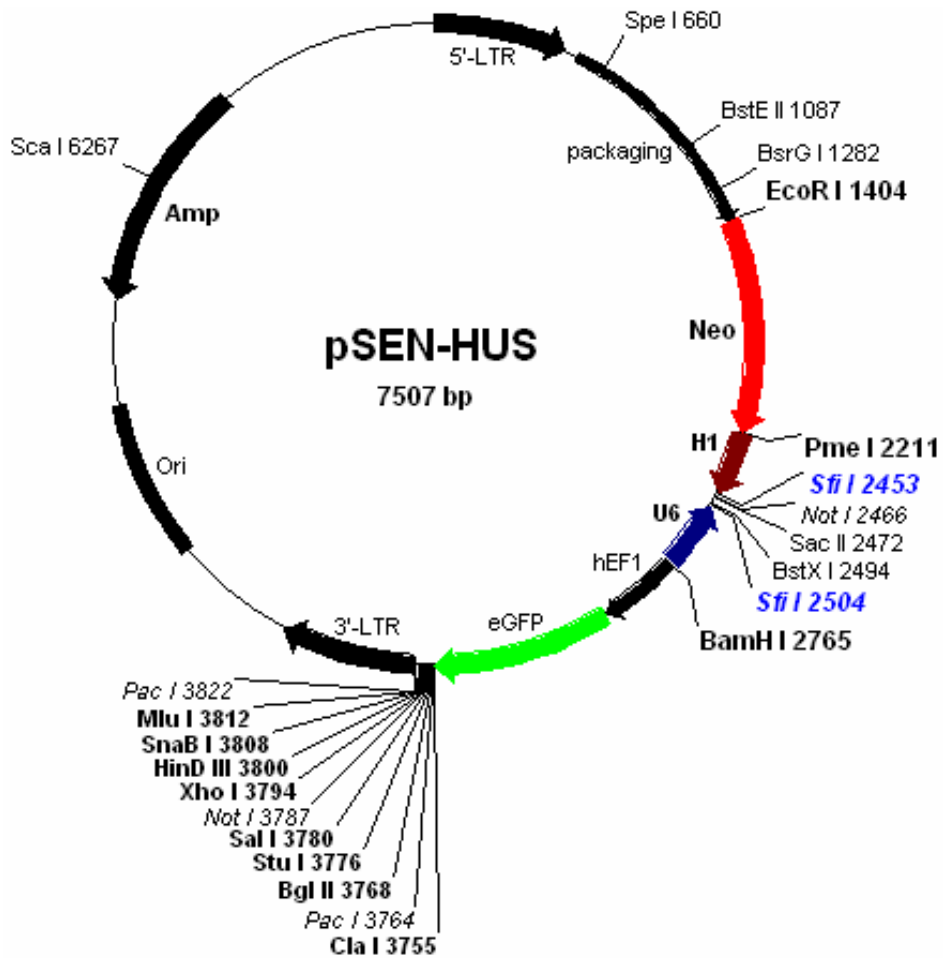


Vector: pSEN-HUS

Antibiotic Selection: Amp

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

Date of Construction: July, 2007



Sfi I Site Stuffer and siRNA Cassette Design:

H1>>> **ggccaaaacGGCC**^{EcoRV}gatata**cGCGGCCGC**^{Not I}ggaacagctatga**CCAtgacgcTGGCCg**^{M13Rev}ttttggcc**ccgg**^{BstX I}ttttgCGG**C**ctatagcgc**ccggc**ctttgtcgata**ctggtactg**cgaccggcaaa**accgg**<<<U6

Sfi I Digestion

5' -GGCCAAA	A(n19-27nt)TTTT	TGGC-3'
3' -CCGGT	TTTT(n19-27nt)A	AAAACCGG-5'

BstB I	TT`CG,AA	2224								
Bsp120 I	G`GGCC,C	2262			Bbv I	(13)	931	939	1614	1656
Apa I	G,GGCC`C	2266					2177	3289	3573	3580
Sac II	CC,GC`GG	2472					5313	5316	5522	6216
BstX I	CCAN,NNNN`NTGG	2494			Bcn I	(18)	6827			
BamH I	G`GATC,C	2765					164	399	400	571
BspM II	T`CCGG,A	2768					724	1546	1706	3068
BsaB I	GATNN NNATC	2770					3722	4035	4270	4271
Mun I	C`AATT,G	2853					5275	5971	6322	6823
Cla I	AT`CG,AT	3755			Bfa I	(15)	6858	7209		
Bgl II	A`GATC,T	3768					31	219	661	673
Stu I	AGG CCT	3776					1394	2275	2868	3017
Sal I	G`TCGA,C	3780					3772	3900	4090	5389
Acc I	GT`MK,AC	3781			Bgl I	(4)	5642	5977	7412	
HinC II	GTY RAC	3782			Bgl II	(1)	2453	2504	5907	7025
Hind II	GTY RAC	3782			Bpm I	(5)	3768			
Paer7 I	C`TCGA,G	3794					3482	3722	3837	5857
Xho I	C`TCGA,G	3794					7475			
HinD III	A`AGCT,T	3800			Bsa I	(7)	476	530	1149	2427
SnaB I	TAC GTA	3808					4325	4346	5848	
Mlu I	A`CGCG,T	3812			BsaA I	(3)	1845	2639	3808	
Sca I	AGT ACT	6267			BsaB I	(1)	2770			
Number of enzymes = 29										

The following enzymes do not cut in pSEN-HUS:

Avr II	Bbs I	Bbv II	Bcl I	Blp I
BsiW I	Bsm I	Bst1107 I	Dra III	Eco72 I
Esp I	Fse I	Hpa I	Nru I	Nsi I
PflM I	Pml I	Spl I	Srf I	Xca I

pSEN-HUS: sites sorted by name:

Aat II	(3)	745	2237	6709	BsaW I	(8)	1572	2768	2785	2860	
Acc I	(1)	3781					3025	5100	5247	6078	
Acc65 I	(2)	401	4272		BseR I	(5)	464	1293	1332	3068	
Aci I	(83)	197	203	566	588		4334				
		688	727	860	901	Bsg I	(4)	2978	3166	3263	3587
		1042	1133	1199	1298	BsiC I	(1)	2224			
		1317	1355	1450	1513	BsiE I	(13)	592	727	1450	2457
		1607	1671	1772	1775		2469	2781	3030	3790	
		2015	2055	2060	2110		4810	5234	6157	6306	
		2126	2152	2245	2260	BsiHKA I	(9)	7053			
		2279	2465	2469	2471		338	1654	1844	3647	
		2882	2919	2999	3256		4209	5212	6373	6458	
		3297	3364	3403	3541	BsmA I	(21)	6955			
		3654	3714	3717	3786		107	475	531	609	
		3790	4068	4074	4370		734	832	949	1073	
		4584	4687	4743	4753		1132	1150	1328	2428	
		4777	4820	4827	4848		3854	3977	4324	4345	
		4939	4967	5094	5113		5849	6623	6776	6820	
		5234	5344	5479	5488	BsmB I	(7)	7492			
		5850	5941	6132	6178		733	831	1072	1131	
		6299	6343	6420	6529		1329	6777	6819		
		6628	6675	6849	6888	BsmF I	(12)	172	185	564	729
		6898	6924	6962	6975		764	1205	1692	2340	
		7001	7058	7317	6975		2809	4043	4056	7188	
Afl II	(3)	35	1006	3904		BsoF I	(53)	727	901	917	920
Afl III	(2)	3812	4894				925	928	1133	1450	
Age I	(2)	2860	3025				1502	1513	1603	1608	
Aha II	(11)	742	1398	1541	2234		1645	1686	1773	1776	
		2340	6324	6706	7010		1779	2015	2111	2152	
		7193	7307	7328			2166	2466	2469	2999	
Ahd I	(4)	1020	4317	4363	5787		3197	3256	3278	3562	
Alu I	(39)	30	34	336	580		3569	3620	3623	3717	
		668	676	1647	2105		3787	3790	4719	4800	
		2217	2480	3012	3058		4818	4821	4939	5094	
		3091	3163	3196	3412		5237	5302	5305	5511	
		3460	3571	3745	3802		5839	6178	6205	6300	
		3899	3903	4207	4526		6529	6816	6925	7029	
		4559	4654	4718	4836		7102				
		5062	5152	5198	5455	Bsp120 I	(1)	2262			
		5976	6076	6139	6818	Bsp1286 I	(2)	1844	3647		
		6837	7082	7438		BspH I	(4)	5614	6622	6727	7251
Alw I	(19)	453	1051	1357	1719	BspM I	(2)	1428	1809		
		1786	1965	2761	2772	BspM II	(1)	2768			
		2778	3533	3730	5456	Bsr I	(20)	374	1030	1058	1484
		5542	5542	5639	5640		1685	2267	2895	2916	
		6104	6419	6425			3650	4245	4695	5301	
AlwN I	(2)	4028	5310				5314	5428	5834	5952	
Apa I	(1)	2266					5995	6262	6434	7140	
Apal I	(3)	5208	6454	6951		BsrB I	(6)	1042	2154	2247	4586
Apo I	(2)	872	1404				4827	6628			
Asc I	(2)	368	4239			BsrD I	(3)	1774	5848	6022	
Ase I	(5)	2676	4537	4665	4724	BsrG I	(1)	1282			
		5959				BssH II	(6)	317	368	1938	2292
Asp718	(2)	401	4272				4188	4239			
Ava I	(8)	331	397	498	2827	BssS I	(5)	2133	3218	5067	6451
		2929	3794	4202	4268		6758				
Ava II	(14)	186	199	254	551	BstB I	(1)	2224			
		690	1219	2057	3694	BstE II	(1)	1087			
		4057	4070	4125	5925	BstN I	(23)	241	548	735	748
		6147	7402				1169	1194	1217	1237	
BamH I	(1)	2765					1267	1928	2305	3083	
Ban I	(18)	244	401	1142	1397		3208	3320	3395	3449	
		1540	1575	2339	2788		4112	4634	4922	5043	
		2863	3073	4115	4272		5056	7129	7406		
		4638	5735	7009	7192	BstU I	(32)	317	319	370	903
		7306	7327				905	1135	1607	1908	
Ban II	(8)	338	351	1906	2266		1940	2260	2294	2296	
		4209	4222	7259	7273		2465	2471	2882	3366	
Bbe I	(7)	1401	1544	2343	7013		3684	3786	3814	4188	
		7196	7310	7331			4190	4241	4741	4743	

Aat II	G,ACGT`C	3	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	83
Afl I II	C`TTAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	2	Aha II	GR`CG,YC	11
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	39
Alw I	GGATC 8/9	19	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	5	Asp718	G`GTAC,C	4
Ava I	C`YGR,G	8	Ava II	G`GWC,C	14
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	18	Ban II	G,RCY`C	8
Bbe I	G,CGCG`C	7	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	-	Bcn I	CC,S`GG	18
Bfa I	C`TA,G	15	Bgl I	GCCN,NNN`NGGC	4
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	7
Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	11	BsaJ I	C`CNNG,G	41
BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	5
Bsg I	GTGCAG 22/20	4	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	13	BsiHKA I	G,WGCW`C	9
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	21	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	53
Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	4	BspM I	ACCTGC 10/14	2
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	20
BsrB I	GAG CGG	6	BsrD I	GCAATG, 8	3
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	6
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	1
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	23	BstU I	CG CG	12
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	32
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	48
Cfr10 I	R`CCGG,Y	9	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	12	Dde I	C`TNA,G	21
Dpn I	GA TC	34	DpnII	`GATC,	34
Dra I	TTT AAA	6	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	5
Eae I	Y`GGCC,R	19	Eag I	C`GGCC,G	5
Ear I	CTCTTC 7/10	9	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	8	Eco72 I	CAC GTG	-
EcoN I	CCTNN,N`NNAGG	3	EcoO109 I	RG`GNC,CY	6
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	23
EcoR V	GAT ATC	4	Ehe I	GGC GCC	7
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	53
Pok I	GGATG 14/18	13	Fse I	GG,CCGG`CC	-

Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	21
Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	8
Hae II	R,CGCC`Y	12	Hae III	GG CC	42
Hga I	GACGC 9/14	11	HgiA I	G,WGCW`C	9
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	53
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	11	Hinp I	G`CG,C	53
Hpa I	GTT AAG	-	Hpa II	C`CG,G	40
Hph I	GGTGA 12/11	20	Kas I	G`GGCC,C	7
Kpn I	G,GTAC`Y	2	Mae I	C`TA,G	15
Mae II	A`CG,T	19	Mae III	`GTNAC,	26
Mbo I	`GATC,	34	Mbo II	GAAGA 12/11	20
Mlu I	A`CGCG,T	1	Mme I	TCRCAC 25/23	6
Mnl I	CCTC 10/10	61	Msc I	TGG CC	3
Mse I	T`TA,A	31	Msl I	CAYNN NNRTG	5
Msp I	C`CG,G	40	MspA I	CMG CKG	12
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	7	Nci I	CC`S,GG	18
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	2
Nla III	,CATG`	30	Nla IV	GGN NCC	39
Not I	GC`GGCC,GC	2	Nru I	TCG CGA	-
Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	5
NspB II	CMG CKG	12	NspH I	R,CATG`Y	5
Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	1
Pal I	GG CC	42	PEIM I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Psp1406 I	AA`CG,TT	3	PspA I	C`CCGG,G	2
Pst I	C,TGCA`G	4	Pvu I	CG,AT`CG	3
Pvu II	CAG CTG	5	Rsa I	GT AC	12
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	4	Sau3A I	`GATC,	34
Sau96 I	G`GNC,C	32	Sca I	AGT ACT	1
ScrF I	CC`N,GG	41	Sec I	C`CNNG,G	41
SfaN I	GCATC 9/13	26	Sfc I	C`TRYA,G	10
Sfi I	GGCCN,NNN`NGGCC	2	Sma I	CCC GGG	2
SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	2	Spl I	C`GTAC,G	3
Srf I	GGCC GGGC	-	Ssp I	AAT ATT	-
Stu I	AGG CCT	1	Sty I	C`CWWG,G	9
Taq I	T`CG,A	22	TFI I	G`AWT,C	10
Tsp45 I	`GTSAC,	12	Tth111 I	GACN`N,NGTC	5
Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	5
Xba I	T`CTAG,A	2	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNNTGG-	-	Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	2
Xma III	C`GGCC,G	5	Xmm I	GAANN NNTTTC	3