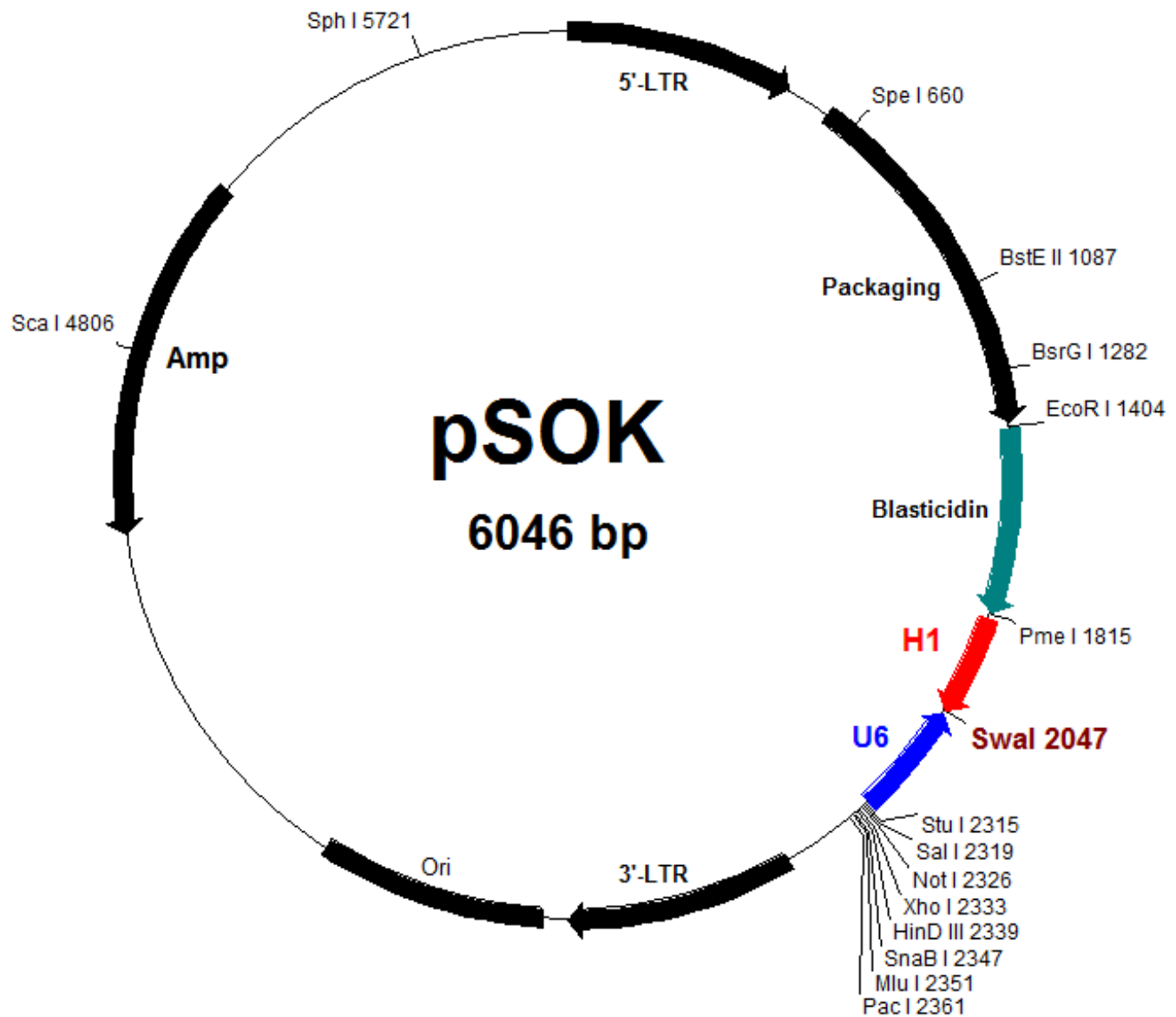


Vector: pSOK (simplified one-step siRNA knockdown destination vector)

Antibiotic Selection: Amp

Creator(S): Fang Deng, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: June, 2013



pSOK Full-Length Sequence

TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGAAGGCATGGAAAATACATAAAGTGAAGTGAAGTGA
 GATCAAGGTTAGGAACAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCCCTCCCGGCTCAGGGCCAAGAACAG
 ATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTTCCAGGGTGCSSCAAGGACCTGAAATGACCCTGTGC
 CTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCGCTTCTGCTCCCCGAGCTCAATAAAAAGAGCCCAACCCCTCACT
 CGGCGCGCCAGTCTCCGATAGACTGCGTCGCCCCGGTACCCTGATTCCCAATAAAGCCTCTTGCTGTTTTGCATCCGAATCGTGGACTCGC
 TGATCCTTGGGAGGGTCTCCTCAGATTGATTGACTGCCACCTCGGGGGTCTTTCATTTGGAGGTTCCACCAGAGATTTGGAGACCCTGCC
 CAGGGACCACCACCCCCCGCCGGGAGGTAAGCTGGCCAGCGGTCTGTTTCGTGTCTGTCTCTGTCTTTGTGCGTGTGTTGTGCCGGCATCT
 AATGTTTTGCGCTGCGTCTGTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGAAGTGCAGAGTTCTGAACACCCGGCCG
 CAACCCTGGGAGACGTCCCAGGGACTTTGGGGCCGTTTTTGTGGCCGACCTGAGGAAGGGAGTTCGATGTGGAATCCGACCCCGTCAAGGA
 TATGTGGTCTGGTAGGAGACGAGAACCATAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGAACCGAAGCCGCGCGTCTT
 GTCTGCTGCAGCGTGCAGCATCGTTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAATTAGGGCCAGACTGTTACCAC
 TCCCTTAAGTTTGACCTTAGGTCACTGGAAAGATGTCGAGCGGATCGCTCACAACCAGTTCGGTAGATGTCAAGAAGAGACGTTGGGTTACC
 TTCTGCTCTGCAGAATGGCCAACCTTTAACGTCGGATGGCCGCGAGACGGCACCTTTAACCGAGACCTCATCACCCAGGTTAAGATCAAGG
 TCTTTTACCTGGCCCGCATGGACACCCAGACCAGGTCCCTTACATCGTGACCTGGGAAGCCTTGCTTTTACCCCTCCCTGGGTCAA
 GCCCTTTGTACACCCTAAGCCTCCGCTCCTCTTCTCCATCCGCCCGTCTCTCCCTTGAACCTCCTCGTTCGACCCCGCCTCGATCC
 TCCCTTTATCCAGCCCTCACTCCTTCTTAGGCGCCGGAATTCACCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGA
 GCAACGGCTACAATCAACAGCATCCCATCTCTGAAGACTACAGCGTCGCCAGCGCAGCTCTCTTAGCGACGGCCGCATCTTCACTGGTG
 TCAATGTATATCATTACTGGGGACCTTGTGCAGAACTCGTGGTGTGGGCACTGCTGTGCTGCGGCAGCTGGCAACCTGACTTGTAT
 CGTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGCCCTGCGGACGGTCCGACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCC
 ATAGTGAAGGACAGTGCATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTaagtttaaacag
 cttaattcgaacgctgacgtcatcaaccgctccaaggaatcgcgggccagtgctactagcggggaacaccagcgcgctgcgccctgg
caggaagatggctgtgagggacaggggagtgccgctgcaatattgcatgtcgctatgtgtctgggaaatcaccataaacgtgaaatg
tctttggatttgggaatcttataagttctgtatgagaccaATTTAAATtcctttccacaagatatataaagccaagaaatcgaaatacttt
caagttacgtaagcatatgatagtcattttaaaacataattttaaaactgcaaaactaccaagaaattattactttctacgtcacgta
ttgtactaatatctttgtgtttacagtcaaatatttctaattatctcttaacagccttgatcgtatatgcaaatatgaaggaatcat
gggaaatagggcctcttctgcccagccttggatctaggcctgtgcagcgggccgctcgagaagctttacgtaacgcgtttaaattaaCGA
 TAAAATAAAGATTTTTATTTAGTCTCCAGAAAAGGGGGGAATGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATT
 TTGCAAGGCATGGAAAATACATAAAGTGAAGTTCAGATCAAGGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGAT
 ATCTGTGGTAAGCAGTTCCCTGCCCGGCTCAGGGCCAAGAACAGATGGTCCCGAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCAT
 CAGATGTTTTCCAGGGTGCSSCAAGGACCTGAAATGACCCTGTGCCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTTCGCGCG
 CTTCTGCTCCCCGAGCTCAATAAAAAGAGCCCAACCCCTCACTCGGCGCGCCAGTCTCCGATAGACTGCGTCGCCCCGGTACCCTGTGA
 TCCAATAAACCCCTTTCAGTTGTCATCCGACTTGTGGTCTCGCTGTTCCCTGGGAGGGTCTCCTCTGAGTGATTGACTACCCGTCAAGCCG
 GGCTTTTCATGGGTAACAGTTTCTTGAAGTTGGAGAACAACATTCTGAGGGTAGGAGTCAATATTAAGTAATCCTGACTCAATTAGCCAC
 TGTTTTGAATCCACATACTCCAATACTCCTGAAATAGTTCAATTATGGACAGCGCAGAAGAGCTGGGGAGAATTAATTCGTAATCATGGTCA
 TAGCTGTTTTCTGTGTGAAATTTGTTATCCGCTCACAATCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAAT
 GAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCATTAATGAATCGGCCA
 ACGCGCGGGGAGAGGCGGTTTTGCGTATTGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTCGGTTCGGTTCGGGCGAGCG
 GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG
 CCAGGAACCGTAAAAAGGCCGCTTGTGCGGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACGCTCAAGTCAGAG
 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCCTGCCGCTTACC
 GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCCGGTGTAGGTTCGTTCCGCT
 CCAAGCTGGGCTGTGTGCAGAACCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACA
 CGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT
 AACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAGAGTTGGTAGCTCTTGATCCG
 GCAAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGAT
 CTTTTTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTCAACCTAGATC
 CTTTTAAATTAATAAGTATTAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCAC
 CTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGTTGCCTGACTCCCCGCTGCTGTAGATAAATACGATACGGGAGGGCTTACCATCTGG
 CCCAGTGTGCAATGATACCGCGAGACCCACGCTCACCAGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGA
 AGTGGTCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCCGCCAGTTAATAGTTTGGCGCA
 ACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCTTGGTATGGCTTCAATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
 TACATGATCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTATCACTC
 ATGGTTATGGCAGCACTGCATAATTTCTTACTGTATGCCATCCGTAAGATGCTTTTTCTGTGACTGGTGGTACTCAACCAAGTCATTCT
 GAGAATAGTGTATGCGGCGACCGAGTTGCTCTTCCCGGCTCAATACGGGATAATACCGGCCACATAGCAGAACCTTTAAAAGTGTCTCAT
 CATTGAAAACGTTCTTCCGGGCGAAAACCTCAAGGATCTTACCCTGTTGAGATCCAGTTTCGATGTAACCCACTCGTGCACCCAACTGA
 TCTTACGATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGAAAAAAGGGAATAAGGGCGACACGGA
 AATGTTGAATACTCATACTCTTCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTAT

TTAGAAAAATAAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC
TATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGA AACCTCTGACACATGCAGCTCCCGGAGACGG
TCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCTGGCTTAACATA
TGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCCGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGC
CATTCGCCATTAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTG
CAAGGCGATTAAAGTTGGGTAACGCCAGGGTTTCCCAGTACGACGTTGTAAAACGACGGCGCAAGGAATGGTGCATGCAAGGAGATGGCG
CCCAACAGTCCCCCGGCCACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGCCCAGTGGCGAGCCCGATCTTCCCCAT
CGGTGATGTCGGCGATATAGCGCCAGCAACCGCACCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGCGATTAGTCCA
ATTTGTTAAAGACAGGATATCAGTGGTCCAGGCTCTAGTTTGACTCAACAATATCACCAGCTGAAGCCTATAGAGTACGACCCATAGATA
AAATAAAAGATTTTATTTAGTCTCCAGAAAAGGGGGGAA

Unique enzymes in pSOK:

Spe I	A`CTAG,T	660
BstE II	G`GTNAC,C	1087
BsrG I	T`GTAC,A	1282
EcoR I	G`AATT,C	1404
Nco I	C`CATG,G	1411
Bbv II	GAAGAC 7/11	1497
Bbs I	GAAGAC 8/12	1498
Bsg I	GTGCAG 22/20	1600
Nru I	TCG CGA	1644
BsaB I	GATNN NNATC	1711
Pme I	CTTT AAAC	1815
BsiC I	TT`CG,AA	1828
BstB I	TT`CG,AA	1828
Bsp120 I	G`GGCC,C	1866
Apa I	G,GGCC`C	1870
SwaI	ATTT AAAT	2047
Stu I	AGG CCT	2315
Sal I	G`TCGA,C	2319
Acc I	GT`MK,AC	2320
HinC II	GTY RAC	2321
Hind II	GTY RAC	2321
Not I	GC`GGCC,GC	2326
PaeR7 I	C`TCGA,G	2333
Xho I	C`TCGA,G	2333
HinD III	A`AGCT,T	2339
SnaB I	TAC GTA	2347
Mlu I	A`CGCG,T	2351
PacI	TTA ATTAA	2359
Sca I	AGT ACT	4806
Sph I	G,CATG`C	5721

Number of enzymes = 30

Apo I	(3)	872	1404	2048
Asc I	(2)	368	2778	
Ase I	(5)	2218	3076	3204 3263
		4498		
Asp718	(2)	401	2811	
Ava I	(6)	331	397	498 2333
		2741	2807	
Ava II	(13)	186	199	254 551
		690	1219	1572 2596
		2609	2664	4464 4686
		5941		
Ban I	(14)	244	401	1142 1397
		1687	1943	2654 2811
		3177	4274	5548 5731
		5845	5866	
Ban II	(8)	338	351	1677 1870
		2748	2761	5798 5812
Bbe I	(6)	1401	1947	5552 5735
		5849	5870	
Bbs I	(1)	1498		
Bbv I	(9)	931	939	1524 1629
		3852	3855	4061 4755
		5366		
Bbv II	(1)	1497		
Bcn I	(14)	164	399	400 571
		724	2574	2809 2810
		3814	4510	4861 5362
		5397	5748	
Bfa I	(14)	31	219	661 673
		1394	1522	1879 2311
		2439	2629	3928 4181
		4516	5951	
Bgl I	(2)	4446	5564	
Bpm I	(3)	2376	4396	6014
Bsa I	(7)	476	530	1149 2031
		2864	2885	4387
BsaA I	(2)	2181	2347	
BsaB I	(1)	1711		
BsaH I	(10)	742	1398	1838 1944
		4863	5245	5549 5732
		5846	5867	
BsaJ I	(33)	161	240	250 397
		461	497	546 547
		694	733	734 746
		747	1167	1236 1245
		1265	1266	1411 1716
		1854	1907	2303 2571
		2650	2660	2807 2870
		3172	3593	5667 5745
		5751		
BsaW I	(3)	3639	3786	4617
BseR I	(4)	464	1293	1332 2873
Bsg I	(1)	1600		
BsiC I	(1)	1828		
BsiE I	(10)	592	727	1532 1648
		2329	3349	3773 4696
		4845	5592	
BsiHKA I	(6)	338	2748	3751 4912
		4997	5494	
BsmA I	(22)	107	475	531 609
		734	832	949 1073
		1132	1150	1328 1431
		2032	2393	2516 2863
		2884	4388	5162 5315
		5359	6031	
BsmB I	(7)	733	831	1072 1131
		1329	5316	5358
BsmF I	(11)	172	185	564 729
		764	1205	1585 1944
		2582	2595	5727
BsoF I	(36)	727	901	917 920
		925	928	1133 1513
		1532	1606	1609 1612
		1615	1618	1782 2326
		2329	3258	3339 3357
		3360	3478	3633 3776
		3841	3844	4050 4378
		4717	4744	4839 5068
		5355	5464	5568 5641
Bsp120 I	(1)	1866		
BspH I	(4)	4153	5161	5266 5790
Bsr I	(17)	374	1030	1058 1546
		1570	1871	2784 3234
		3840	3853	3967 4373
		4491	4534	4801 4973

The following enzymes do not cut in pSOK:

Age I	Avr II	BamH I	Bcl I	Bgl II
Blp I	BsiW I	Bsm I	Bsp1286 I	BspM I
BspM II	Bst1107 I	BstX I	Cla I	Dra III
Eco72 I	Esp I	Fse I	Hpa I	Mun I
Nsi I	PfI M I	Pml I	Rsr II	Sac II
Sfi I	Spl I	Srf I	Xca I	Xcm I

pSOK: sites sorted by name:

Aat II	(3)	745	1841	5248
Acc I	(1)	2320		
Acc65 I	(2)	401	2811	
Aci I	(60)	197	203	566 588
		688	727	860 901
		1042	1133	1199 1298
		1317	1355	1532 1614
		1681	1849	1864 1883
		2325	2329	2607 2613
		2909	3123	3226 3282
		3292	3316	3359 3366
		3387	3478	3506 3633
		3652	3773	3883 4018
		4027	4389	4480 4671
		4717	4838	4882 4959
		5068	5167	5214 5388
		5427	5437	5463 5501
		5514	5540	5597 5856
Afl II	(3)	35	1006	2443
Afl III	(2)	2351	3433	
Aha II	(10)	742	1398	1838 1944
		4863	5245	5549 5732
		5846	5867	
Ahd I	(4)	1020	2856	2902 4326
Alu I	(29)	30	34	336 580
		668	676	1515 1620
		1821	2341	2438 2442
		2746	3065	3098 3193
		3257	3375	3601 3691
		3737	3994	4515 4615
		4678	5357	5376 5621
		5977		
Alw I	(13)	453	1051	1357 1727
		2314	3995	4081 4081
		4178	4179	4643 4958
		4964		
AlwN I	(2)	2567	3849	
Apa I	(1)	1870		
ApaL I	(3)	3747	4993	5490

		3204	3263	4139	4191
		4196	4210	4263	4498
		4537	4902	5274	5455
		5652	5922		
Msl I	(3)	1993	4578	4737	
Msp I	(24)	163	398	569	630
		723	1401	2573	2808
		3151	3640	3787	3813
		4003	4407	4441	4508
		4618	4860	5361	5395
		5747	5870	5879	5894
MspA1 I	(10)	588	1620	2909	3257
		3775	4020	4961	5427
		5621	5977		
Nae I	(2)	631	5880		
Nar I	(6)	1398	1944	5549	5732
		5846	5867		
Nci I	(14)	163	398	399	570
		723	2573	2808	2809
		3813	4509	4860	5361
		5396	5747		
Nco I	(1)	1411			
Nde I	(2)	2110	5497		
NgoM I	(2)	629	5878		
Nhe I	(2)	30	2438		
Nla III	(19)	62	1205	1415	1964
		2277	2470	2924	3091
		3437	4157	4648	4658
		4736	4772	5165	5270
		5354	5721	5794	
Nla IV	(33)	188	201	246	403
		521	552	692	761
		893	1144	1221	1399
		1573	1689	1868	1945
		2598	2611	2656	2813
		3179	3465	3504	4276
		4370	4411	4622	5212
		5550	5733	5757	5847
		5868			
Not I	(1)	2326			
Nru I	(1)	1644			
Nsp7524 I	(4)	1960	3433	5350	5717
NspB II	(10)	588	1620	2909	3257
		3775	4020	4961	5427
		5621	5977		
NspH I	(4)	1964	3437	5354	5721
PacI	(1)	2359			
PaeR7 I	(1)	2333			
Pal I	(31)	129	173	584	726
		762	774	987	1111
		1132	1197	1416	1531
		1868	2286	2315	2328
		2538	2583	3274	3448
		3459	3477	3911	4369
		4449	4716	5303	5601
		5750	5758	5882	5993
Ple I	(3)	799	2976	3812	
Pme I	(1)	1815			
PpuM I	(4)	254	1219	1572	2664
Psp1406 I	(2)	4552	4925		
PspA I	(2)	397	2807		
Pst I	(3)	921	929	1105	
Pvu I	(3)	1648	4696	5592	
Pvu II	(4)	1620	3257	5621	5977
Rsa I	(8)	403	659	1284	2190
		2813	4806	5482	5993
Sac I	(2)	338	2748		
Sal I	(1)	2319			
Sap I	(2)	3055	3317		
Sau3A I	(25)	92	457	1044	1176
		1361	1645	1706	1720
		2307	2501	3999	4074
		4085	4093	4171	4183
		4288	4629	4647	4693
		4951	4968	5004	5589
		5813			
Sau96 I	(29)	127	171	186	199
		254	551	690	760
		773	985	1196	1219
		1572	1866	1867	2285
		2536	2581	2596	2609
		2664	4368	4447	4464
		4686	5302	5599	5756
		5941			
Sca I	(1)	4806			
ScrF I	(32)	163	241	398	399
		548	570	723	735
		748	1169	1194	1217
		1237	1267	1717	1909
		2573	2651	2808	2809
		3173	3461	3582	3595
		3813	4509	4860	5361
		5396	5668	5747	5945
Sec I	(33)	161	240	250	397
		461	497	546	547
		694	733	734	746
		747	1167	1236	1245
		1265	1266	1411	1716
		1854	1907	2303	2571
		2650	2660	2807	2870
		3172	3593	5667	5745
		5751			
SfaN I	(20)	185	444	641	938

		1485	1542	1674	1720
		2595	2853	3529	4581
		4774	5021	5382	5474
		5512	5550	5866	5878
Sfc I	(10)	15	917	925	1101
		1496	2423	3698	3889
		4567	5985		
Sma I	(2)	399			
SnaB I	(1)	2347			
Spe I	(1)	660			
Sph I	(1)	5721			
Ssp I	(3)	1955	2976	5130	
Stu I	(1)	2315			
Sty I	(8)	250	461	1245	1411
		1854	2303	2660	2870
SwaI	(1)	2047			
Taq I	(12)	794	1038	1349	1360
		1705	1828	2083	2320
		2334	2971	3533	4977
Tfi I	(10)	442	802	1437	1769
		1859	2017	2270	3011
		3268	3408		
Tsp45 I	(8)	1022	1231	1874	2176
		4582	4793	5369	5680
Tth111 I	(4)	390	811	1217	2800
Tth111 II	(8)	146	422	613	632
		2555	4022	4031	4061
Vsp I	(5)	2218	3076	3204	3263
		4498			
Xba I	(2)	218	2628		
Xho I	(1)	2333			
Xho II	(7)	2307	4074	4085	4171
		4183	4951	4968	
Xma I	(2)	397	2807		
Xma III	(3)	724	1529	2326	
Xmn I	(3)	3039	3077	4925	

Site usage in pSOK:

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	60
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	10
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	29
Alw I	GGATC 8/9	13	AlwN I	CAG,NNN`CTG	2
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	5	Asp718	G`GTAC,C	2
Ava I	C`YCGR,G	6	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	-
Ban I	G`GYRC,C	14	Ban II	G,RCYC`C	8
Bbe I	G,CGCC`C	6	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	9	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	14
Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	2	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	10	BsaJ I	C`CNNG,G	33
BsaW I	W`CCGG,W	3	Bse I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	36
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	-
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	17
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	5
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	18	BstU I	CG CG	25
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	7
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	34
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
Csp6 I	G`TA,C	8	Dde I	C`TNA,G	19
Dpn I	GA TC	25	DpnII	`GATC,	25
Dra I	TTT AAA	7	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
Ear I	CTCTC 7/10	7	Eco47 III	AGC GCT	2
Eco57 I	CTGAAG 21/19	4	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	7
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	18
EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	36
Fok I	GGATG 14/18	11	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	11
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	7
Hae II	R,CGCC`Y	10	Hae III	GG CC	31
Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	6
HgiE II	ACNNNNNNGGT	-1/132	Hha I	G,CG`C	40
Hinc II	GTY RAC	1	Hind II	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	18
HinI I	GR`CG,YC	10	HinP I	G`CG,C	40
Hpa I	GTT AAC	-	Hpa II	C`CG,G	24
Hph I	GGTGA 12/11	14	Kas I	G`CGCG,C	6
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	14
Mae II	A`CG,T	13	Mae III	`GTNAC,	22
Mbo I	`GATC,	25	Mbo II	GAAGA 12/11	16
Mlu I	A`CCGG,T	1	Mme I	TCCRC 25/23	6

pSOK Vector

Mnl I	CCTC 10/10	49	Msc I	TGG CCA	3	Rsr II	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Mse I	T`TA,A	30	Msl I	CAYNN NNRTG	3	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Msp I	C`CG,G	24	MspA1 I	CMG CKG	10	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	25
Mun I	C`AATT,G	-	Nae I	GCC GGC	2	Sau96 I	G`GNC,C	29	Sca I	AGT ACT	1
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	14	ScrF I	CC`N,GG	32	Sec I	C`CNNG,G	33
Nco I	C`CATG,G	1	Nde I	CA`TA,TG	2	SfaN I	GCATC 9/13	20	Sfc I	C`TRYA,G	10
Ngom I	G`CCGG,C	2	Nhe I	G`CTAG,C	2	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
Nla III	,CATG`	19	Nla IV	GGN NCC	33	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1	Sph I	G,CATG`C	1	Spl I	C`GTAC,G	-
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	4	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	3
NspB II	CMG CKG	10	NspH I	R,CATG`Y	4	Stu I	AGG CCT	1	Sty I	C`CWWG,G	8
PacI	TTA ATTAA	1	Paer7 I	C`TCGA,G	1	SwaI	ATTT AAAT	1	Taq I	T`CG,A	12
Pal I	GG CC	31	PflM I	CCAN,NNN`NTGG	-	Tfi I	G`AWT,C	10	Tsp45 I	`GTSAC,	8
Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1	Tth111 I	GACN`N,NGTC	4	Tth111 II	CAARCA 16/14	8
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4	Vsp I	AT`TA,AT	5	Xba I	T`CTAG,A	2
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2	Xca I	GTA TAC	-	Xcm I	CCANNNN,N`NNNTGG-	-
Pst I	C,TGCA`G	3	Pvu I	CG,AT`CG	3	Xho I	C`TCGA,G	1	Xho II	R`GATC,Y	7
Pvu II	CAG CTG	4	Rsa I	GT AC	8	Xma I	C`CCGG,G	2	Xma III	C`GGCC,G	-