(6)	586	1113	1418	4492
		2559	2684	2796	2871			4503	4955		
		2925	3695	4217	4505	Hae II	(10)	927	1403	2509	4355
		4626	4639	6712	6989			4725	6596	6779	6833
BstU I	(26)	319	321	372	905			6893	6914		
		907	1137	1646	1873	Hae III	(36)	130	175	586	728
		2842	3160	3244	3341			764	776	989	1113
		3357	3771	3773	3824			1134	1199	1418	1533

		1897	2090	2587	2687		3997	4326	4375	4585
		2976	3088	3338	3363		4658	4909	5309	5390
		3374	3582	3627	4318		5536	5742	6337	6395
		4492	4503	4521	4955		6655	6939		
		5413	5493	5760	6347					
		6645	6794	6802	6926	Msc I	(3)	586	1113	1418
Hga I	(12)	383	644	897	1493	Mse I	(27)	36	1009	1121
		2338	3331	3835	4587			1175	1816	2430
		5165	5897	6455	6924			3401	3405	3488
HgiA I	(7)	340	3123	3792	4795			4120	4248	4307
		5956	6041	6538				5235	5240	5254
HgiE II	(2)	5056	6536					5542	5581	5946
Hha I	(41)	321	323	372	374	Msl I	(4)	6499	6696	6966
		650	907	926	1402	Msp I	(30)	2178	3000	5622
		1514	2508	2803	2844			165	400	571
		3160	3244	3773	3775			725	1403	2542
		3824	3826	4101	4261			2665	3196	3251
		4326	4354	4387	4657			3617	3852	4195
		4724	4824	4998	5107			4831	4857	5047
		5500	5593	5930	6262			5485	5552	5662
		6362	6465	6595	6616			6405	6439	6791
		6749	6778	6832	6892			6923	6938	
		6913				MspAl I	(10)	590	1622	3953
HinC II	(1)	3345						4819	5064	6005
Hind II	(1)	3345				Nae I	(2)	6665	7021	
HinD III	(1)	3329				Nar I	(5)	633	6924	
Hinf I	(16)	444	452	793	804			1400	6593	6776
		1439	1771	2223	4012			6911		6890
		4034	4055	4312	4377	Nci I	(17)	165	400	401
		4452	4848	5365	7003			725	2543	3197
HinI I	(12)	744	1400	1935	1988			3617	3852	3853
		2071	2257	5907	6289			5553	5904	6405
		6593	6776	6890	6911			6791		6440
HinP I	(41)	319	321	370	372	Nco I	(3)	1413	2173	2512
		648	905	924	1400	Nde I	(2)	2047	6541	
		1512	2506	2801	2842	Ngom I	(2)	631	6922	
		3158	3242	3771	3773	Nhe I	(2)	30	3482	
		3822	3824	4099	4259	Nla III	(25)	62	1207	1417
		4324	4352	4385	4655			2177	2516	2750
		4722	4822	4996	5105			2975	3170	3215
		5498	5591	5928	6260			3968	4135	4481
		6360	6463	6593	6614			5692	5702	5780
		6747	6776	6830	6890			6209	6314	6398
		6911						6838		6765
Hpa II	(30)	165	400	571	632	Nla IV	(38)	190	203	248
		725	1403	2542	2605			523	554	694
		2665	3196	3251	3365			895	1146	1223
		3617	3852	4195	4684			1575	1691	2280
		4831	4857	5047	5451			3089	3255	3303
		5485	5552	5662	5904			3363	3642	3655
		6405	6439	6791	6914			3857	4223	4509
		6923	6938					5320	5414	5455
Hph I	(21)	1159	1185	1403	2188			6256	6594	6777
		2527	2532	2860	2884			6891	6912	6801
		3013	3374	3380	5214	Not I	(1)	3336		
		5441	5855	6063	6096	Nru I	(1)	1646		
		6380	6389	6882	6927	Nsp7524 I	(3)	4477	6394	6761
		7008				NspB II	(10)	590	1622	3953
Kas I	(5)	1399	6592	6775	6889			4819	5064	6005
		6910						6665	7021	6471
Kpn I	(2)	407	3859			NspH I	(3)	4481	6398	6765
Mae I	(16)	31	221	663	675	Pal I	(36)	130	175	586
		1396	1524	2405	2503			764	776	989
		3238	3320	3483	3673			1134	1199	1418
		4972	5225	5560	6995			1897	2090	2587
Mae II	(18)	744	1083	1124	1935			2976	3088	3338
		1947	1988	2071	2152			3374	3582	3627
		2257	2488	2578	2791			4492	4503	4521
		2962	5180	5596	5969			5413	5493	5760
		6289	6731					6645	6794	6802
Mae III	(24)	39	996	1024	1089	Ple I	(3)	801	4020	4856
		1233	1874	1961	2310	Pme I	(1)	1817		
		2696	3185	3229	3491	PpuM I	(5)	256	1221	1574
		3969	4833	4896	5012			3708		3301
		5295	5626	5684	5837	Psp1406 I	(2)	5596	5969	
		6025	6413	6704	6724	PspA I	(2)	399	3851	
Mbo I	(32)	93	459	1046	1178	Pst I	(3)	923	931	1107
		1363	1647	1708	1722	Pvu I	(3)	1650	5740	6636
		2398	2411	3013	3161	Pvu II	(4)	1622	4301	6665
		3199	3247	3322	3349	Rea I	(15)	405	661	1286
		3545	5043	5118	5129			2057	2112	2145
		5137	5215	5227	5332			2353	2943	3225
		5673	5691	5737	5995			5850	6526	7037
		6012	6048	6633	6857	Sac I	(2)	340	3792	
Mbo II	(20)	1088	1301	1447	1504	Sal I	(1)	3343		
		1532	2487	2757	2802	Sap I	(2)	4099	4361	
		2805	2998	3320	4115	Sau3A I	(32)	93	459	1046
		4349	5138	5211	5966			1363	1647	1708
		6044	6153	6641	6853			2398	2411	3013
Mlu I	(1)	3355						3199	3247	3322
Mme I	(6)	831	1108	3916	3968			3545	5043	5118
		4691	4875					5137	5215	5227
Mnl I	(58)	218	370	389	434			5673	5691	5737
		462	486	508	512			6012	6048	6633
		568	778	874	1170	Sau96 I	(34)	128	173	188
		1273	1306	1312	1315			256	553	692
		1321	1351	1354	1369			775	987	1198
		1376	1392	1456	1797			1574	1896	2089
		1798	2354	2472	2522			3087	3170	3301
		2603	2609	2702	2840			3362	3580	3625
		2852	2903	3023	3305			3653	3708	5412
		3314	3361	3670	3822			5508	5730	6346
		3841	3886	3913	3937			6800	6985	6643
						Sca I	(1)	5850		

ScrF I	(41)	165	243	400	401	BsaH I	GR`CG, YC	12	BsaJ I	C`CNNG, G	37
		550	572	725	737	BsaW I	W`CCGG, W	4	BseR I	GAGGAG 16/14	6
		750	1171	1196	1219	Bsg I	GTGCAG 22/20	4	BsiC I	TT`CG, AA	-
		1239	1269	1719	1903	BsiE I	CG, RY`CG	10	BsiHKA I	G, WGCW`C	7
		2096	2543	2559	2684	BsiW I	C`GTAC, G	-	Bsm I	GAATG, C 7	-
		2796	2871	2925	3197	BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
		3365	3617	3695	3852	BsmF I	GGGAC 15/19	14	BsoF I	GC`N, GC	45
		3853	4217	4505	4626	Bsp120 I	G`GGCC, C	1	Bsp1286 I	G, DGCH`C	1
		4639	4857	5553	5904	BspH I	T`CATG, A	4	BspM I	AC2TGC 10/14	-
		6405	6440	6712	6791	BspM II	T`CCGG, A	1	Bsr I	ACT, GG`	18
		6989				BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
Sec I	(37)	163	242	252	399	BsrG I	T`GTAC, A	2	Bssh II	G`CGCG, C	4
		463	499	548	549	BssS I	C`TCGT, G	5	Bst1107 I	GTA TAC	-
		696	735	736	748	BstB I	TT`CG, AA	-	BstE II	G`GTNAC, C	1
		749	1169	1238	1247	BstN I	CC`W, GG	24	BstU I	CG CG	26
		1267	1268	1413	1718	BstX I	CCAN, NNNN`NTGG	-	BstY I	R`GATC, Y	10
		2173	2512	2542	2682	Bsu36 I	CC`TNA, GG	2	Cac8 I	GCN NGC	39
		2845	2869	2924	3615	Cfr10 I	R`CCGG, Y	5	ClA I	AT`CG, AT	-
		3694	3704	3851	3914	Csp6 I	G`TA, C	15	Dde I	C`TNA, G	21
		4216	4637	6711	6789	Dpn I	GA TC	32	DpnII	`GATC,	32
SfaN I	(25)	187	446	643	940	Dra I	TTT AAA	4	Dra III	CAC, NNN`GTG	5
		1487	1544	1676	1722	Drd I	GACNN, NN`NNGTC	3	Dsa I	C`CRYG, G	-
		2171	2613	2889	2904	Eae I	Y`GGCC, R	14	Eag I	C`GGCC, C	3
		3003	3639	3897	4573	Ear I	CTCTTC 7/10	8	Eco47 III	AGC GCT	2
		5625	5818	6065	6426	Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	-
		6518	6556	6594	6910	EcoN I	CCTNN`N, NNAGG	3	EcoO109 I	RG`GNC, CY	7
		6922				EcoR I	G`AATT, C	2	EcoR II	`CCWGG,	24
Sfc I	(10)	15	919	927	1103	EcoR V	GAT ATC	3	Ehe I	GGC GCC	5
		1498	3467	4742	4933	Esp I	GC`TNA, GC	-	Fnu4H I	GC`N, GC	45
		5611	7029			Fok I	GGATG 14/18	13	Fse I	GG, CCGG`CC	-
Sma I	(2)	401	3853			Fsp I	TGC GCA	2	Gdi II	`YGGC, CG	14
SnaB I	(1)	2153				Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	6
Spe I	(1)	662				Hae II	R, CGCG`Y	10	Hae III	GG CC	36
Sph I	(1)	6765				Hga I	GAGCG 9/14	12	HgiA I	G, WGCW`C	7
Ssp I	(2)	4020	6174			HgiE II	ACNNNNNNNGGT -1/132	-	Hha I	G, CG`C	41
Sty I	(8)	252	463	1413		Hinc II	GTY RAC	1	Hind II	GTY RAC	1
		2173	2512	3704	3914	Hind III	A`AGCT, T	1	Hinf I	G`ANT, C	16
Taq I	(15)	796	1040	1351	1362	HinI I	GR`CG, YC	12	HinP I	G`CG, C	41
		1707	2563	2857	2884	Hpa I	GTT AAC	-	Hpa II	C`CG, G	30
		2899	3028	3307	3344	Hph I	GGTGA 12/11	21	Kas I	G`CGCG, C	5
		4015	4577	6021		Kpn I	G, GTAC`C	2	Mae I	C`TA, G	16
Tfi I	(7)	444	804	1439	1771	Mae II	A`CG, T	18	Mae III	GTNAC,	24
		4055	4312	4452		Mbo I	`GATC,	32	Mbo II	GAGA 12/11	20
Tsp45 I	(8)	1024	1233	2696	3185	Mlu I	A`CGCG, T	1	Mme I	TCCRAC 25/23	6
		5626	5837	6413	6724	Mnl I	CCTC 10/10	58	Msc I	TGG CCA	3
Tth111 I	(4)	392	813	1219	3844	Mse I	T`TA, A	27	Msl I	CAYNN NNRTG	4
Tth111 II	(9)	147	424	615	634	Msp I	C`CG, G	30	MspA I	CMG CKG	10
		2996	3599	5066	5075	Mun I	C`AATT, G	-	Nae I	GCC GGC	2
		5105				Nar I	GG`CG, CC	5	Nci I	CC`S, GG	17
Vsp I	(4)	4120	4248	4307	5542	Nco I	C`CATG, G	3	Nde I	CA`TA, TT	2
Xba I	(2)	220	3672			NgoM I	G`CCGG, C	2	Nhe I	G`CTAG, C	2
Xho II	(10)	2398	3013	3322	3349	Nla III	, CATG`	25	Nla IV	GGN NCC	38
		5118	5129	5215	5227	Not I	GC`GGCC, GC	1	Nru I	TCG CGA	1
		5995	6012			Nsi I	A, TGCA`T	-	Nsp7524 I	R`CATG, Y	3
Xma I	(2)	399	3851			NspB II	CMG CKG	10	NspH I	R, CATG`Y	3
Xma III	(3)	726	1531	3336		Paer7 I	C`TCGA, G	-	Pal I	GG CC	36
Xmn I	(4)	3313	4083	4121	5969	PflM I	CCAN, NNN`NTGG	-	Ple I	GAGTC 9/10	3
						Pme I	CTTT AAAC	1	Pml I	CAC GTG	-
						PpuM I	RG`GWC, CY	5	Psp1406 I	AA`CG, TT	2
						PspA I	C`CCGG, G	2	Pst I	C, TGCA`G	3
						Pvu I	CG, AT`CG	3	Pvu II	CAG CTG	4
						Rsa I	GT AC	15	Rsr II	CG`GWC, CG	-
						Sac I	G, AGCT`C	2	Sac II	CC, GC`GG	-
						Sal I	G`TCGA, C	1	Sap I	GCTCTTC 8/11	2
						Sau3A I	`GATC,	32	Sau96 I	G`GNC, C	34
						Sca I	AGT ACT	1	ScrF I	CC`N, GC	41
						Sec I	C`CNNG, G	37	SfaN I	GCATC 9/13	25
						Sfc I	C`TRYA, G	10	Sfi I	GGCCN, NNN`NGGCC	-
						Sma I	CCC GGG	2	SnaB I	TAC GTA	1
						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	-
						Sty I	C`CWWG, G	8	Taq I	T`CG, A	15
						Tfi I	G`AWT, T	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`CTAG, A	2
						Xca I	GTA TAC	-	Xcm I	CCANNNN, N`NNNTGG-	-
						Xho I	C`TCGA, G	-	Xho II	R`GATC, Y	10
						Xma I	C`CCGG, G	2	Xma III	C`GGCC, G	3

Site usage in pSCX-His:

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, RGCY`C	8
Bbe I	G, CGCC`C	5	Bbs I	GAAGAC 8/12	1
Bbv I	GACAGC 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