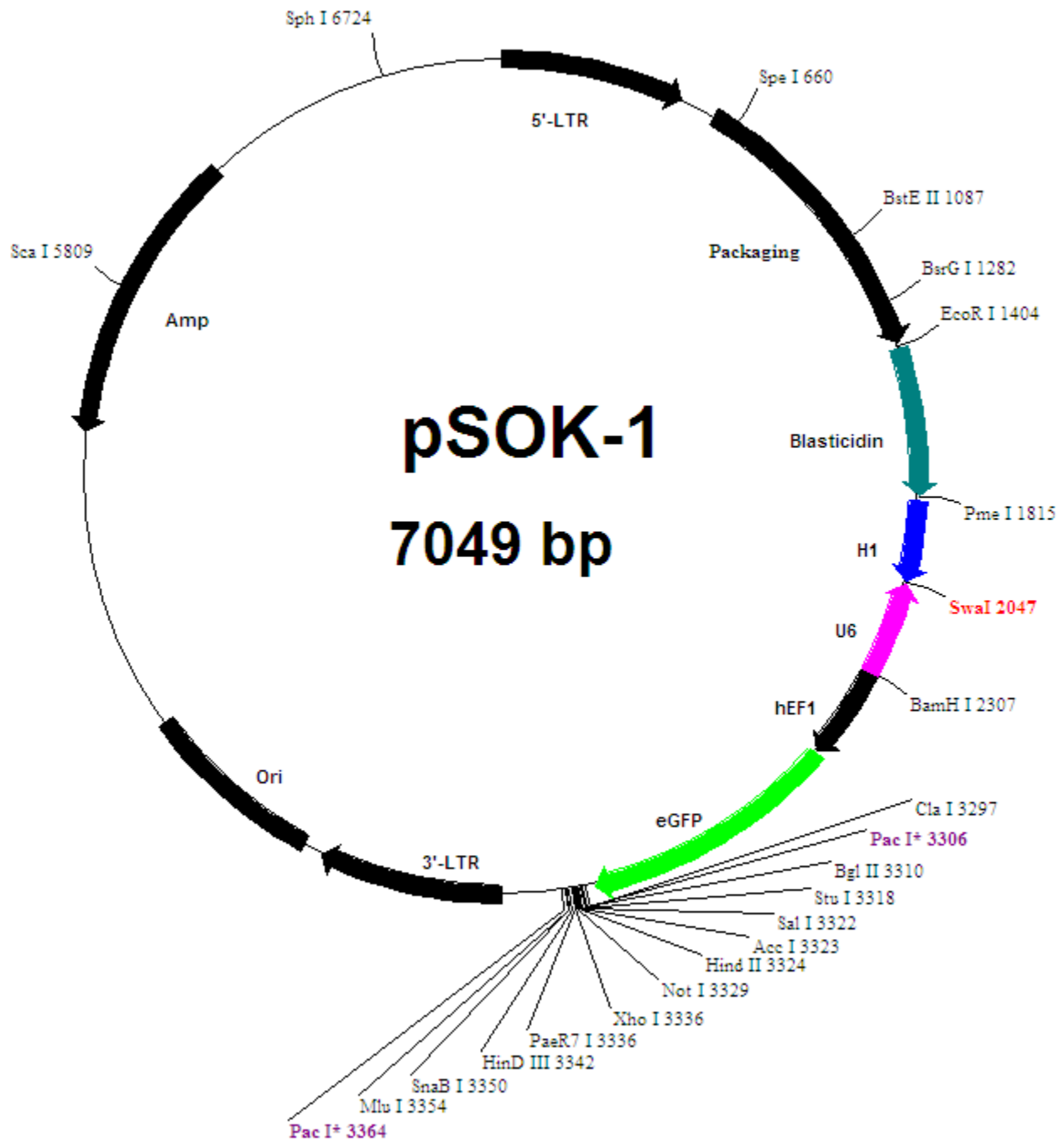


**Vector:** pSOK-1 (with eGFP cassette)

**Antibiotic Selection:** Amp

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

**Date of Construction:** June, 2013



## pSOK1 Full-Length Sequence

TGAAAGACCCACCTGTAGGTTTGGCAAGCTAGCTTAAGTAACGCCATTTTGC AAGGCATGGAAAAACATAAATGAGAATA  
 GAGAAGTTAGATCAAGGTTAGGAACAGAGAGACAGCAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCC TCCCCG  
 GCTCAGGGCCAAGAACAGATGGTCCCCAGATGCGGTCCCGCCCTCAGCAGTTTCTAGAGAACCATCAGATGTTTCCAGGGTG  
 CCCC AAGGACCTGAAATGACCCGTGCTTATTTGAACTAACCAATCAGTTTCGCTTCTCGCTTCTGTTCGCGCGCTTCTGCT  
 CCCC GAGCTCAATAAAAAGAGCCCAACCCCTCCTCGGCGGCCAGTCC TCCGATAGACTGCGTGC CCGGGTACCCGTAT  
 TCCCAATAAAGCCTCTTGTGCTTTGCATCCGAATCGTGGACTCGCTGATCCTTGGGAGGGTCTCCTCAGATTGATTGACTGC  
 CCACCTCGGGGGTCTTTTCAATTTGGAGGTTCCACCGAGATTTGGAGACCCCTGCC CAGGGACCACCGACCCCCCGCCGGGAG  
 GTAAGCTGGCCAGCGGTGCTTTCGTGTCTGTCTCTGCTTTTGTGCGTGT TTTGTGCCGGCATCTAATGTTTGCCTGCGTCT  
 GTACTAGTTAGCTAACTAGCTCTGTATCTGGCGGACCCGTGGTGGAACTGACGAGTTCTGAACACCCGGCCGCAACCC TGGG  
 AGACGTCC CAGGGACTTTGGGGGCCGTTTTTGTGGCCCGACCTGAGGAAGGGAGTCGATGTGGAATCCGACCCCGTCAGGAT  
 ATGTGGTTCTGGTAGGAGACGAGAACC TAAAACAGTTCCCGCCTCCGTCTGAATTTTTGCTTTTCGGTTTGGAAACCGAAGCCG  
 CGCGTCTTGTCTGCTGCAGCGCTGCAGCATCGTTCTGTGTTGTCTCTGTCTGACTGTGTTTCTGTATTTGTCTGAAAAT TAG  
 GGCCAGACTGTTACCAC TCCCTTAAGTTTGACCTTAGGTCAC TGGAAAGATGTCGAGCGGATCGCTCACAACCAGTCGGTAG  
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 TAACCGAGACCTCATCACC CAGGTTAAGATCAAGGCTTTTTACCTGGCCCGCATGGACACCCAGACCAGGTC CCCC TACATC  
 GTGACCTGGGAAGCCTTGGCTTTTGACCCCCCTCCCTGGGTCAAGCCCTTTGTACACCC TAAAGCCTCCGCTCCTCTTCTC  
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 GGCTaag **tttaaac** agctt **aattcgaacgctgacgtcatcaaccgctccaaggaatcgcgggccagtggtcaacta**  
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**tttgcattgctgtatgtgtttctgggaaatcaccataaacgtgaaatgtctttggatttgggaaatcttataagttc**  
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**agcatatgatagtcatttttaaaacataattttaaaactgcaactaccaagaatattactttctacgtcac**  
**gtattttgtactaataatctttgtgtttacagtc aaattaattctaattatctcttaacagccttgatogtata**  
**tgcaataatgaaggaatcatgggaaatagggccctcttctgcccgaacct** **ggatctgcatCGCTCCGGTG**  
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**AGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTG** **CTAGCGCTACCGGTCCGCCACC**  
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 GCAGTTCC T G C C C C G G T C A G G G C C A A G A A C A G A T G G T C C C C A G A T G C G G T C C C G C C T C A G C A G T T T C T A G A G A A C C A T C A  
 G A T G T T T C C A G G G T G C C C A A G G A C C T G A A A T G A C C C T G T G C C T T A T T T G A A C T A A C C A A T C A G T T C G C T T C T G C T T C T G T  
 T C G C G C G C T T C T G C T C C C C G A G C T C A A T A A A A G A G C C C A C A A C C C C T C A C T C G G C G C G C C A G T C C T C C G A T A G A C T G C G T C G  
 C C C G G T A C C C G T G A T C C A A T A A A C C C T C T T G C A G T T G C A T C C G A C T T G T G G T C T C G C T G T T C C T T G G G A G G G T C C C T C T  
 G A G T G A T T G A C T A C C C G T C A G C G G G G T C T T T C A T G G G T A A C A G T T T C T T G A A G T T G G A G A A C A A C A T T C T G A G G G T A G G A G  
 T C G A A T A T T A A G T A A T C C T G A C T C A A T T A G C C A C T G T T T T G A A T C C A C A T A C T C C A A T A C T C C T G A A A T A G T T C A T T A T G G A  
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 C C A C A C A C A T A C G A G C C G G A A G C A T A A A G T G T A A A G C C T G G G G T G C C T A A T G A G T G A G C T A A C T C A C A T T A A T T G C G T T G C  
 G C T C A C T G C C C G C T T T C C A G T C G G G A A C C T G T C G T G C C A G C T G C A T T A A T G A A T C G G C C A A C G C G C G G G A G A G C G G T T T  
 G C G T A T T G G G C G C T C T T C C G T T C C T C G T C A C T G A C T C G C T G C G C T C G G T C G T T C G G C T G C G G C G A G C G G T A T C A G C T C A C  
 T C A A A G G C G G T A A T A C G G T T A T C C A C A G A A T C A G G G G A T A A C G C A G G A A G A A C A T G T G A G C A A A A G G C C A G C A A A A G G C C A  
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		5002	5077	5088	5096
		5174	5186	5291	5632
		5650	5696	5954	5971
		6007	6592	6816	
Sau96 I	(32)	127	171	186	199
		254	551	690	760
		773	985	1196	1219
		1572	1866	1867	2285
		2752	3153	3236	3539
		3584	3599	3612	3667
		5371	5450	5467	5689
		6305	6602	6759	6944
Sca I	(1)	5809			
ScrF I	(39)	163	241	398	399
		548	570	723	735
		748	1169	1194	1217
		1237	1267	1717	1909
		2609	2625	2750	2862
		2937	2991	3263	3576
		3654	3811	3812	4176
		4464	4585	4598	4816
		5512	5863	6364	6399
		6671	6750	6948	
Sec I	(40)	161	240	250	397
		461	497	546	547
		694	733	734	746
		747	1167	1236	1245
		1265	1266	1411	1716
		1854	1907	2303	2472
		2578	2608	2748	2911
		2935	2990	3574	3653
		3663	3810	3873	4175
		4596	6670	6748	6754
SfaN I	(24)	185	444	641	938
		1485	1542	1674	1720
		2679	2955	2970	3069
		3598	3856	4532	5584
		5777	6024	6385	6477
		6515	6553	6869	6881

Sfc I	(10)	15	917	925	1101
		1496	3426	4701	4892
		5570	6988		
Sma I	(2)	399	3812		
SnaB I	(1)	3350			
Spe I	(1)	660			
Sph I	(1)	6724			
Ssp I	(3)	1955	3979	6133	
Stu I	(1)	3318			
Sty I	(9)	250	461	1245	1411
		1854	2303	2578	3663
		3873			
SwaI	(1)	2047			
Taq I	(18)	794	1038	1349	1360
		1705	1828	2083	2629
		2923	2950	2965	3094
		3297	3323	3337	3974
		4536	5980		
Tfi I	(10)	442	802	1437	1769
		1859	2017	2270	4014
		4271	4411		
Tsp45 I	(10)	1022	1231	1874	2176
		2762	3251	5585	5796
		6372	6683		
Tth111 I	(4)	390	811	1217	3803
Tth111 II	(9)	146	422	613	632
		3062	3558	5025	5034
		5064			
Vsp I	(5)	2218	4079	4207	4266
		5501			
Xba I	(2)	218	3631		
Xho I	(1)	3336			
Xho II	(10)	2307	2313	3079	3310
		5077	5088	5174	5186
		5954	5971		
Xma I	(2)	397	3810		
Xma III	(3)	724	1529	3329	
Xmn I	(3)	4042	4080	5928	