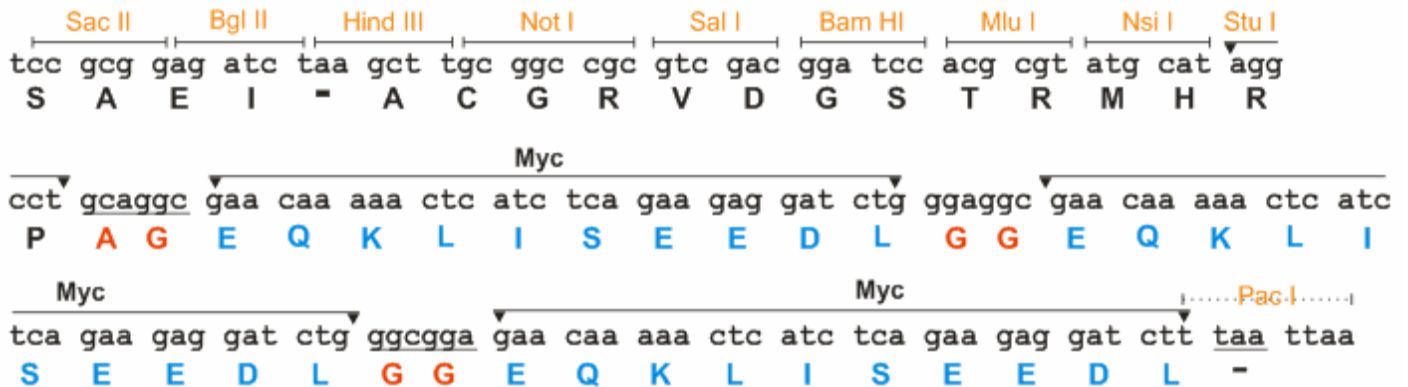
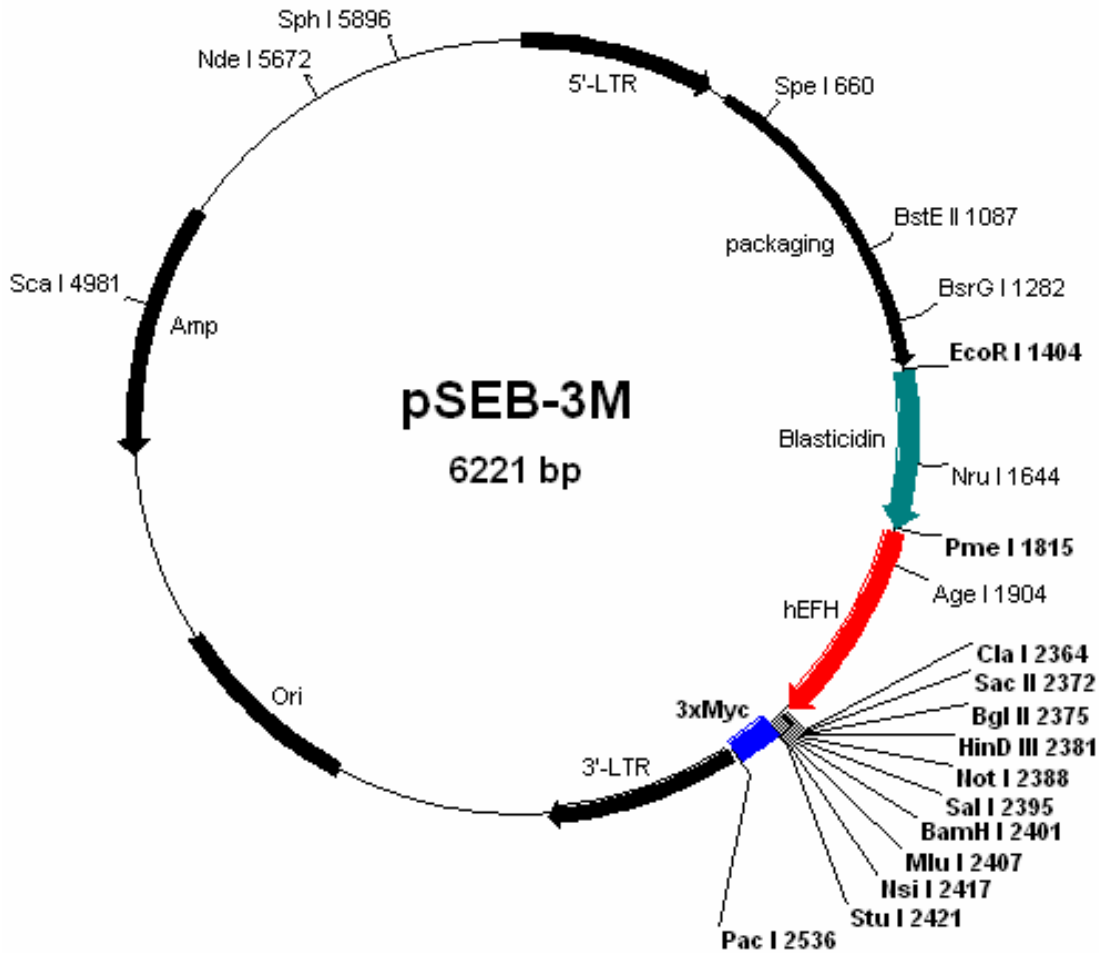


Vector: pSEB-3M (3xMyc tags)

Antibiotic Selection: Amp

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

Date of Construction: August, 2007



pSEB-3M (human EF1a/HLTV hybrid promoter) Full-Length Sequence

TGAAAGACC CACCTGTAGG TTTGGCAAGC TAGCTTAAGT AACGCCATT TGC AAGGCATGGAAAATACATACTAGAGATA TAGAGAAGTT AGATCAAGG TTAGAGACAGAGACAGACAGAGAATATGGGCCAAACAGGATATCTGTGGTAAGCAGTTCTCTCCCGGTCCAGGGCCAAGAACAGATTGGTCCCAGATGCGGTCCC...

Unique enzymes in pSEB-3M:

Table with 4 columns: Enzyme Name, Recognition Site, and Count. Includes Spe I (1), BstE II (1), BsrG I (1), EcoR I (1), Nco I (1), Bbv II (1), Bbs I (1), Nru I (1), BsaB I (1), Pme I (1), Mun I (1), Age I (1), Cla I (1), Sac II (1).

Table with 4 columns: Enzyme Name, Recognition Site, and Count. Includes Bgl II (1), Hind III (1), Not I (1), Sal I (1), Acc I (1), Hinc II (1), Hind II (1), BamH I (1), Mlu I (1), Nsi I (1), Stu I (1), Pac I (1), Sca I (1), Nde I (1), Sph I (1), and a total of 29 enzymes.

		4236			
Vsp I	(4)	3251	3379	3438	4673
Xba I	(2)	218	2803		
Xho II	(12)	2337	2375	2401	2454
		2490	2526	4249	4260
		4346	4358	5126	5143
Xma I	(2)	397	2982		
Xma III	(3)	724	1529	2388	
Xmn I	(3)	3214	3252	5100	

Site usage in pSEB-3M:

Aat II	G,ACGT`C	2	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	68
Afl III	C`TTAA,G	3	Afl IIII	A`CRYG,T	2
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	9
Ahd I	GACNN,N`NNGTC	4	Alu I	AG CT	33
Alw I	GGATC 8/9	19	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	3
Apo I	R`AATT,Y	2	Asc I	GG`CGCG,CC	2
Ase I	AT`TA,AT	4	Asp718	G`GTAC,C	2
Ava I	C`KGR,G	7	Ava II	G`GWC,C	13
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	17	Ban II	G,RGCY`C	8
Bbe I	G,CGCC`C	6	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	-	Bon I	CC,S`GG	15
Bfa I	C`TA,G	16	Bgl I	GCCN,NNN`NGGC	2
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	7
BsaA I	YAC GTR	-	BsaB I	GATNN NNATC	1
BsaH I	GR`CG,YC	9	BsaJ I	C`CNNG,G	33
BsaW I	W`CCGG,W	5	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
BsiE I	CG,RY`CG	10	BsiHKA I	G,WGCW`C	6
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	7
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	41
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	-
BspH I	T`CATG,A	4	BspM I	ACTTCC 10/14	-
BspM II	T`CCCG,A	-	Bsr I	ACT,GG`	18
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	BSSH II	G`CGCG,C	4
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	1
BstN I	CC`W,GG	17	BstU I	CG CG	26
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	12
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	39
Cfr10 I	R`CCGG,Y	8	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	8	Dde I	C`TNA,G	26
Dpn I	GA TC	31	DpnII	`GATC,	31
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	-
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	11	Eag I	C`GGCC,G	3
Ear I	CTCTTC 7/10	9	Eco47 III	AGC GCT	3
Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-

EcoN I	CCTNN`N,NNAGG	4	EcoO109 I	RG`GNC,CY	6
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	17
EcoR V	GAT ATC	3	Ehe I	GGC GCC	6
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	41
Fok I	GGATG 14/18	12	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,CGCG`Y	12	Hae III	GG CC	31
Hga I	GACGC 9/14	12	HgiA I	G,WGCW`C	6
HgiE II	ACNNNNNNNGGT -1/132	-	Hha I	G,CG`C	43
Hinc III	GTY RAC	1	Hind II	GTY RAC	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	17
Hinf I	GR`CG,YC	9	Hinp I	G`CG,C	43
Hpa I	GTT AAC	-	Hpa II	C`CG,G	31
Hph I	GGTGA 12/11	13	Kas I	G`GGCC,C	6
Kpn I	G,GTAC`C	2	Mae I	C`TA,G	16
Mae II	A`CG,T	10	Mae III	`GTNAC,	20
Mbo I	`GATC,	31	Mbo II	GAAGA 12/11	17
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	6
Mnl I	CCTC 10/10	57	Msc I	TGG CCA	3
Mse I	T`TA,A	26	Msl I	CAYNN NNRTG	2
Msp I	C`CG,G	31	MspA I	CMG CKG	12
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	6	Nci I	CC`S,GG	15
Nco I	C`CATG,G	1	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	3
Nla III	,CATG	18	Nla IV	GGN NCC	38
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	4
NspB II	CMG CKG	12	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	-
Pal I	GG CC	31	Pf1M I	CCAN,NNN`NTGG	-
Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	4
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	8
Rsr I	CG`GWC,CG	-	Sac I	G,AGCT`C	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	31
Sau96 I	G`GNC,C	27	Sca I	AGT ACT	1
ScrF I	CC`N,GG	32	Sec I	C`CNNG,G	33
SfaN I	GCATC 9/13	21	Sfc I	C`TRYA,G	11
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	Spl I	C`GTAC,G	-
Srf I	GGC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`GWWG,G	7
Taq I	T`CG,A	12	Tfi I	G`AWT,C	7
Tsp45 I	`GTSAC,	7	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`NNNNNTGG-	-	Xho I	C`TCGA,G	2
Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	-
Xma III	C`GGCC,G	3	Xmn I	GAANN NNTTC	3
GAANN NNTTC	3				