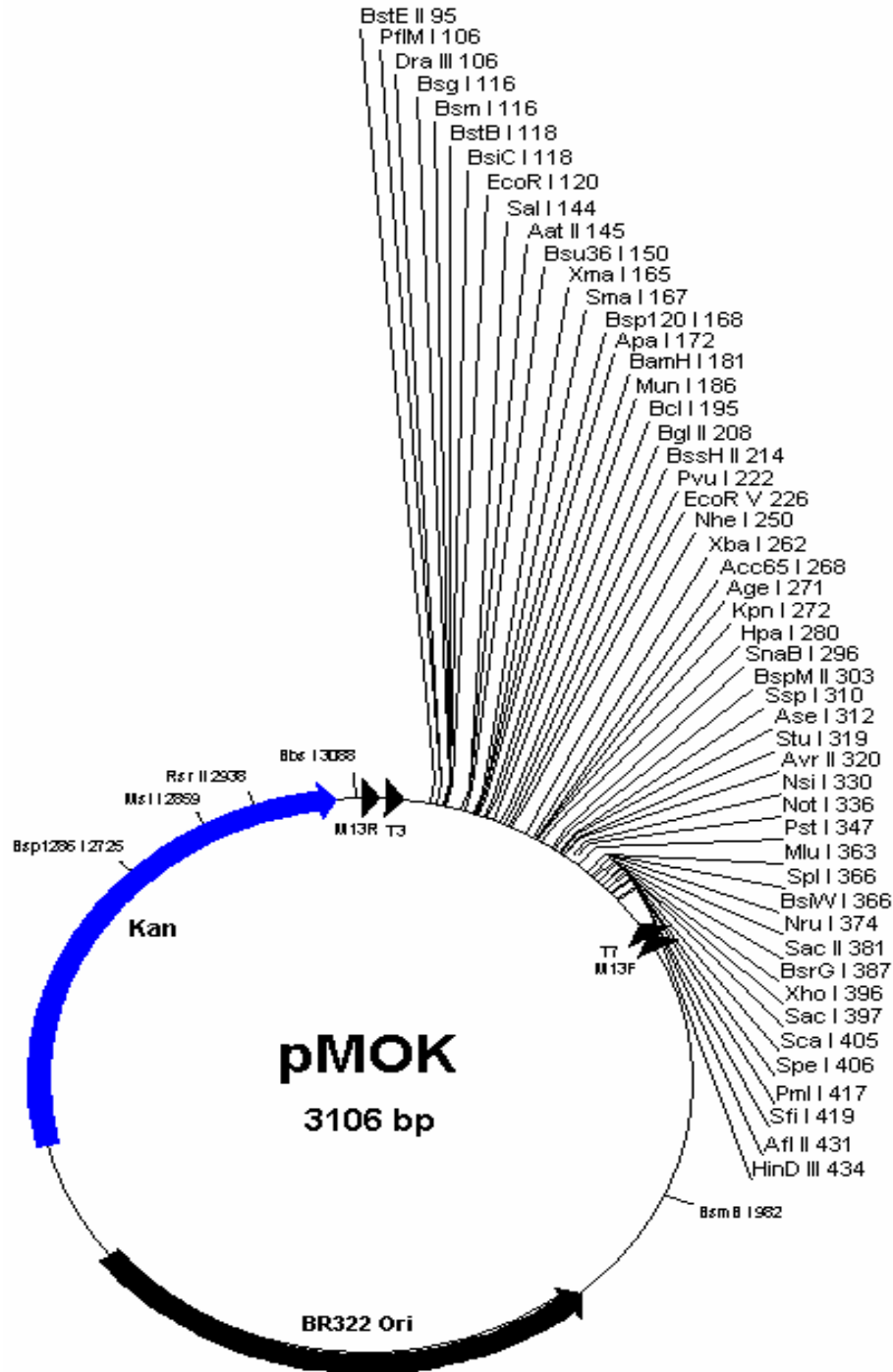


Vector: pMOK

Antibiotic Selection: Kan

Creator(s): Jinyong Luo, Molecular Oncology Lab of The University of Chicago Medical Center

Date of Construction: June, 2006



pMOK Full-Length Sequence

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACCCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTG
GAGCCATGGCTGGTGACCACGTCGTGGAAATGCCCTTCGAATTCAGCACCTGCACATGGGACGTCGACCTGAGGTAATTTATAAC
CCGGGCCCTATATATGGATCCAATTGCAATGATCATCATGACAGATCTGCGCGCGATCGATATCAGCGCTTTAAATTTGCGC
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CTCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGACTTTCGCTTCAAGaatt

Unique enzymes in pMOK:

BstE II	G`GTNAC,C	95	BspM II	T`CCGG,A	303
Pf1M I	CCAN,NNN`NTGG	106	Ssp I	AAT ATT	310
Dra III	CAC,NNN`GTG	106	Ase I	AT`TA,AT	312
Bsm I	GAATG,C 7	116	Vsp I	AT`TA,AT	312
Bsg I	GTGCAG 22/20	116	Stu I	AGG CCT	319
BsiC I	TT`CG,AA	118	Avr II	C`CTAG,G	320
BstB I	TT`CG,AA	118	Nsi I	A,TGCA`T	330
EcoR I	G`AATT,C	120	Not I	GC`GGCC,GC	336
Sal I	G`TCGA,C	144	Pst I	C,TGCA`G	347
Aat II	G,ACGT`C	145	Mlu I	A`CGCG,T	363
Bsu36 I	CC`TNA,GG	150	BsiW I	C`GTAC,G	366
PspA I	C`CCGG,G	165	Spl I	C`GTAC,G	366
Xma I	C`CCGG,G	165	Nru I	TCG CGA	374
Sma I	CCC GGG	167	Sac II	CC,GC`GG	381
Bsp120 I	G`GGCC,C	168	BsrG I	T`GTAC,A	387
Eco109 I	RG`GNC,CY	169	Paer7 I	C`TCGA,G	396
Apa I	G,GGCC`C	172	Xho I	C`TCGA,G	396
BamH I	G`GATC,C	181	Sac I	G,AGCT`C	397
Mun I	C`AATT,G	186	Sca I	AGT ACT	405
Bcl I	T`GATC,A	195	Spe I	A`CTAG,T	406
Bgl II	A`GATC,T	208	Eco72 I	CAC GTG	417
BssH II	G`CGCG,C	214	Pml I	CAC GTG	417
Pvu I	CG,AT`CG	222	Sfi I	GGCCN,NNN`NGGCC	419
EcoR V	GAT ATC	226	Bgl I	GCCN,NNN`NGGC	419
Nhe I	G`CTAG,C	250	Afl II	C`TTAA,G	431
Xba I	T`CTAG,A	262	Hind III	A`AGCT,T	434
Acc65 I	G`GTAC,C	268	BsmB I	CGTCTC 7/11	982
Asp718	G`GTAC,C	268	Bsp1286 I	G, DGCH`C	2725
Age I	A`CCGG,T	271	Msl I	CAYNN NNRTG	2859
Kpn I	G,GTAC`C	272	Rsr II	CG`GWC,CG	2938
Hpa I	GTT AAC	280	Bbs I	GAAGAC 8/12	3088
SnaB I	TAC GTA	296	Bbv II	GAAGAC 7/11	3089
			Number of enzymes =	64	

The following enzymes do not cut in pMOK:

Asc I	Blp I	Bsa I	BseR I	BstX I
EcoN I	Esp I	Fse I	Pac I	Pme I

BssS I	(2)	1512	3014		
Bst1107 I	(2)	299	1112		
BstB I	(1)	118			
BstE II	(1)	95			
BstN I	(4)	1367	1488	1501	2809
BstU I	(13)	216	218	365	374
		380	871	940	942
		1045	1386	1967	2488
		2789			
BstY I	(9)	181	208	533	1980
		1991	2077	2089	2593
		2839			
Bsu36 I	(1)	150			
Cac8 I	(24)	216	248	252	290
		343	350	438	556
		598	816	1270	1356
		1393	1953	2316	2502
		2721	2787	2793	2821
		2825	2866	2870	2924
Cfr10 I	(4)	271	288	2741	2922
Cla I	(2)	222	358		
Csp6 I	(7)	68	269	367	388
		404	1146	2727	
Dde I	(6)	150	609	1149	1614
		2023	2189		
Dpn I	(17)	183	197	210	221
		535	1907	1982	1993
		2001	2079	2091	2196
		2595	2673	2754	2763
		2841			
DpnII	(17)	181	195	208	219
		533	1905	1980	1991
		1999	2077	2089	2194
		2593	2671	2752	2761
		2839			
Dra I	(3)	237	2098	2117	
Dra III	(1)	106			
Drd I	(3)	1034	1447	2449	
Dsa I	(3)	87	378	2854	
Eae I	(7)	336	411	516	2328
		2502	2893	2920	
Eag I	(2)	336	2328		
Ear I	(3)	1223	2766	2976	
Eco47 III	(2)	232	595		
Eco57 I	(3)	1886	2567	2999	
Eco72 I	(1)	417			
Eco109 I	(1)	169			
EcoR I	(1)	120			
EcoR II	(4)	1365	1486	1499	2807
EcoR V	(1)	226			
Ehe I	(2)	353	2423		
Fnu4H I	(33)	336	339	346	552
		633	930	933	979
		1076	1129	1245	1263
		1266	1384	1539	1682
		1747	1750	1956	2331
		2383	2394	2484	2489
		2526	2567	2654	2657
		2660	2896	2992	3033
		3047			
Fok I	(9)	337	560	622	700
		886	1027	2198	2746
		2771			
Fsp I	(2)	245	2524		
Gdi II	(7)	335	337	515	2327
		2329	2892	2919	
Gsu I	(2)	101	867		
Hae I	(6)	319	413	1354	1365
		1817	2504		
Hae II	(6)	234	355	597	1217
		1587	2425		
Hae III	(15)	170	319	338	413
		422	518	814	1354
		1365	1383	1817	2330
		2504	2895	2922	
Hga I	(4)	876	1035	1449	2027
HgiA I	(6)	397	429	1159	1657
		2535	2725		
HgiE II	(2)	1157	1918		
Hha I	(22)	216	218	233	246
		354	596	942	1045
		1075	1216	1249	1519
		1586	1686	1860	1969
		2416	2424	2488	2525
		2791	3051		
Hinc II	(2)	146	280		
Hind II	(2)	146	280		
Hind III	(1)	434			
Hinf I	(8)	497	895	1239	1314
		1710	2227	2907	3041
HinI I	(3)	142	352	2422	
HinP I	(22)	214	216	231	244
		352	594	940	1043
		1073	1214	1247	1517
		1584	1684	1858	1967
		2414	2422	2486	2523
		2789	3049		
Hpa I	(1)	280			
Hpa II	(20)	166	272	289	304
		531	678	985	1019
		1546	1693	1719	1909
		2327	2404	2426	2454
		2585	2675	2742	2923

pMOK: sites sorted by name:

Aat II	(1)	145			
Acc I	(3)	145	298	1111	
Acc65 I	(1)	268			
Aci I	(44)	335	339	378	380
		630	633	644	800
		816	871	927	1012
		1051	1061	1103	1128
		1166	1179	1205	1222
		1265	1272	1293	1384
		1412	1539	1558	1679
		1789	1924	1933	2252
		2331	2394	2488	2552
		2653	2656	2896	2936
		2941	2991	3007	3033
Afl II	(1)	431			
Afl III	(3)	363	384	1339	
Age I	(1)	271			
Aha II	(3)	142	352	2422	
Ahd I	(2)	2232	3092		
Alu I	(20)	9	31	64	254
		348	395	436	477
		864	921	932	981
		1000	1281	1507	1597
		1643	1900	2528	2986
Alw I	(11)	177	188	540	1901
		1987	1987	2084	2085
		2600	2667	2846	
AlwN I	(2)	130	1755		
Apa I	(1)	172			
ApaL I	(3)	425	1155	1653	
Apo I	(2)	120	238		
Ase I	(1)	312			
Asp718	(1)	268			
Ava I	(2)	165	396		
Ava II	(2)	626	2938		
Avr II	(1)	320			
BamH I	(1)	181			
Ban I	(5)	268	351	2180	2421
		2456			
Ban II	(3)	172	397	2787	
Bbe I	(2)	355	2425		
Bbs I	(1)	3088			
Bbv I	(10)	357	941	990	1087
		1758	1761	1967	2495
		2537	3058		
Bbv II	(1)	3089			
Bcl I	(1)	195			
Bcn I	(9)	167	168	532	680
		986	1021	1720	2427
		2587			
Bfa I	(6)	251	263	321	407
		1834	2087		
Bgl I	(1)	419			
Bgl II	(1)	208			
Bpm I	(2)	102	868		
BsaA I	(4)	296	417	1093	2726
BsaB I	(2)	224	538		
BsaH I	(3)	142	352	2422	
BsaJ I	(7)	87	165	320	378
		1499	2585	2854	
BsaW I	(5)	271	303	1545	1692
		2453			
Bsg I	(1)	116			
BsIC I	(1)	118			
BsIE I	(6)	222	339	378	1255
		1679	2331		
BsiHKA I	(6)	397	429	1159	1657
		2535	2725		
BsiW I	(1)	366			
Bsm I	(1)	116			
BsmA I	(2)	983	2255		
BsmB I	(1)	982			
BsmF I	(3)	153	612	2573	
BsoF I	(33)	336	339	346	552
		633	930	933	979
		1076	1129	1245	1263
		1266	1384	1539	1682
		1747	1750	1956	2331
		2383	2394	2484	2489
		2526	2567	2654	2657
		2660	2896	2992	3033
		3047			
Bsp120 I	(1)	168			
Bsp1286 I	(1)	2725			
BspH I	(3)	201	2059	2256	
BspM I	(3)	138	2309	2690	
BspM II	(1)	303			
Bsr I	(10)	518	648	672	1087
		1118	1746	1759	1873
		2365	2566		
BsrB I	(3)	1272	2254	3035	
BsrD I	(2)	198	2655		
BsrG I	(1)	387			
BssH II	(1)	214			

Mun I	C`AATT,G	1	Nae I	GCC GGC	2	Sap I	GCTCTTC 8/11	3	Sau3A I	`GATC,	17
Nar I	GG`CG,CC	2	Nci I	CC`S,GG	9	Sau96 I	G`GNC,C	6	Sca I	AGT ACT	1
Nco I	C`CATG,G	2	Nde I	CA`TA,TG	2	ScrF I	CC`N,GG	13	Sec I	C`CNNG,G	7
NgoM I	G`CCGG,C	2	Nhe I	G`CTAG,C	1	SfaN I	GCATC 9/13	17	Sfc I	C`TRYA,G	5
Nla III	,CATG`	19	Nla IV	GGN NCC	11	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	1
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	1	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Nsi I	A,TGCA`T	1	Nsp7524 I	R`CATG,Y	6	Sph I	G,CATG`C	2	Spl I	C`GTAC,G	1
NspB II	CMG CKG	7	NspH I	R,CATG`Y	6	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	1
Pac I	TTA,AT`TAA	-	Paer7 I	C`TCGA,G	1	Stu I	AGG CCT	1	Sty I	C`CWWG,G	3
Pal I	GG CC	15	Pf1M I	CCAN,NNN`NTGG	1	Taq I	T`CG,A	12	Tfi I	G`AWT,C	4
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	-	Tsp45 I	`GTSAC,	6	Tth111 I	GACN`N,NGTC	3
Pml I	CAC GTG	1	PpuM I	RG`GWC,CY	-	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	1	Xba I	T`CTAG,A	1	Xca I	GTA TAC	2
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Pvu II	CAG CTG	3	Rsa I	GT AC	7	Xho II	R`GATC,Y	9	Xma I	C`CCGG,G	1
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	1	Xma III	C`GGCC,G	2	Xmn I	GAANN NNITC	2
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1						

