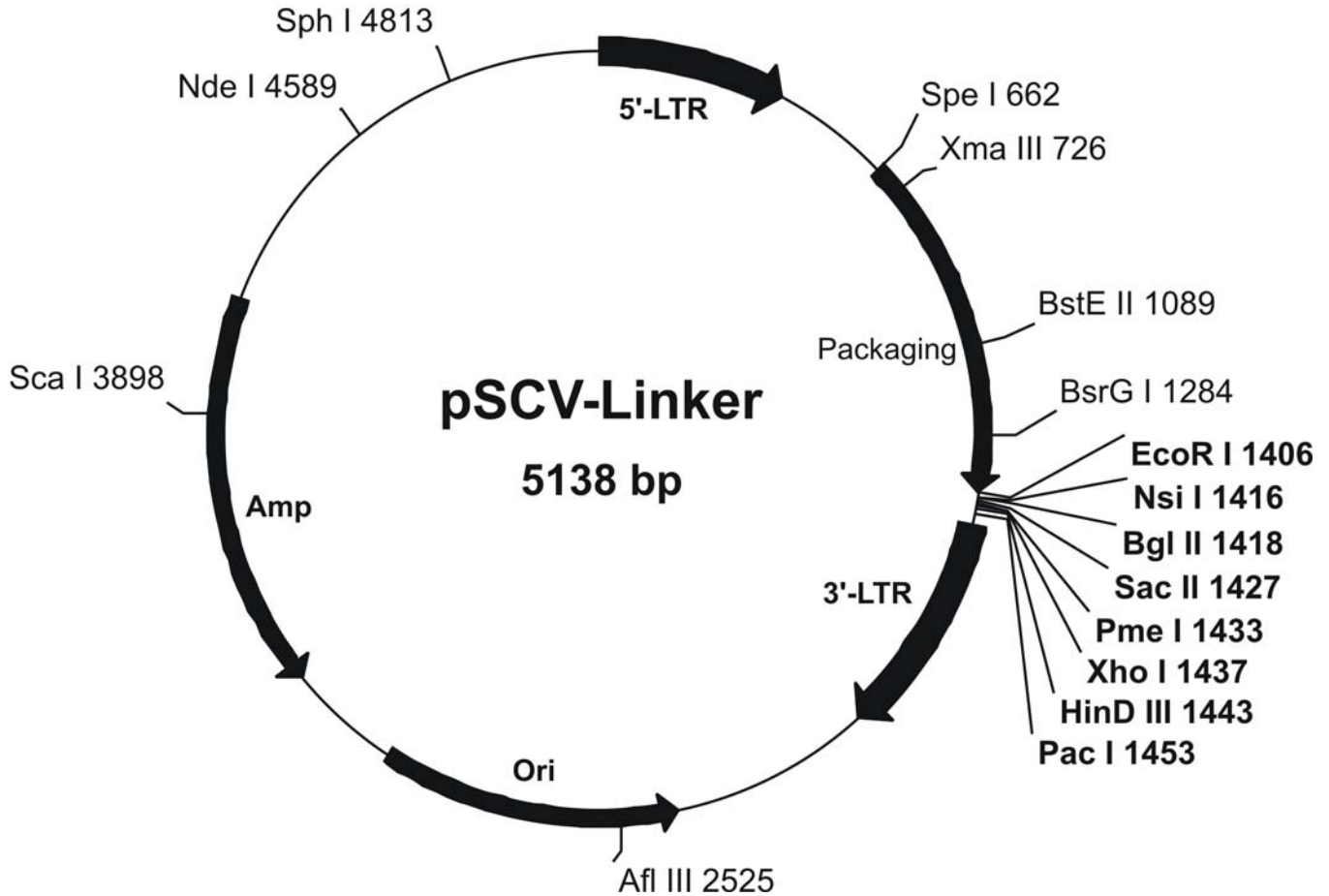


Name of Vector: pSCV-Linker
Antibiotic Selection: Amp
Created by: Hong Yin
(He Lab @ The University of Chicago)
Date of Creation: March 2005



pSCV-Linker Sequence

TGAAAGACCC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATTT TGCAAGGCATGGAAAATACA
TAACTGAGAA TAGAGAAGTT CAGATCAAGG TTAGGAACAG AGAGACAGCAGAATATGGGC CAAACAGGAT
ATCTGTGGTA AGCAGTTCCCT GCCCCGGCTC AGGGCCAAGAACAGATGGTC CCCAGATGCG GTCCCCGCCCT
CAGCAGTTTC TAGAGAACCA TCAGATGTTTTCCAGGGTGCC CCAAGGACCT GAAATGACCC TGTGCCTTAT
TTGAACTAAC CAATCAGTTCGCTTCTCGCT TCTGTTTCGCG CGCTTCTGCT CCCCAGACTC AATAAAAAGAG
CCCACAACCCCTCACTCGGC GCGCCAGTCC TCCGATAGAC TGCGTCGCCC GGGTACCCGT ATTCCCAATA
AAGCCTCTTG CTGTTTGCAT CCGAATCGTG GACTCGCTGA TCCTTGGGAG GGTCTCCTCAGATTGATTGA
CTGCCACCT CGGGGGTCTT TCATTTGGAG GTTCCACCGA GATTTGGAGACCCCTGCCA GGGACCACCG
ACCCCCCGC CGGGAGGTAA GCTGGCCAGC GGTGTTTTCGTGTCTGTCTC TGTCTTTGTG CGTGTTTGTG
CCGGCATCTA ATGTTTGCAG CTGCGTCTGTACTAGTTTAC TAACCTAGCTC TGTATCTGGC GGACCCGTGG
TGGAACCTGAC GAGTCTGAACACCCGGCCG CAACCTTGGG AGACGTCCA GGGACTTTGG GGGCCGTTTT
TGTGCCCCGACCTGAGGAAG GGAGTCGATG TGAATCCGA CCCCCTCAGG ATATGTGGTT CTGGTAGGAG
ACGAGAACCT AAAACAGTTC CCGCCTCCGT CTGAATTTTT GCTTTCGGTT TGGAAACCGAAGCCGCGCGTC
TTGTCTGCTG CAGCGCTGCA GCATCGTTCT GTGTTGTCTC TGTCTGACTGTGTTTCTGTA TTTGTCTGAA
AATTAGGGCC AGACTGTTAC CACTCCCTTA AGTTTGACCTTAGGTCCTG GAAAGATGTC GAGCGGATCG
CTCACAACTA GTCGGTAGAT GTCAAGAAGAGACGTTGGGT TACCTTCTGC TCTGCAGAAT GGCCAACCTT
TAACGTCGGA TGGCCGCGAGACGGCACCTT TAACCGAGAC CTCATCACC AGGTTAAGAT CAAGGTCTTT
TCACCTGGCCCGCATGGACA CCCAGACCAG GTCCCTACA TCGTGACCTG GGAAGCCTTG GCTTTTGACC
CCCTCCCTG GGTCAAGCCC TTTGTACACC CTAAGCTCC GCCTCCTTT CCTCCATCCGCCCGTCTCT
CCCCCTGAA CTTCTCGTT CGACCCCGCC TCGATCCTCC CTTTATCCAGCCCTCACTCC TTCTTAGGC
GCCGGAATTCa tgc ata gat ctc cgc ggg ttt aaa ctc gag aag ctt tta att aaCGATAA
AATAAAGAT TTTATTTAGT CTCCAGAAAAAGGGGGGAAT GAAAGACCCC ACCTGTAGGT TTGGCAAGCT
AGCTTAAGTA ACGCCATTTTGCAAGGCATG GAAAATACAT AACTGAGAAAT AGAGAAGTTC AGATCAAGGT
TAGGAACAGAGAGACAGCAG AATATGGGCC AAACAGGATA TCTGTGGTAA GCAGTTCCTG CCCCAGCTCA
GGCCAAGAA CAGATGGTCC CCAGATGCGG TCCCGCCCTC AGCAGTTTCT AGAGAACCATCAGATGTTTC
CAGGGTGCCC CAAGGACCTG AAATGACCTA GTGCCATTAT TGAACCTAACCAATCAGTTCG CTTCTCGCTT
CTGTTGCGC GCTTCTGCTC CCCGAGCTA ATAAAAGAGCCCAACCCC TCACTCGGC CGCCAGTCTT
CCGATGACT CGTTCGCCG GGTACCCGTGTATCCAATAA ACCCTCTGC AGTTGCATCC GACTGTGGT
CTCGCTGTTT CTTGGGAGGGTCTCCTCTGA GTGATTGACT ACCCGTCAGC GGGGGTCTTT CATGGGTAAC
AGTTTCTTGAAAGTTGGAGAA CAACATTTCTG AGGGTAGGAG TCGAATATTA AGTAATCCTG ACTCAATTAG
CCACTGTTTT GAATCCACAT ACTCCAATAC TCCTGAAATA GTTCATTATG GACAGCGCAGAAGAGCTGGG
GAGAATTAAT TCGTAATCAT GGTACATAGCT GTTTCCTGTG TGAAATTGTTATCCGCTCAC AATTCCACAC
AACATACGAG CCGGAAGCAT AAAGTGTA AAAAGGCTGCTAATGAGT GAGCTAACTC ACATTAATTG
CGTTGCGCTC ACTGCCCGCT TTCCAGTCGGGAAACCTGTC GTGCCAGCTG CATTAAATGAA TCGGCCAACG
CGCGGGGAGA GCGGTTTGCATATTGGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT GCGCTCGGTC
GTTCCGCTGCGGCGAGCGGT ATCAGCTCAC TCAAAGGCG TAATACGGTT ATCCACAGAA TCAGGGGATA
ACGACGAAA GAACATGTGA GCAAAAAGCC AGCAAAAAGC CAGGAACCGT AAAAAGGCCGCTTGCTGGC
GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCTCAAGTCAGAG GTGGCGAAAC
CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCTGGAAGCTCCCTCGT GCGCTCTCCT GTTCCGACCC
TGCCGCTTAC CGGATACCTG TCCGCTTTTCCCTTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG
TAGGTATCTC AGTTCCGGTGTAGGTCGTTTCG CTCCAAGCTG GGCTGTGTGC ACGAACCCCC CGTTCAGCCC
GACCCTGCGCCTTATCCGG TAACTATCGT CTTGAGTCCA ACCCGGTAAG ACACGACTTA TCGCCACTGG
CAGCAGCCAC TGGTAACAGG ATTAGCAGAG CGAGGTATGT AGGCGGTGCT ACAGAGTTCCTGAAGTGGTG
GCCTAACTAC GGCTACACTA GAAGGACAGT ATTTGGTATC TCGCTCTGCTGAAGCCAGT TACCTTCGGA
AAAAGAGTTG GTAGCTCTTG ATCCGGCAA CAAACCACCGCTGGTAGCGG TGGTTTTTTT GTTTGCAAGC
AGCAGATTAC GCGCAGAAA AAAGATCTCAAGAAGATCC TTTGATCTTT TCTACGGGT CTGACGCTCA
GTGGAACGAA AACTCACGTTAAGGGATTTT GGTACATGAGA TTATCAAAAA GGATCTTCAC CTAGATCCTT
TTAAATTAATAAATGAAGTTT TAAATCAATC TAAAGTATAT ATGAGTAAAC TTGGTCTGAC AGTTACCAAT
GCTTAATCAG TGAGGCACCT ATCTCAGCGA TCTGTCTATT TCGTTTCATCC ATAGTTGCTGACTCCCCGT
CGTGAGATA ACTACGATC GGGAGGGCTT ACCATCTGGC CCCAGTGCTGCAATGATACC GCGAGACCCA
CGCTCACCGG CTCCAGATTT ATCAGCAATA AACCAGCCAGCCGGAAGGGC CGAGCGCAGA AGTGGTCTG
CAACTTTATC CGCTCCATC CAGTCTATTAATTGTTGCCG GGAAGCTAGA GTAAGTAGTT CGCCAGTTAA
TAGTTTGCAG AACGTTGTTGCCATTGCTAC AGGCATCGTG GTGTCACGCT CGTCGTTTGG TATGGCTTCA
TTCAGTCCGGTTCCCAACG ATCAAGGCGA GTTACATGAT CCCCATGTT GTGCAAAAA GCGTTAGCT
CCTTCGGTCC TCCGATCGTT GTCAGAAGTA AGTTGGCCGC AGTGTATCA CTCATGTTATGGCAGCACT
GCATAATCT CTTACTGTCA TGCCATCCGT AAGATGCTTT TCTGTGACTGGTGAGTACTC AACCAAGTCA
TTCTGAGAAT AGTGTATGCG GCGACCGAGT TGCTCTTGGCCGGCGTCAAT ACGGGATAAT ACCGCGCCAC
ATAGCAGAAC TTTAAAAGTG CTCATCATTTGGAAAACGTTT TTCGGGGCGA AAACCTCAA GGATCTTACC

GCTGTTGAGA TCCAGTTCGATGTAACCCAC TCGTGCACCC AACTGATCTT CAGCATCTTT TACTTTTACC
 AGCGTTTCTGGGTGAGCAAA AACAGGAAGG CAAAATGCCG CAAAAAAGGG AATAAGGGCG ACACGGAAAT
 GTTGAATACT CATACTTTC CTTTTTCAAT ATTATTGAAG CATTATCAG GGTATTGTCTCATGAGCGG
 ATACATATTT GAATGTATT AGAAAAATA ACAAAATAGGG GTTCCGCGCACATTTCCCC AAAAGTGCCA
 CCTGACGTTT AAGAAACCAT TATTATCATG ACATTAACTATAAAAAATAG GCGTATCACG AGGCCCTTTC
 GTCCTCGCGG TTTCCGGTGAT GACGGTGAAAACCTCTGACA CATGCAGCTC CCGGAGACGG TCACAGCTTG
 TCTGTAAGCG GATGCCGGGAGCAGACAAGC CCGTCAGGGC GCGTCAGCGG GTGTTGGCGG GTGTCCGGGC
 TGGCTTAACTATGCGGCATC AGAGCAGATT GACTGAGAG TGCACCATAT GCGGTGTGAA ATACCCGACA
 GATGCGTAAG GAGAAAATAC CGCATCAGGC GCCATTCCGC ATTACAGGCTG CGCAACTGTTGGGAAGGGCG
 ATCGGTGCGG GCCTCTTCGC TATTACGCCA GCTGGCGAAA GGGGGATGTGCTGCAAGGCG ATTAAGTTGG
 GTAACGCCAG GTTTTTCCA GTCACGACGT TGTAAAACGACGGCGCAAGG AATGGTGCAT GCAAGGAGAT
 GCGGCCAAC AGTCCCCCGG CCACGGGGCTGCCACCATA CCCACGCCGA AACAAGCGCT CATGAGCCCG
 AAGTGGCGAG CCCGATCTTCCCATCGGTG ATGTCGGCGA TATAGGCGC AGCAACCGCA CCTGTGGCGC
 CGGTGATGCCGGCCAGATG CGTCCGGCGT AGAGGCGATT AGTCCAATTT GTTAAAGACA GGATATCAGT
 GTCCAGGCT CTAGTTTTGA CTCAACAATA TCACCAGCTG AAGCCTATAG AGTACGAGCCATAGATAAAA
 TAAAAGATTT TATTTAGTCT CCAGAAAAAG GGGGGAA

Unique enzymes in pSCV-Linker:

Spe I	A`CTAG,T	662
Eag I	C`GGCC,G	726
Xma III	C`GGCC,G	726
BstE II	G`GTNAC,C	1089
BsrG I	T`GTAC,A	1284
EcoR I	G`AATT,C	1406
Nsi I	A,TGCA`T	1416
Bgl II	A`GATC,T	1418
Sac II	CC,GC`GG	1427
Pme I	CTTT AAAC	1433
Paer7 I	C`TCGA,G	1437
Xho I	C`TCGA,G	1437
HinD III	A`AGCT,T	1443
Pac I	TTA,AT`TAA	1453
Afl III	A`CRYG,T	2525
Sca I	AGT ACT	3898
Nde I	CA`TA,TG	4589
Sph I	G,CATG`C	4813

Number of enzymes = 18

Ava I	(6)	333	399	500	1437
Ava II	(12)	1833	1899		
Ban I	(12)	188	201	256	553
Ban II	(6)	692	1221	1688	1701
Bbe I	(5)	1756	3556	3778	5033
Bbv I	(7)	246	403	1144	1399
Bcn I	(14)	1746	1903	2269	3366
Bfa I	(11)	4640	4823	4937	4958
Bgl I	(2)	340	353	1840	1853
Bgl II	(1)	4890	4904		
Bpm I	(3)	1403	4644	4827	4941
Bsa I	(6)	4962			
BsaH I	(8)	933	941	2944	2947
BsaJ I	(29)	3153	3847	4458	
Bsm I	(20)	166	401	402	573
BsmB I	(7)	726	1666	1901	1902
BsmF I	(9)	2906	3602	3953	4454
BsoF I	(26)	4489	4840		
Bsp I	(4)	31	221	663	675
BspH I	(4)	1396	1531	1721	3020
Bar I	(14)	3273	3608	5043	
BsrB I	(4)	3538	4656		
BsrD I	(2)	1418			
BsrG I	(1)	1468	3488	5106	
BssH II	(4)	478	532	1151	1956
BssS I	(3)	1977	3479		
BstE II	(1)	744	1400	3955	4337
BstN I	(16)	4641	4824	4938	4959
BstU I	(20)	163	242	252	399
		463	499	548	549
		696	735	736	748
		749	1169	1238	1247
		1267	1268	1424	1663
		1742	1752	1899	1962
		2264	2685	4759	4837
		4843			
		2731	2878	3709	
		466	1295	1334	1965
		594	729	2441	2865
		3788	3937	4684	
		340	1840	2843	4004
		4089	4586		
		108	477	533	611
		736	834	951	1075
		1134	1152	1330	1485
		1608	1955	1976	3480
		4254	4407	4451	5123
		735	833	1074	1133
		1331	4408	4450	
		174	187	566	731
		766	1207	1674	1687
		4819			
		729	903	919	922
		927	930	1135	2350
		2431	2449	2452	2570
		2725	2868	2933	2936
		3142	3470	3809	3836
		3931	4160	4447	4556
		4660	4733		
		3245	4253	4358	4882
		376	1032	1060	1876
		2326	2932	2945	3059
		3465	3583	3626	3893
		4065	4771		
		1044	2217	2458	4259
		3479	3653		
		1284			
		319	370	1819	1870
		2698	4082	4389	
		1089			
		243	550	737	750
		1171	1196	1219	1239
		1269	1743	2265	2553
		2674	2687	4760	5037
		319	321	372	905

The following enzymes do not cut in pSCV-Linker:

Acc I	Age I	Apa I	Avr II	BamH I
Bbs I	Bbv II	Bcl I	Blp I	BsaA I
BsaB I	Bsg I	BsiC I	BsiW I	Bsm I
Bsp120 I	Bsp1286 I	BspM I	BspM II	Bst1107 I
BstB I	BstX I	Cla I	Dra III	Eco72 I
Esp I	Fse I	HinC II	Hind II	Hpa I
Mlu I	Mun I	Nco I	Not I	Nru I
PflM I	Pml I	Rsr II	Sal I	Sfi I
SnaB I	Spl I	Srf I	Stu I	Xca I

pSCV-Linker: sites sorted by name:

Aat II	(2)	747	4340
Acc65 I	(2)	403	1903
Aci I	(54)	199	205
		690	729
		1044	1135
		1319	1357
		1699	1705
		2318	2374
		2451	2458
		2598	2725
		2975	3110
		3572	3763
		3974	4051
		4306	4480
		4555	4593
		4689	4948
Afl II	(3)	35	1008
Afl III	(1)	2525	
Aha II	(8)	744	1400
		4641	4824
Ahd I	(4)	1022	1948
Alu I	(26)	30	34
		670	678
		1534	1838
		2285	2349
		2783	2829
		3707	3770
		4713	5069
Alw I	(11)	455	1053
		3173	3173
		3735	4050
AlwN I	(3)	159	1659
ApaL I	(3)	2839	4085
Apo I	(2)	874	1406
Asc I	(2)	370	1870
Ase I	(4)	2168	2296
Asp718	(2)	403	1903

BsaW I	(3)	2731	2878	3709	
BseR I	(4)	466	1295	1334	1965
BsiE I	(7)	594	729	2441	2865
BsiHKA I	(6)	340	1840	2843	4004
BsmA I	(20)	4089	4586		
		108	477	533	611
		736	834	951	1075
		1134	1152	1330	1485
		1608	1955	1976	3480
		4254	4407	4451	5123
BsmB I	(7)	735	833	1074	1133
BsmF I	(9)	1331	4408	4450	
		174	187	566	731
		766	1207	1674	1687
		4819			
BsoF I	(26)	729	903	919	922
		927	930	1135	2350
		2431	2449	2452	2570
		2725	2868	2933	2936
		3142	3470	3809	3836
		3931	4160	4447	4556
		4660	4733		
BspH I	(4)	3245	4253	4358	4882
Bar I	(14)	376	1032	1060	1876
		2326	2932	2945	3059
		3465	3583	3626	3893
		4065	4771		
BsrB I	(4)	1044	2217	2458	4259
BsrD I	(2)	3479	3653		
BsrG I	(1)	1284			
BssH II	(4)	319	370	1819	1870
BssS I	(3)	2698	4082	4389	
BstE II	(1)	1089			
BstN I	(16)	243	550	737	750
		1171	1196	1219	1239
		1269	1743	2265	2553
		2674	2687	4760	5037
BstU I	(20)	319	321	372	905

		907	1137	1426	1819			4641	4824	4938	4959
		1821	1872	2372	2374	HinP I	(35)	319	321	370	372
		2572	3153	3483	3976			648	905	924	1400
		4308	4408	4410	4513			1819	1821	1870	1872
BstY I	(7)	1418	3166	3177	3263			2147	2307	2372	2400
		3275	4043	4060				2433	2703	2770	2870
Bsu36 I	(2)	783	1020					3044	3153	3546	3639
Cac8 I	(29)	28	32	321	372			3976	4308	4408	4511
		584	588	633	652			4641	4662	4795	4824
		1201	1528	1532	1821			4878	4938	4959	
		1872	2318	2347	2456	Hpa II	(24)	165	400	571	632
		2542	2579	3139	3530			725	1403	1665	1900
		4543	4691	4711	4715			2243	2732	2879	2905
		4811	4852	4900	4942			3095	3499	3533	3600
		4972						3710	3952	4453	4487
Cfr10 I	(4)	631	3498	4961	4970			4839	4962	4971	4986
Csp6 I	(7)	404	660	1285	1904	Hph I	(12)	1159	1185	3262	3489
		3897	4573	5084				3903	4111	4144	4428
Dde I	(18)	75	169	210	478			4437	4930	4975	5056
		783	1020	1292	1575	Kas I	(5)	1399	4640	4823	4937
		1669	1710	1979	2050			4958			
		2800	3209	3375	3915	Kpn I	(2)	407	1907		
		4341	4576			Mae I	(11)	31	221	663	675
Dpn I	(22)	95	461	1048	1180			1396	1531	1721	3020
		1365	1420	1595	3093			3273	3608	5043	
		3168	3179	3187	3265	Mae II	(8)	744	1083	1124	3228
		3277	3382	3723	3741			3644	4017	4337	4779
		3787	4045	4062	4098	Mae III	(18)	39	996	1024	1089
		4683	4907					1233	1539	2017	2881
DpnII	(22)	93	459	1046	1178			2944	3060	3343	3674
		1363	1418	1593	3091			3732	3885	4073	4461
		3166	3177	3185	3263			4752	4772		
		3275	3380	3721	3739	Mbo I	(22)	93	459	1046	1178
		3785	4043	4060	4096			1363	1418	1593	3091
		4681	4905					3166	3177	3185	3263
Dra I	(4)	1433	3284	3303	3995			3275	3380	3721	3739
Drd I	(2)	2633	4502					3785	4043	4060	4096
Dsa I	(3)	696	1424	4843				4681	4905		
Eae I	(8)	584	726	1111	1132	Mbo II	(11)	1088	1301	2163	2397
		2364	3806	4840	4972			3186	3259	4014	4092
Eag I	(1)	726						4201	4689	4901	
Ear I	(6)	1072	1313	2147	2409	Mme I	(6)	831	1108	1964	2016
		4213	4701					2739	2923		
Eco47 III	(2)	925	4879			Mnl I	(42)	218	370	389	434
Eco57 I	(3)	3072	4086	5090				462	486	508	512
EcoN I	(2)	786	1394					568	778	874	1170
EcoO109 I	(5)	256	1221	1756	4394			1273	1306	1312	1315
		4848						1321	1351	1354	1369
EcoR I	(1)	1406						1376	1392	1718	1870
EcoR II	(16)	241	548	735	748			1889	1934	1961	1985
		1169	1194	1217	1237			2045	2374	2423	2633
		1267	1741	2263	2551			2706	2957	3357	3438
		2672	2685	4758	5035			3584	3790	4385	4443
EcoR V	(3)	141	1641	5026				4703	4987		
Ehe I	(5)	1401	4642	4825	4939	Msc I	(2)	586	1113		
		4960				Mse I	(25)	36	1009	1121	1151
Fnu4H I	(26)	729	903	919	922			1175	1432	1449	1453
		927	930	1135	2350			1536	2070	2168	2296
		2431	2449	2452	2570			2355	3231	3283	3288
		2725	2868	2933	2936			3302	3355	3590	3629
		3142	3470	3809	3836			3994	4366	4547	4744
		3931	4160	4447	4556			5014			
		4660	4733			Msl I	(2)	3670	3829		
Fok I	(9)	425	1142	1302	1924	Msp I	(24)	165	400	571	632
		3384	3565	3852	4495			725	1403	1665	1900
		4739						2243	2732	2879	2905
Fsp I	(2)	3640	4663					3095	3499	3533	3600
Gdi II	(7)	725	727	1131	2365			3710	3952	4453	4487
		3805	4841	4973				4839	4962	4971	4986
Gsu I	(3)	1469	3489	5107		MspAI I	(10)	590	1426	2001	2349
Hae I	(5)	586	1113	2540	2551			2867	3112	4053	4519
		3003						4713	5069		
Hae II	(9)	927	1403	2403	2773	Nae I	(2)	633	4972		
		4644	4827	4881	4941	Nar I	(5)	1400	4641	4824	4938
		4962						4959			
Hae III	(25)	130	175	586	728	Nci I	(14)	165	400	401	572
		764	776	989	1113			725	1665	1900	1901
		1134	1199	1630	1675			2905	3601	3952	4453
		2366	2540	2551	2569			4488	4839		
		3003	3461	3541	3808	Nde I	(1)	4589			
		4395	4693	4842	4850	Ngm I	(2)	631	4970		
		4974				Nhe I	(2)	30	1530		
Hga I	(9)	383	644	897	1883	Nla III	(17)	62	1207	1414	1562
		2635	3213	3945	4503			2016	2183	2529	3249
		4972						3740	3750	3828	3864
HgiA I	(6)	340	1840	2843	4004			4257	4362	4446	4813
		4089	4586					4886			
HgiE II	(2)	3104	4584			Nla IV	(29)	190	203	248	405
Hha I	(35)	321	323	372	374			523	554	694	763
		650	907	926	1402			895	1146	1223	1401
		1821	1823	1872	1874			1690	1703	1748	1905
		2149	2309	2374	2402			2271	2557	2596	3368
		2435	2705	2772	2872			3462	3503	3714	4304
		3046	3155	3548	3641			4642	4825	4849	4939
		3978	4310	4410	4513			4960			
		4643	4664	4797	4826	Nsi I	(1)	1416			
		4880	4940	4961		Nsp7524 I	(3)	2525	4442	4809	
HinD III	(1)	1443				NspB II	(10)	590	1426	2001	2349
Hinf I	(13)	444	452	793	804			2867	3112	4053	4519
		2060	2082	2103	2360			4713	5069		
		2425	2500	2896	3413	NspH I	(3)	2529	4446	4813	
		5051				Pac I	(1)	1453			
HinI I	(8)	744	1400	3955	4337	Paer7 I	(1)	1437			

Pal I	(25)	130	175	586	728	Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
		764	776	989	1113	Ava I	C`YCGR,G	6	Ava II	G`GWC,C	12
		1134	1199	1630	1675	Avr II	C`CTAG,G	-	BamH I	G`GATC,C	-
		2366	2540	2551	2569	Ban I	G`GYRC,C	12	Ban II	G,RCGY`C	6
		3003	3461	3541	3808	Bbe I	G,CGCG`C	5	Bbs I	GAAGAC 8/12	-
		4395	4693	4842	4850	Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
		4974				Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	14
Ple I	(3)	801	2068	2904		Bfa I	C`TA,G	11	Bgl I	GCCN,NNN`NGGC	2
Pme I	(1)	1433				Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
PpuM I	(3)	256	1221	1756		Bpm I	CTGGAG 22/20	3	Bsa I	GCTCTC 7/11	6
Psp1406 I	(2)	3644	4017			BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	-
PspA I	(2)	399	1899			BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	29
Pst I	(3)	923	931	1107		BsaW I	W`CCGG,W	3	BseR I	GAGGAG 16/14	4
Pvu I	(2)	3788	4684			Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	-
Pvu II	(3)	2349	4713	5069		BsiE I	CG,RY`CG	7	BsiHKA I	G,WGCW`C	6
Rsa I	(7)	405	661	1286	1905	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
		3898	4574	5085		BsmA I	GTCTC`/9	20	BsmB I	CGTCTC 7/11	7
Sac I	(2)	340	1840			BsmF I	GGGAC 15/19	9	BsoF I	GC`N,GC	26
Sac II	(1)	1427				Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
Sap I	(2)	2147	2409			BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
Sau3A I	(22)	93	459	1046	1178	BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	14
		1363	1418	1593	3091	BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
		3166	3177	3185	3263	BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	4
		3275	3380	3721	3739	BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	-
		3785	4043	4060	4096	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
		4681	4905			BstN I	CC`w,GG	16	BstU I	CG CG	20
Sau96 I	(25)	128	173	188	201	BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	7
		256	553	692	762	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	29
		775	987	1198	1221	Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
		1628	1673	1688	1701	Csp6 I	G`TA,C	7	Dde I	C`TNA,G	18
		1756	3460	3539	3556	Dpn I	GA TC	22	DpnII	`GATC,	22
		3778	4394	4691	4848	Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	-
		5033				Drd I	GACNN,NN`NNGTC	2	Dsa I	C`CRYG,G	3
Sca I	(1)	3898				Eae I	Y`GGCC,R	8	Eag I	C`GGCC,G	1
ScrF I	(30)	165	243	400	401	Ear I	CTCTTC 7/10	6	Eco47 III	AGC GCT	2
		550	572	725	737	Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
		750	1171	1196	1219	EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	5
		1239	1269	1665	1743	EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	16
		1900	1901	2265	2553	EcoR V	GAT ATC	3	Ehe I	GGC GCC	5
		2674	2687	2905	3601	Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	26
		3952	4453	4488	4760	Fok I	GGATG 14/18	9	Fse I	GG,CCGG`CC	-
		4839	5037			Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
Sec I	(29)	163	242	252	399	Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	5
		463	499	548	549	Hae II	R,CGCG`Y	9	Hae III	GG CC	25
		696	735	736	748	Hga I	GAGCG 9/14	9	HgiA I	G,WGCW`C	6
		749	1169	1238	1247	HgiE II	ACCNNNNNGGT -1/132	-	Hha I	G,CG`C	35
		1267	1268	1424	1663	Hinc II	GTY RAC	-	Hind II	GTY RAC	-
		1742	1752	1899	1962	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	13
		2264	2685	4759	4837	HinI I	GR`CG,YC	8	HinP I	G`CG,C,	35
		4843				Hpa I	GTT AAC	-	Hpa II	C`CG,G	24
SfaN I	(16)	187	446	643	940	Hph I	GGTGA 12/11	12	Kas I	G`GGCC,C	5
		1687	1945	2621	3673	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	11
		3866	4113	4474	4566	Mae II	A`CG,T	8	Mae III	`GTNAC,	18
		4604	4642	4958	4970	Mbo I	`GATC,	22	Mbo II	GAAGA 12/11	11
Sfc I	(9)	15	919	927	1103	Mlu I	A`CGCG,T	-	Mme I	TCCRAC 25/23	6
		1515	2790	2981	3659	Mnl I	CCTC 10/10	42	Msc I	TGG CCA	2
		5077				Mse I	T`TA,A	25	Msl I	CAYNN NNRTG	2
Sma I	(2)	401	1901			Msp I	C`CG,G	24	MspA1 I	CMG CKG	10
Spe I	(1)	662				Mun I	C`AATT,G	-	Nae I	GCC GGC	2
Sph I	(1)	4813				Nar I	GG`CG,CC	5	Nci I	CC`S,GG	14
Sep I	(2)	2068	4222			Nco I	C`CATG,G	-	Nde I	CA`TA,TT	1
Sty I	(5)	252	463	1247	1752	Ngom I	G`CCGG,C	2	Nhe I	G`CTAG,C	2
		1962				Nla III	,CATG`	17	Nla IV	GGN NCC	29
Taq I	(8)	796	1040	1351	1362	Not I	GC`GGCC,GC	-	Nru I	TCG CGA	-
		1438	2063	2625	4069	Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	3
Tfi I	(5)	444	804	2103	2360	NspB II	CMG CKG	10	NspH I	R,CATG`Y	3
		2500				Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	1
Tsp45 I	(6)	1024	1233	3674	3885	Pal I	GG CC	25	Pflm I	CCAN,NNN`NTGG	-
		4461	4772			Ple I	GAGTC 9/10	3	Pme I	CTTT AAC	1
Tth111 I	(4)	392	813	1219	1892	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Tth111 II	(8)	147	424	615	634	Psp1406 I	AA`CG,TT	2	PspA I	C`COGG,G	2
		1647	3114	3123	3153	Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	7
Vsp I	(4)	2168	2296	2355	3590	Pvu II	CAG CTG	3	Rsa I	GT AC	2
Xba I	(2)	220	1720			Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Xho I	(1)	1437				Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	-
Xho II	(7)	1418	3166	3177	3263	Sap I	GCCTCTC 8/11	2	Sau3A I	`GATC,	22
		3275	4043	4060		Sau96 I	G`GNC,C	25	Sca I	AGT ACT	1
Xma I	(2)	399	1899			ScrF I	CC`N,GG	30	Sec I	C`CNNG,G	29
Xma III	(1)	726				SfaN I	GCATC 9/13	16	Sfc I	C`TRYA,G	9
Xmn I	(3)	2131	2169	4017		Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
						SnaB I	TAC GTA	-	Spe I	A`CTAG,T	1
						Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
						Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
						Stu I	AGG CCT	-	Sty I	C`CWGG,G	5
						Taq I	T`CG,A	8	Tfi I	G`AWT,C	5
						Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	4
						Tth111 II	CAARCA 16/14	8	Vsp I	AT`TA,AT	4
						Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
						Xcm I	CCANNNN,N`NNNNTGG-	2	Xho I	C`TCGA,G	1
						Xho II	R`GATC,Y	7	Xma I	C`COGG,G	2
						Xma III	C`GGCC,G	1	Xmn I	GAANN NNTTC	3

Site usage in pSCV-Linker:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	-
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	54
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	1
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	26
Alw I	GGATC 8/9	11	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	-	ApAL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2