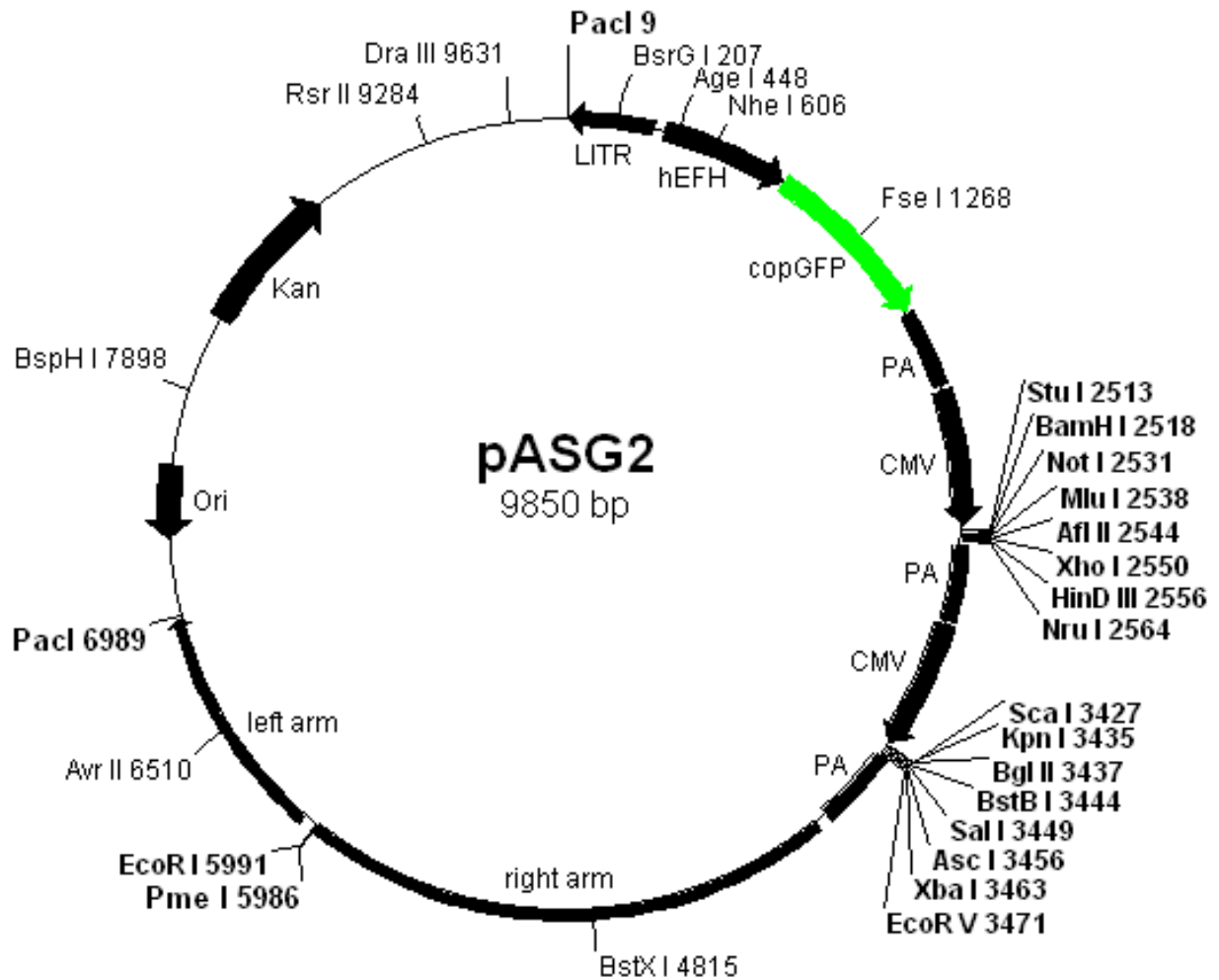


Vector: pASG2 (adenoviral shuttle vector with hEFH-copGFP + 2xCMV-PA)

Antibiotic Selection: Kan

Creator(s): Liang Chen, Molecular Oncology Lab of The University of Chicago

Date of Construction: November, 2008



AGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCACCGCTGGTAGCGGTGGTTTTT
TTGTTTGCAGCAGCAGATTACGCCGAGAAAAAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGG
GATTTTTGGTATGAGATTATCAAAAAGGATCTTACCTAGATCCCTTTAAATCAAAATGAAAGTTTAAATCAACTAAAAGTATATAGTAACTTGGTCTGAC
AGTTACCAATGCTTAAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTTCATCATAGTTCGCTGACTCCCGCTCGTGTAGATAAATACGATACGGGAGG
GCTTACCATCTGGCCCGCAGTGTGCAATGATACCGCGAGACCAGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCGAGAAG
TGGTCTGCAACTTTATCCGCCCTCCATCCAGTCTATTAATTTGTGCCGGGAAGCTAGAGTAAGTATGTTCCCGCAGTAAATAGTTTGGCAGACGTTGTTGNMNNNNAA
AAAGGATCTTACACTAGATCTTTACGTAGAAAAGCCTCCGAGAAACGGTCTGACCCCGATGAAATGTCAGTACTGTTGGTACGAGGAAACCCG
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TGGCTGGCCACGAGCAGCGCGTTCCTTGCGCAGCTGTGCTCGACGTGTGCTCGACGTTGTGCACTGAAGCGGAAGGAGTGGCTGCTATTTGGCGAAAGTGGCCGAGGATCTTCTGT
CATCTCACCTTGGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGGCGCGCTGCATACGCTTGATCCGGCTACCTGCCATTCCGACCACCAAGCGAAACA
TCGCATCGAGCAGCAGCAGCTCGGATGGAAAGCCGCTTTGTGATCAGATGATCTGGACGAAGAGCATCAGGGGCTCGCCGCAAGCCGAACTGTTCCGCGAGGTC
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TATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGTACGAGTTCCTCTGAATTTTGTAAAATTTTGTAAATCAGCTCATTTTTTAAACCAATA
GGCCGAAATCGGCAACATCCCTTATAAATCAAAGAATAGACCGGATAGGGTGTAGTGTGTTCCAGTTTGGACAAGAGTCCACTATTAAAGAACGTGGACTCC
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ACCCTAAAGGGGACCCCGATTTAGCTTACGCGGAAGAACCGCGAGAGTGGCGAGAAGGAAGGAAAGAACGCAAGAGGAGCGGGCGCTAGGGCGCTGGCAAG
TGTAGCGTACGCTGCGCTAACACACCACCCCGCGCTTAATGCGCCGNNN

Unique enzymes in pASG2:

BsrG I	T`GTAC,A	207				6907	7018	7044	7061	
Age I	A`CCGG,T	448				7104	7111	7132	7223	
Nhe I	G`CTAG,C	606				7251	7378	7397	7518	
Bsu36 I	CC`TNA,GG	655				8225	8355	8478	8574	
Blp I	GC`TNA,GC	1099				8677	8740	8834	8898	
Esp I	GC`TNA,GC	1099				8999	9002	9242	9282	
Xmn I	GAANN NNTTC	1162				9287	9337	9353	9379	
Fse I	GG,CCGG`CC	1268				9521	9660	9775	9802	
Stu I	AGG CCT	2513				9830				
BamH I	G`GATC,C	2518	Afl II	(1)	2544					
Not I	GC`GGCC,GC	2531	Afl III	(4)	158	2538	6137	7178		
Mlu I	A`CGCG,T	2538	Age I	(1)	448					
Afl II	C`TTAA,G	2544	Aha II	(14)	899	1073	2027	2080		
Paer7 I	C`TCGA,G	2550			2163	2349	2941	2994		
Xho I	C`TCGA,G	2550			3077	3263	4771	5724		
HinD III	A`AGCT,T	2556			8520	8768				
Nru I	TCG CGA	2564	Ahd I	(2)	4335	8071				
Sca I	AGT ACT	3427	Alu I	(53)	25	600	606	610		
Acc65 I	G`GTAC,C	3431			748	889	1005	1244		
Asp718	G`GTAC,C	3431			1250	1403	1445	1542		
Kpn I	G,GTAC`C	3435			1560	2471	2549	2558		
Bgl II	A`GATC,T	3437			2718	3385	3624	3848		
BsiC I	TT`CG,AA	3444			4081	4173	4453	4539		
BstB I	TT`CG,AA	3444			4589	4739	5081	5108		
Sal I	G`TCGA,C	3449			5178	5184	5387	5707		
Asc I	GG`CGCG,CC	3456			5764	5851	6095	6310		
Xba I	T`CTAG,A	3463			6634	7120	7346	7436		
EcoR V	GAT ATC	3471			7482	7739	8260	8389		
BstX I	CCAN,NNNN`NTGG	4815			8442	8468	8514	8605		
Bst1107 I	GTA TAC	5971			8874	9332	9461	9679		
Xca I	GTA TAC	5971			9718					
Pme I	CTTT AAAC	5986	Alw I	(33)	877	905	1608	1677		
EcoR I	G`AATT,C	5991			1679	2486	2514	2525		
Avr II	C`CTAG,G	6510			2573	3400	3479	3738		
BspH I	T`CATG,A	7898			4186	4278	4477	4868		
Rsr II	CG`GWC,CG	9284			5031	5409	6993	7000		
Dra III	CAC,NNN`GTG	9631			7740	7826	7923	7923		
						7924	8324	8325	8588	
Number of enzymes = 37						8605	8635	8946	9013	
						9192				

The following enzymes do not cut in pASG2:

BsiW I	Pvu I	Sfi I	Spe I	Spl I	AlwN I	(6)	4015	4173	4258	5979	
							7594	8392			
					Apa I	(3)	1513	4828	5134		
					ApaL I	(2)	4714	7492			
					Apo I	(7)	257	2753	3659	4725	
					Asc I	(1)	5991	9433	9444		
					Ase I	(5)	5	2525	6466	6985	
										8243	
					Asp718	(1)	3431				
					Ava I	(7)	415	517	1309	2550	
							4145	4325	6400		
					Ava II	(9)	917	1657	4329	4353	
							5378	5519	5597	8209	
							9284				
					Avr II	(1)	6510				
					BamH I	(1)	2518				
					Ban I	(23)	376	451	707	898	
							979	1024	1072	1135	
							1297	1648	1761	2370	
							3284	3431	4511	4932	
							5723	6627	8019	8519	
							8767	8802	9668		
					Ban II	(10)	622	1513	3850	3907	
							4063	4828	5134	5853	
							9133	9706			
					Bbe I	(5)	902	1076	5727	8523	
							8771				
					Bbs I	(2)	1885	5617			
					Bbv I	(22)	378	1358	1412	2727	
							3633	3808	3811	4003	
							4030	4090	4182	5117	
							5133	5193	5716	6576	
							7597	7600	7806	8841	
							8883	9404			

EcoR II	(20)	1753	1993	2186	2907	7053	7086	7356	7423
		3100	4369	4546	4840	7523	7697	7806	8199
		4885	4965	5371	5490	8292	8422	8520	8591
		5577	5643	5842	5874	8760	8768	8832	8869
		7204	7325	7338	9153	9135	9395	9779	9787
EcoR V	(1)	3471				9813	9832	9834	9843
Ehe I	(5)	900	1074	5725	8521	Hpa I (2)	2702	3608	
		8769				Hpa II (51)	203	374	449
Esp I	(1)	1099					761	773	805
Fnu4H I	(82)	367	587	646	661		977	1265	1301
		692	939	969	1014		1661	1670	2584
		1041	1149	1188	1227		3881	4146	4326
		1234	1269	1347	1401		4711	4961	5063
		1434	1530	1543	2531		5153	5562	5621
		2534	2716	3622	3797		5927	6098	6258
		3800	3803	3806	3809		6401	7385	7532
		3992	4001	4004	4013		7748	8152	8186
		4016	4019	4079	4171		8375	8502	8673
		4461	4835	4838	5106		8772	8800	8931
		5109	5122	5179	5182		9088	9269	9733
		5185	5275	5448	5567	Hph I (17)	120	967	1321
		5618	5686	5705	5727		3194	4396	5386
		5808	6016	6562	6565		5857	5953	6275
		7084	7102	7105	7223		7915	8142	8316
		7378	7521	7586	7589		9633		
		7795	8123	8574	8677	Kas I (5)	898	1072	5723
		8729	8740	8830	8835		8767		8519
		8872	8913	9000	9003	Kpn I (1)	3435		
		9006	9242	9338	9379	Mae I (18)	456	607	733
		9393	9811				1705	1912	2497
Fok I	(22)	184	258	651	1327		3411	3464	3694
		1468	1480	1914	4077		7673	7926	8261
		4407	4606	4902	4944		8469	9782	
		5178	5786	8037	8218		81	113	187
		8390	8573	8635	9092	Mae II (37)	846	1106	1238
		9117	9481				2027	2039	2080
Fse I	(1)	1268					2244	2349	2941
Fsp I	(2)	8293	8870				2994	3077	3158
Gdi II	(12)	940	1265	1267	2530		4375	4605	4870
		2532	5642	5854	6251		6811	6816	6882
		8673	8675	9238	9265		7881	8297	8340
Gsu I	(3)	3892	6520	8142			9071	9575	9587
Hae I	(8)	285	2513	4906	5577		9740		9630
		7193	7204	7656	8850	Mae III (41)	77	109	183
Hae II	(16)	372	779	902	1076		266	337	875
		1481	4503	5271	5618		1966	2053	2402
		5727	6554	7056	7426		2880	2967	3316
		8523	8771	9782	9790		4038	4385	4778
Hae III	(43)	285	660	765	941		5391	5540	5942
		1040	1264	1268	1511		6280	6642	6700
		1989	2182	2513	2533		6812	6817	6861
		2903	3096	3880	4324		6915	7534	7597
		4557	4826	4840	4906		7996	8888	9194
		4964	5132	5209	5490		9816		6262
		5577	5643	5693	5814		881	909	959
		5857	6252	6661	7193	Mbo I (50)	1322	1337	1612
		7204	7222	7656	8114		1681	2490	2501
		8194	8676	8850	9241		2568	2577	2596
		9268	9481	9623			3415	3437	3474
Hga I	(9)	712	2430	2530	3344		3502	3731	4179
		3878	4778	5627	7288		4481	4861	4894
		7866					5075	5413	6993
HgiA I	(10)	1066	1367	3820	3850		7744	7819	7830
		4718	5478	5853	7496		7916	7928	8033
		8881	9071				8329	8581	8598
HgiE II	(3)	1750	5116	7757			8628	8939	9017
Hha I	(64)	88	202	233	350		9107	9185	9098
		371	398	470	641	Mbo II (16)	1070	1318	1889
		778	873	901	1075		4859	5060	5097
		1427	1480	1621	3458		7050	7839	7912
		3460	3866	4187	4313		9128	9338	9420
		4315	4317	4502	4922	Mlu I (1)	2538		9770
		5270	5515	5559	5571	Mme I (5)	3963	4158	7392
		5573	5587	5617	5637		9607		7576
		5702	5704	5726	5772	Mnl I (66)	56	304	424
		5807	6044	6553	6911		608	650	704
		7055	7088	7358	7425		1014	1212	1254
		7525	7699	7808	8201		1530	1699	1741
		8294	8424	8522	8593		1862	2446	2523
		8762	8770	8834	8871		2657	2666	3360
		9137	9397	9781	9789		3524	3563	3572
		9815	9834	9836	9845		4223	4228	4343
Hinc II	(4)	2702	3451	3608	4112		4677	4792	4922
Hind II	(4)	2702	3451	3608	4112		5437	5531	5584
Hind III	(1)	2556					5711	5714	5726
Hinf I	(22)	679	798	1908	2315		5919	6047	6322
		3229	4135	4255	4388		6512	6536	6794
		4676	5232	5784	6328		7076	7286	7359
		6342	6364	7078	7153		8010	8091	8237
		7549	8066	9253	9387		8619	8683	8819
		9558	9580				9368	9659	9176
HinI I	(14)	899	1073	2027	2080	Msc I (3)	285	5577	8850
		2163	2349	2941	2994	Mse I (35)	5	9	743
		3077	3263	4771	5724		2545	2640	2701
		8520	8768				3607	4154	4233
HinP I	(64)	86	200	231	348		5170	5218	5985
		369	396	468	639		6291	6466	6605
		776	871	899	1073		6831	6985	6989
		1425	1478	1619	3456		7936	7941	7955
		3458	3864	4185	4311		8243	8282	9441
		4313	4315	4500	4920		9470	9568	9838
		5268	5513	5557	5569	Msl I (6)	2270	3184	4813
		5571	5585	5615	5635		6072	9205	
		5700	5702	5724	5770	Msp I (51)	203	374	449
		5805	6042	6551	6909		761	773	805

Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	1	Hph I	GGTGA 12/11	17	Kas I	G`GCGC,C	5
Bpm I	CTGGAG 22/20	3	Bsa I	GGTCTC 7/11	6	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	18
BsaA I	YAC GTR	9	BsaB I	GATNN NNATC	5	Mae II	A`CG,T	37	Mae III	`GTNAC,	41
BsaH I	GR`CG,YC	14	BsaJ I	C`CNNG,G	43	Mbo I	`GATC,	50	Mbo II	GAAGA 12/11	16
BsaW I	W`CCGG,W	12	BseR I	GAGGAG 16/14	4	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	5
Bsg I	GTGCAG 22/20	9	BsiC I	TT`CG,AA	1	Mnl I	CCTC 10/10	66	Msc I	TGG CCA	3
BslE I	CG,RY`CG	8	BsiHKA I	G,WGCW`C	10	Mse I	T`TA,A	35	Msl I	CAYNN NNRTG	6
BslW I	C`GTAC,G	-	Bsm I	GAATG,C 7	6	Msp I	C`CG,G	51	MspAl I	CMG CKG	16
BsmA I	CTCTC`/9	13	BsmB I	CGTCTC 7/11	2	Mun I	C`AATT,G	4	Nae I	GCC GCG	5
BsmF I	GGGAC 15/19	12	BsoF I	GC`N,GC	82	Nar I	GG`CG,CC	5	Nci I	CC`S,GG	19
Bsp120 I	G`GGCC,C	3	Bsp1286 I	G,DGCH`C	4	Nco I	C`CATG,G	8	Nde I	CA`TA,TG	2
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	10	Ngm I	G`CCGG,C	5	Nhe I	G`CTAG,C	1
BspM II	T`CCGG,A	2	Bsr I	ACT,GG`	22	Nla III	,CATG`	43	Nla IV	GCN NCC	49
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	3	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1
BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	6	Nsi I	A,TGCA`T	2	Nsp7524 I	R`CATG,Y	11
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	1	NspB II	CMG CKG	16	NspH I	R,CATG`Y	11
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	2	Pac I	TTA,AT`TAA	2	PaeR7 I	C`TCGA,G	1
BstN I	CC`W,GG	20	BstU I	CG CG	44	Pal I	GG CC	43	PflM I	CCAN,NNN`NTGG	4
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	19	Ple I	GAGTC 9/10	5	Pme I	CTTT AAAC	1
Bsu36 I	CC`TNA,GG	1	Cac8 I	GCN NGC	67	Pml I	CAC GTG	2	PpuM I	RG`GWC,CY	2
Cfr10 I	R`CCGG,Y	16	Cla I	AT`CG,AT	3	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	3
Csp6 I	G`TA,C	22	Dde I	C`TNA,G	16	Pst I	C,TGCA`G	5	Pvu I	CG,AT`CG	-
Dpn I	GA TC	50	DpnII	`GATC,	50	Pvu II	CAG CTG	7	Rsa I	GT AC	22
Dra I	TTT AAA	8	Dra III	CAC,NNN`GTG	1	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	2
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	15	Sac II	CC,GC`GG	3	Sal I	G`TCGA,C	1
Eae I	T`GGCC,R	12	Eag I	C`GGCC,G	3	Sap I	GCCTCTC 8/11	4	Sau3A I	`GATC,	50
Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	4	Sau96 I	G`GNC,C	33	Sca I	ACT ACT	1
Eco57 I	CTGAAG 21/19	10	Eco72 I	CAC GTG	2	ScaF I	CC`N,GG	39	Sec I	C`CNNG,G	43
EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	6	Sfa I	GCCTC 9/13	24	Sfc I	C`TRYA,G	8
EcoR I	G`AATT,C	1	EcoR II	`CWGG,	20	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	3
EcoR V	GAT ATC	1	Ehe I	GGC GCC	5	SnaB I	TAC GTA	3	Spe I	A`CTAG,T	-
Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	82	Sph I	G,CATG`C	4	Spl I	C`GTAG,C	-
Fok I	GGATG 14/18	22	Fse I	GG,CCGG`CC	1	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	-
Fsp I	TGT GCA	2	Gai II	`YGGC,CG	12	Stu I	AGG CCT	1	Sty I	C`CWG,G	14
Gsu I	CTGGAG 21/19	3	Hae I	WGG CCW	8	Taq I	T`CG,A	23	Tfi I	G`AWT,C	7
Hae II	R,GCGC`Y	16	Hae III	GG CC	43	Tsp45 I	`GTSAC,	20	Tth111 I	GACN`N,NGTC	2
Hga I	GACGC 9/14	9	HgiA I	G,WGCW`C	10	Tth111 II	CAARCA 16/14	12	Vsp I	AT`TA,AT	5
HgiE II	ACCNNNNNNGGT -1/133	4	Hha I	G,CG`C	64	Xba I	T`CTAG,A	1	Xca I	GTA TAC	1
Hinc II	GTY RAC	4	Hind II	GTY RAC	4	Xcm I	CCANNNN,N`NNNNTGG4	1	Xho I	C`TCGA,G	1
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	22	Xho II	R`GATC,Y	19	Xma I	C`CCGG,G	3
HinI I	GR`CG,YC	14	HinP I	G`CG,C	64	Xma III	C`GGCC,G	3	Xmm I	GAANN NNYTC	1
Hpa I	GTT AAC	2	Hpa II	C`CG,G	51						