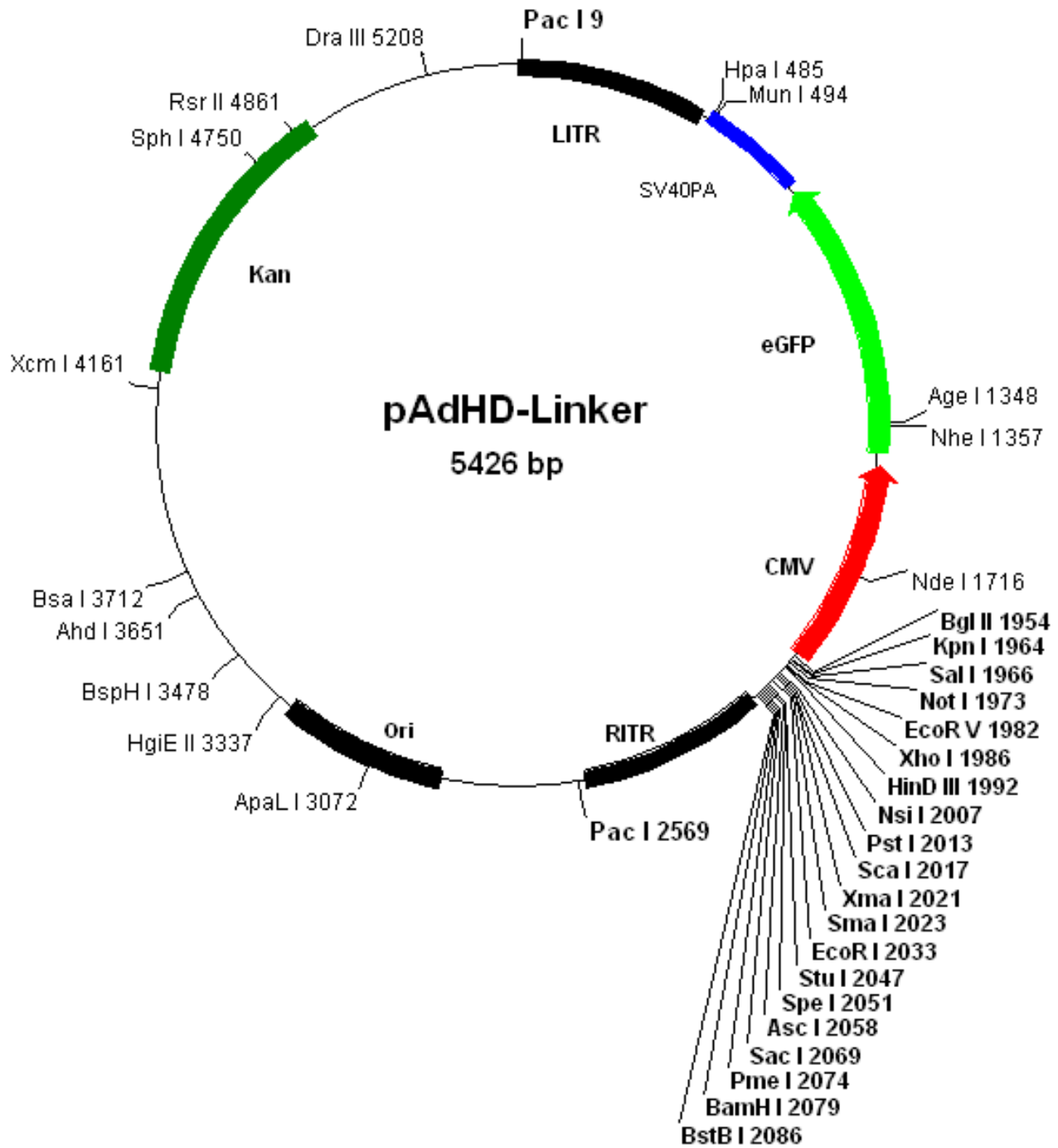


Vector: pAdHD-Linker (adenoviral Helper-dependent shuttle vector)

Antibiotic Selection: Kan

Creator(s): Wei Jiang, Molecular Oncology Lab of The University of Chicago

Date of Construction: June, 2009



Hae III	(22)	285 1266 2047 2802 4253 5058	765 1675 2241 3236 4427 5200	877 1868 2773 3694 4818 4845	1166 1975 2784 3774 4845	MspA1 I	(5)	2141 4451	3100	3345	4091
Hga I	(5)	1422 3446	1977	2034	2868	Mun I	(1)	494			
HgiA I	(5)	734 4648	2069	3076	4458	Nae I	(2)	4847	5311		
HgiE II	(1)	3337				Nar I	(2)	4097	4345		
Hha I	(36)	88 695 2060 2635 3105 3874 4339 4714 5392	202 1011 2062 2668 3279 4001 4347 4974 5411	233 1052 2133 2938 3388 4099 4411 5358 5413	350 1357 2491 3005 3781 4170 4448 5366 5422	Nci I	(9)	655 3138 4509	1309 3834	2022 3952	2023 4349
HinC II	(2)	485	1968			Nco I	(3)	1337	1588	4777	
Hind II	(2)	485	1968			Nde I	(1)	1716			
Hind III	(1)	1992				Ngom I	(2)	4845	5309		
Hinf I	(10)	615 3129 5135	1539 3646 5157	2658 4830	2733 4964	Nhe I	(1)	1357			
HinI I	(6)	1506 4097	1692 4345	1775	1828	Nla III	(17)	162 1077 1652 4219 4807	642 1107 2762 4564	687 1341 3482 4750	882 1592 4038 4781
HinP I	(36)	86 693 2058 2633 3103 3872 4337 4712 5390	200 1009 2060 2666 3277 3999 4345 4972 5409	231 1050 2131 2936 3386 4097 4409 5364 5411	348 1355 2489 3003 3779 4168 4446 5364 5420	Nla IV	(17)	764 2081 3601 4346 5280	1302 2209 3695 4381	1485 2790 3736 5247	1962 2829 4098 5268
Hpa I	(1)	485				Not I	(1)	1973			
Hpa II	(27)	203 1186 2022 3328 3952 4349 4665	604 1246 2965 3732 4079 4377 4846	619 1309 3112 3766 4250 4508 5310	655 1349 3138 3833 4327 4598	Nsi I	(1)	2007			
Hph I	(13)	120 1322 3495 5210	841 1327 3722	970 1578 3893	994 2458 4524	Nsp7524 I	(3)	158	2758	4746	
Kas I	(2)	4096	4344			NspB II	(5)	2141 4451	3100	3345	4091
Kpn I	(1)	1964				NspH I	(3)	162	2762	4750	
Mae I	(13)	397 1998 3506 5359	598 2052 3841	1358 2091 3904	1949 3253 4046	Pac I	(2)	9	2569		
Mae II	(26)	81 1060 1692 2279 2494 4461 5207	113 1273 1775 2391 3461 4648 5317	187 1506 1816 2396 3877 5152	889 1611 1828 2462 3917 5164	PaeR7 I	(1)	1986			
Mae III	(28)	77 266 1152 2222 2397 3114 4465	109 337 1450 2280 2441 3177 4771	183 455 1799 2373 2463 3293 5381	218 663 1886 2392 2495 3576 5393	Pal I	(22)	285 1266 2047 2802 4253 5058	765 1675 2241 3236 4427 5200	877 1868 2773 3694 4818 5143	1166 1975 2784 3774 4845
Mbo I	(29)	587 688 2079 3399 3508 4158 4516 4762	600 836 2573 3410 3613 4175 4594	609 1363 2577 3418 3894 4186 4675	650 1954 3324 3496 3906 4205 4684	Ple I	(4)	623	1547	3137	5143
Mbo II	(12)	856 2630 4705	1049 3419 4915	1052 3492 4997	1097 3890 5347	Pme I	(1)	2074			
Mlu I	(2)	358	2027			Psp1406 I	(1)	3877			
Mme I	(3)	2972	3156	5184		PspA I	(1)	2021			
Mnl I	(32)	56 569 1013 1331 2374 2939 3817 4396	304 830 1151 1411 2521 3190 4110 4753	521 950 1244 1994 2656 3590 4196 4945	530 1001 1250 2116 2866 3671 4260 5236	Pst I	(1)	2013			
Msc I	(2)	285	4427			Pvu II	(2)	4091	4451		
Mse I	(24)	5 545 2288 3464 3588 5030	9 1943 2411 3516 3823 5047	363 2073 2565 3521 3862 5145	484 2185 2569 3535 5018 5415	Rsa I	(12)	209 1569 1733	628 1620 1962	910 1653 2017	1412 1708 4651
Msl I	(2)	1587	4782			Rsr II	(1)	4861			
Msp I	(27)	203 1186 2022 3328 3952 4349 4665	604 1246 2965 3732 4079 4377 4846	619 1309 3112 3766 4250 4508 5310	655 1349 3138 3833 4327 4598	Sac I	(1)	2069			
						Sal I	(1)	1966			
						Sap I	(3)	2642	4689	4899	
						Sau3A I	(29)	587 688 2079 3399 3508 4158 4516 4762	600 836 2573 3410 3613 4175 4594	609 1363 2577 3418 3894 4186 4675	650 1954 3324 3496 3906 4205 4684
						Sau96 I	(11)	680 1866 3789	763 2239 4861	1164 3693 5199	1673 3772
						Sca I	(1)	2017			
						ScrF I	(20)	655 1168 1861 2907 3952	927 1293 2022 2920 4349	981 1309 2023 3138 4509	1056 1668 2786 3834 4732
						Sec I	(13)	925 1307 2918 4777	980 1337 3950	1004 1588 4154	1167 2021 4508
						SfaN I	(16)	429 1236 2634 4643	846 1590 2854 4707	945 2013 4304 4775	960 2596 4559 4982
						Sfc I	(3)	2009	3023	3214	
						Sma I	(1)	2023			
						SnaB I	(2)	1612	2397		
						Spe I	(1)	2051			
						Sph I	(1)	4750			
						Stu I	(1)	2047			
						Sty I	(4)	1337	1588	4154	4777
						Taq I	(18)	823 1288 2086 4458 4836	952 1967 2200 4614 5241	967 1987 2576 4638	994 2040 2858 4674
						Tfi I	(3)	2733	4830	4964	
						Tsp45 I	(13)	77 663 2463 5381	109 1152 2495	183 2222 4465	218 2373 4771
						Tth111 I	(1)	4463			
						Tth111 II	(5)	859 4781	3347	3356	3386
						Vsp I	(3)	5	2565	3823	
						Xba I	(1)	597			
						Xcm I	(1)	4161			
						Xho I	(1)	1986			
						Xho II	(15)	600 1954 3496 4158	609 2079 3508 4516	836 3399 3894 4762	1363 3410 3906
						Xma I	(1)	2021			
						Xma III	(2)	1973	4251		

Site usage in pAdHD-Linker:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1	Fok I	GGATG 14/18	12	Fse I	GG,CCGG`CC	-
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	69	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	8
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	4	Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	6
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	6	Hae II	R,CGCC`Y	8	Hae III	GG CC	22
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	30	Hga I	GACGC 9/14	5	Hga I	G,WGCW`C	5
Alw I	GGATC 8/9	22	AlwN I	CAG,NNN`CTG	2	HgiE II	ACNNNNNNNGGT -1/131	-	Hha I	G,CG`C	36
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	1	Hinc II	GTY RAC	2	Hind II	GTY RAC	2
Apo I	R`AATT,Y	5	Asc I	GG`CGCG,CC	1	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	10
Ase I	AT`TA,AT	3	Asp718	G`GTAC,C	1	HinI I	GR`CG,YC	6	HinP I	G`CG,C	36
Ava I	C`YCGR,G	2	Ava II	G`GWC,C	3	Hpa I	GT AAC	1	Hpa II	C`CG,G	27
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1	Hph I	GGTGA 12/11	13	Kas I	G`GGCG,C	2
Ban I	G`GYRC,C	9	Ban II	G,RCY`C	3	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	13
Bbe I	G,CGCC`C	2	Bbs I	GAAGAC 8/12	-	Mae II	A`CG,T	26	Mae III	`GTNAC,	28
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	-	Mbo I	`GATC,	29	Mbo II	GAAGA 12/11	12
Bcl I	T`GATC,A	2	Bcn I	CC,S`GG	9	Mlu I	A`CGCG,T	2	Mme I	TCCRAC 25/23	3
Bfa I	C`TA,G	13	Bgl I	GCCN,NNN`NGGC	4	Mnl I	CCTC 10/10	32	Msc I	TGG CCA	2
Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-	Mse I	T`TA,A	24	Msl I	CAYNN NNRTG	2
Bpm I	CTGGAG 22/20	4	Bsa I	GGTCTC 7/11	1	Msp I	C`CG,G	27	MspAl I	CMG CKG	5
BsaA I	YAC GTR	5	BsaB I	GATNN NNATC	2	Mun I	C`AATT,G	1	Nae I	GCC GGC	2
BsaH I	GR`CG,YC	6	BsaJ I	C`CNN,G	13	Nar I	GG`CG,CC	2	Nci I	CC`S,GG	9
BsaW I	W`CCG,W	7	BseR I	GAGGAG 16/14	1	Nco I	C`CATG,G	3	Nde I	CA`TA,TG	1
Bsg I	GTGCAG 22/20	4	BsiC I	TT`CG,AA	1	NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	1
BsiE I	CG,RY`CG	6	BsiHKA I	G,WGCW`C	5	Nla III	,CATG`	17	Nla IV	GGN`NCC	17
BsiW I	C`GTAC,G	-	Bsm I	GAATC,C 7	2	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
BsmA I	GTCTC`/9	3	BsmB I	CGTCTC 7/11	-	Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	3
BsmF I	GGGAC 15/19	5	BsoF I	GC`N,GC	39	NspB II	CMG CKG	5	NspH I	R,CATG`Y	3
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	1	Pac I	TTA,AT`TAA	22	Paer7 I	C`TCGA,G	1
BspH I	T`CATG,A	1	BspM I	ACCTGC 10/14	3	Pal I	GG CC	22	Pf1M I	CCAN,NNN`NTGG	-
BspM II	T`CCGG,A	1	Bsr I	ACT,GG`	16	Ple I	GAGTC 9/10	4	Pme I	CTTT AAAC	1
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
BsrG I	T`GTAC,A	2	BssH II	G`CGCG,C	2	Psp1406 I	AA`CG,TT	1	PspA I	C`CCGG,G	1
BssS I	C`TCGT,G	3	Bst1107 I	GTA TAC	-	Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-	Pvu II	CAG CTG	2	Rsa I	GT AC	12
BstN I	CC`W,GG	11	BstU I	CG CG	24	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	1
BstX I	CCAN,NNNN`NTGG	-	BstY I	R`GATC,Y	15	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Bsu36 I	CC`TNA,GG	-	Cac8 I	GCN NGC	33	Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	29
Cfr10 I	R`CCGG,Y	7	Cla I	AT`CG,AT	2	Sau96 I	G`GNC,C	11	Sca I	AGT ACT	1
Csp6 I	G`TA,C	12	Dde I	C`TNA,G	6	ScrF I	CC`N,GG	20	Sec I	C`CNNG,G	13
Dpn I	GA TC	29	DpnII	`GATC,	29	SfaN I	GCATC 9/13	16	Sfc I	C`TRYA,G	3
Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	1	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	3	SnaB I	TAC GTA	2	Spe I	A`CTAG,T	1
Eae I	Y`GGCC,R	8	Eag I	C`GGCC,G	2	Sph I	G,CATG`C	1	SpI I	C`GTAC,G	-
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	2	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	-
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-	Stu I	AGG CCT	1	Sty I	C`CWVG,G	4
EcoN I	CCTNN`N,NNAGG	-	Eco0109 I	RG`GNC,CY	-	Taq I	T`CG,A	18	Tfi I	G`AWT,C	3
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	11	Tsp45 I	`GTSAC,	13	Tth111 I	GACN`N,NGTC	1
EcoR V	GAT ATC	1	Ehe I	GGC GCC	2	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	3
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	39	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
						Xcm I	CCANNNN,N`NNNNTGG1	1	Xho I	C`TCGA,G	1
						Xho II	R`GATC,Y	15	Xma I	C`CCGG,G	1
						Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	-