Vector: pMOK

Antibiotic Selection: Kan

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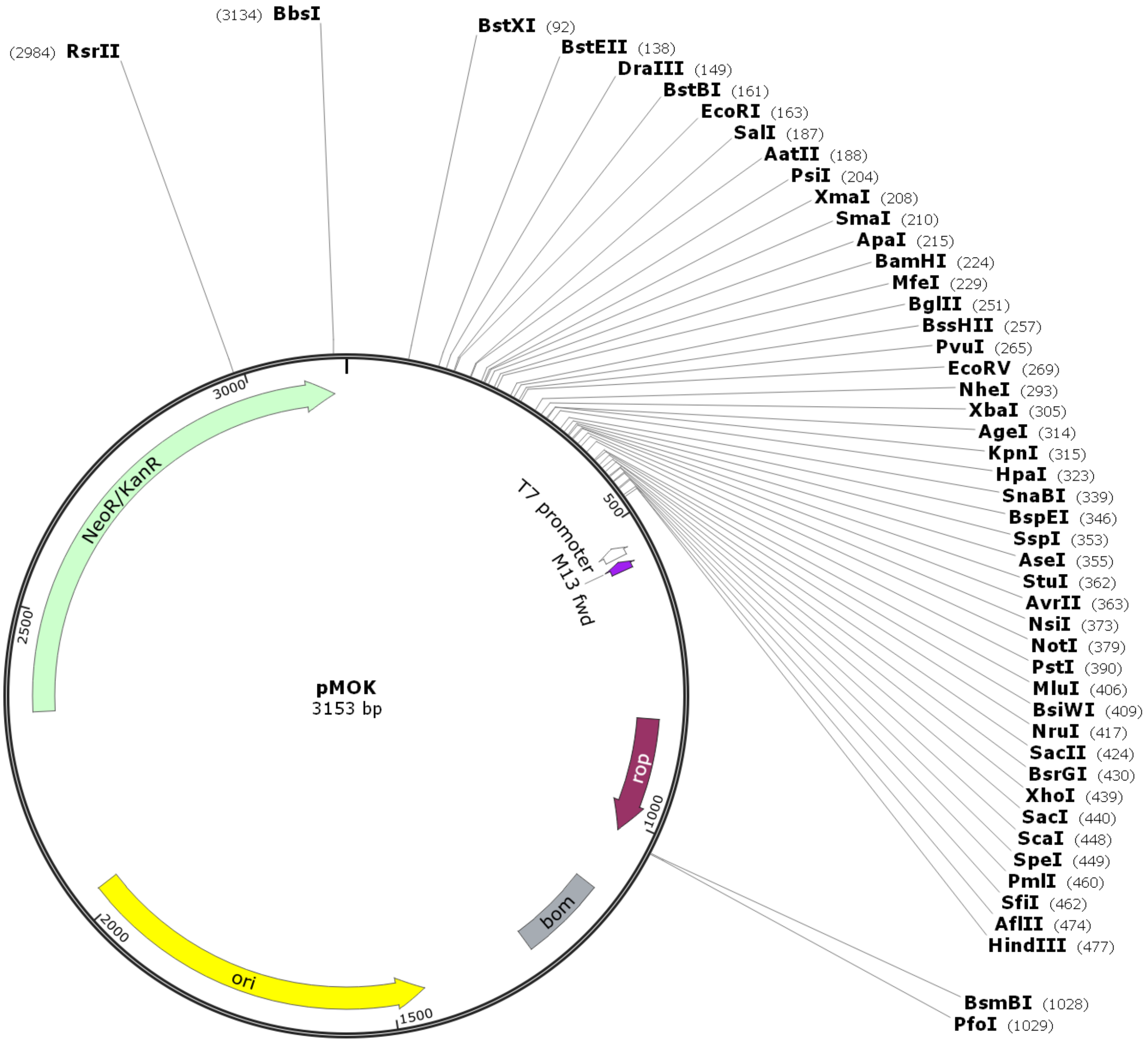
Date of Construction: June, 2006 (updated by Zongyue Zeng @ Nov 12, 2017)



pMOK Vector Full-Length Sequence

GGAAACAGCTATGACCATGATTACGCCAAGCTCGAAATTACCCTCACTAAAGGGAACAAAAGCTGGTACGAGGACAGGCTGG
AGCCATGGGCATGGCTACTCAAGCTGATTTGATGGAGTTGGACATGGCCATGGCTGGTGACCACGTCGTGGAATGCCTTCGA
ATTCAGCACCTGCACATGGGACGTCGACCTGAGGTAATTATAACCCGGGCCCTATATATGGATCCAATTGCAATGATCATCA
TGACAGATCTGCGCGCGATCGATATCAGCGCTTTAAATTTGCGCATGCTAGCTATAGTTCTAGAGGTACCGGTTGTTAACGT
TAGCCGGCTACGTATACTCCGGAATATTAATAGGCCTAGGATGCATATGGCGGCCGCCTGCAGCTGGCGCCATCGATACGCG
TACGTCGCGACCGCGGACATGTACAGAGCTCGAGAAGTACTAGTGGCCACGTGGGCCGTGCACCTTAAGCTTTTAAATAAGG
AGGAATAACATAT**GACCATGATTACGCCAAGCTCCAATTC**GCCCTATAGTGAGTCGTATTACAATTCACTGGCCGTCGTTTT
ACCCGGATCTGCATCGCAGGATGCTGCTGGCTACCCTGTGGAACACCTACATCTGTATTAACGAAGCGCTGGCATTGACCCT
GAGTGATTTTTCTCTGGTCCCGCCGCATCCATACCGCCAGTTGTTTACCCTCACAACGTTCCAGTAACCGGGCATGTTCATC
ATCAGTAACCCGTATCGTGAGCATCCTCTCTCGTTTCATCGGTATCATTACCCCCATGAACAGAAATCCCCCTTACACGGAG
GCATCAGTGACCAAACAGGAAAAAACCGCCCTTAACATGGCCCGCTTTATCAGAAGCCAGACATTAACGCTTCTGGAGAAAC
TCAACGAGCTGGACGCGGATGAACAGGCAGACATCTGTGAATCGCTTCACGACCACGCTGATGAGCTTTACCGCAGCTGCCT
CGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCC
GGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATA
GCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCAC
AGATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGC
GGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGC
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TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCC
GACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG
GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG
GACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACC
ACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCT
TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCAC
CTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGC
TTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCATTCAAATATGTA
TCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT**ATG**ATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCC
GCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAG
CGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATC
GTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGC
GAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGC
TGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGC
CGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGC
ATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTG
GATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCT
TGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTT
CTTGACGAGTTCTTC**TGA**CCTTTCGTCTTCAAGaatt

Unique enzymes in pMOK:

BstE II	G`GTNAC,C	95
PflM I	CCAN,NNN`NTGG	106
Dra III	CAC,NNN`GTG	106
Bsm I	GAATG,C 7	116
Bsg I	GTGCAG 22/20	116
BsiC I	TT`CG,AA	118
BstB I	TT`CG,AA	118
EcoR I	G`AATT,C	120
Sal I	G`TCGA,C	144
Aat II	G,ACGT`C	145
Bsu36 I	CC`TNA,GG	150
PspA I	C`CCGG,G	165
Xma I	C`CCGG,G	165
Sma I	CCC|GGG	167
Bsp120 I	G`GGCC,C	168
EcoO109 I	RG`GNC,CY	169
Apa I	G,GGCC`C	172
BamH I	G`GATC,C	181
Mun I	C`AATT,G	186
Bcl I	T`GATC,A	195
Bgl II	A`GATC,T	208
BssH II	G`CGCG,C	214
Pvu I	CG,AT`CG	222
EcoR V	GAT|ATC	226
Nhe I	G`CTAG,C	250
Xba I	T`CTAG,A	262
Acc65 I	G`GTAC,C	268
Asp718	G`GTAC,C	268
Age I	A`CCGG,T	271
Kpn I	G,GTAC`C	272
Hpa I	GTT|AAC	280
SnaB I	TAC|GTA	296
BspM II	T`CCGG,A	303
Ssp I	AAT|ATT	310
Ase I	AT`TA,AT	312
Vsp I	AT`TA,AT	312
Stu I	AGG|CCT	319
Avr II	C`CTAG,G	320
Nsi I	A,TGCA`T	330
Not I	GC`GGCC,GC	336
Pst I	C,TGCA`G	347
Mlu I	A`CGCG,T	363
BsiW I	C`GTAC,G	366
Spl I	C`GTAC,G	366
Nru I	TCG|CGA	374
Sac II	CC,GC`GG	381
BsrG I	T`GTAC,A	387
PaeR7 I	C`TCGA,G	396
Xho I	C`TCGA,G	396
Sac I	G,AGCT`C	397
Sca I	AGT|ACT	405
Spe I	A`CTAG,T	406
Eco72 I	CAC|GTG	417
Pml I	CAC|GTG	417
Sfi I	GGCCN,NNN`NGGCC	419
Bgl I	GCCN,NNN`NGGC	419
Afl II	C`TTAA,G	431
HinD III	A`AGCT,T	434
BsmB I	CGTCTC 7/11	982
Bsp1286 I	G,DGCH`C	2725
Msl I	CAYNN|NNRTG	2859
Rsr II	CG`GWC,CG	2938

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Bbs I       GAAGAC 8/12     3088
Bbv II      GAAGAC 7/11     3089
Number of enzymes = 64
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The following enzymes do not cut in pMOK:

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Asc I       Blp I       Bsa I       BseR I      BstX I
EcoN I      Esp I       Fse I       Pac I       Pme I
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pMOK: sites sorted by name:

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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
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BsrB I      (3)   1272      2254      3035
BsrD I      (2)   198       2655
BsrG I      (1)   387
BssH II     (1)   214
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
EcoO109 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
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                  531     678     985     1019
                  1546    1693    1719    1909
                  2327    2404    2426    2454
                  2585    2675    2742    2923
Hph I        (5)  106     960     969     2076
                  2601
Kas I        (2)  351     2421
Kpn I        (1)  272
Mae I        (6)  251     263     321     407
                  1834    2087
Mae II       (11) 102     142     282     295
                  369     416     666     1092
                  2042    2538    2725
Mae III      (12) 95      673     696     780
                  993     1088    1695    1758
                  1874    2157    2542    2848
Mbo I        (17) 181     195     208     219
                  533     1905    1980    1991
                  1999    2077    2089    2194
                  2593    2671    2752    2761
                  2839
Mbo II       (7)  1211    2000    2073    2782
                  2992    3074    3089
Mlu I        (1)  363
Mme I        (2)  1553    1737
Mnl I        (18) 53      65      145     259
                  668     726     765     945
                  975     1237    1447    1520
                  1771    2171    2337    2473
                  2830    3022
Msc I        (2)  413     2504
Mse I        (14) 39      236     279     312
                  432     586     806     838
                  1120    2045    2097    2102
                  2116    2169
Msl I        (1)  2859
Msp I        (20) 166     272     289     304
                  531     678     985     1019
                  1546    1693    1719    1909
                  2327    2404    2426    2454
                  2585    2675    2742    2923
MspA1 I      (7)  348     380     932     1051
                  1681    1926    2528
Mun I        (1)  186
Nae I        (2)  290     2924
Nar I        (2)  352     2422
Nci I        (9)  166     167     531     679
                  985     1020    1719    2426
                  2586
Nco I        (2)  87      2854
Nde I        (2)  330     1162
NgoM I       (2)  288     2922
Nhe I        (1)  250
Nla III      (19) 20      91      139     205
                  250     388     466     686
                  750     813     978     1083
                  1343    2063    2260    2641
                  2827    2858    2884
Nla IV       (11) 85      170     183     270
                  353     628     1371    1410
                  2182    2423    2458
Not I        (1)  336
Nru I        (1)  374
Nsi I        (1)  330
Nsp7524 I    (6)  246     384     682     974
                  1339    2823
NspB II      (7)  348     380     932     1051
                  1681    1926    2528
NspH I       (6)  250     388     686     978
                  1343    2827
PaeR7 I      (1)  396
Pal I        (15) 170     319     338     413
                  422     518     814     1354
                  1365    1383    1817    2330
                  2504    2895    2922
PflM I       (1)  106
Ple I        (2)  505     1718
Pml I        (1)  417
Psp1406 I    (2)  282     666
PspA I       (1)  165
Pst I        (1)  347
Pvu I        (1)  222
Pvu II       (3)  348     932     2528
Rsa I        (7)  69      270     368     389
                  405     1147    2728
Rsr II       (1)  2938
Sac I        (1)  397
Sac II       (1)  381
Sal I        (1)  144
Sap I        (3)  1223    2766    2976
Sau3A I      (17) 181     195     208     219
                  533     1905    1980    1991
                  1999    2077    2089    2194
                  2593    2671    2752    2761
                  2839
Sau96 I      (6)  168     169     420     626
                  813     2938
Sca I        (1)  405
ScrF I       (13) 166     167     531     679
                  985     1020    1367    1488
                  1501    1719    2426    2586
                  2809
Sec I        (7)  87      165     320     378
                  1499    2585    2854
SfaN I       (17) 316     539     547     643
                  721     783     1006    1139
                  1177    1215    1435    2381
                  2636    2720    2784    2852
                  3059
Sfc I        (5)  255     343     490     1604
                  1795
Sfi I        (1)  419
Sma I        (1)  167
SnaB I       (1)  296
Spe I        (1)  406
Sph I        (2)  250     2827
Spl I        (1)  366
Ssp I        (1)  310
Stu I        (1)  319
Sty I        (3)  87      320     2854
Taq I        (12) 33      118     145     222
                  358     397     1439    2535
                  2691    2715    2751    2913
Tfi I        (4)  895     1314    2907    3041
Tsp45 I      (6)  95      780     993     1088
                  2542    2848
Tth111 I     (3)  101     1086    2540
Tth111 II    (5)  801     1928    1937    1967
                  2858
Vsp I        (1)  312
Xba I        (1)  262
Xca I        (2)  299     1112
Xho I        (1)  396
Xho II       (9)  181     208     533     1980
                  1991    2077    2089    2593
                  2839
Xma I        (1)  165
Xma III      (2)  336     2328
Xmn I        (2)  114     899
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Site usage in pMOK:

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Aat II      G,ACGT`C          1     Acc I       GT`MK,AC          3
Acc65 I     G`GTAC,C          1     Aci I       C`CG,C            44
Afl II      C`TTAA,G          1     Afl III     A`CRYG,T          3
Age I       A`CCGG,T          1     Aha II      GR`CG,YC          3
Ahd I       GACNN,N`NNGTC     2     Alu I       AG|CT             20
Alw I       GGATC 8/9         11    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        -
Ase I       AT`TA,AT          1     Asp718      G`GTAC,C          1
Ava I       C`YCGR,G          2     Ava II      G`GWC,C           2
Avr II      C`CTAG,G          1     BamH I      G`GATC,C          1
Ban I       G`GYRC,C          5     Ban II      G,RGCY`C          3
Bbe I       G,GCGC`C          2     Bbs I       GAAGAC 8/12       1
Bbv I       GCAGC 13/17       10    Bbv II      GAAGAC 7/11       1
Bcl I       T`GATC,A          1     Bcn I       CC,S`GG           9
Bfa I       C`TA,G            6     Bgl I       GCCN,NNN`NGGC     1
Bgl II      A`GATC,T          1     Blp I       GC`TNA,GC         -
Bpm I       CTGGAG 22/20      2     Bsa I       GGTCTC 7/11       -
BsaA I      YAC|GTR           4     BsaB I      GATNN|NNATC       2
BsaH I      GR`CG,YC          3     BsaJ I      C`CNNG,G          7
BsaW I      W`CCGG,W          5     BseR I      GAGGAG 16/14      -
Bsg I       GTGCAG 22/20      1     BsiC I      TT`CG,AA          1
BsiE I      CG,RY`CG          6     BsiHKA I    G,WGCW`C          6
BsiW I      C`GTAC,G          1     Bsm I       GAATG,C 7         1
BsmA I      GTCTC`/9          2     BsmB I      CGTCTC 7/11       1
BsmF I      GGGAC 15/19       3     BsoF I      GC`N,GC           33
Bsp120 I    G`GGCC,C          1     Bsp1286 I   G,DGCH`C          1
BspH I      T`CATG,A          3     BspM I      ACCTGC 10/14      3
BspM II     T`CCGG,A          1     Bsr I       ACT,GG`           10
BsrB I      GAG|CGG           3     BsrD I      GCAATG, 8         2
BsrG I      T`GTAC,A          1     BssH II     G`CGCG,C          1
BssS I      C`TCGT,G          2     Bst1107 I   GTA|TAC           2
BstB I      TT`CG,AA          1     BstE II     G`GTNAC,C         1
BstN I      CC`W,GG           4     BstU I      CG|CG             13
BstX I      CCAN,NNNN`NTGG    -     BstY I      R`GATC,Y          9
Bsu36 I     CC`TNA,GG         1     Cac8 I      GCN|NGC           24
Cfr10 I     R`CCGG,Y          4     Cla I       AT`CG,AT          2
Csp6 I      G`TA,C            7     Dde I       C`TNA,G           6
Dpn I       GA|TC             17    DpnII       `GATC,            17
Dra I       TTT|AAA           3     Dra III     CAC,NNN`GTG       1
Drd I       GACNN,NN`NNGTC    3     Dsa I       C`CRYG,G          3
Eae I       Y`GGCC,R          7     Eag I       C`GGCC,G          2
Ear I       CTCTTC 7/10       3     Eco47 III   AGC|GCT           2
Eco57 I     CTGAAG 21/19      3     Eco72 I     CAC|GTG           1
EcoN I      CCTNN`N,NNAGG     -     EcoO109 I   RG`GNC,CY         1
EcoR I      G`AATT,C          1     EcoR II     `CCWGG,           4
EcoR V      GAT|ATC           1     Ehe I       GGC|GCC           2
Esp I       GC`TNA,GC         -     Fnu4H I     GC`N,GC           33
Fok I       GGATG 14/18       9     Fse I       GG,CCGG`CC        -
Fsp I       TGC|GCA           2     Gdi II      `YGGC,CG          7
Gsu I       CTGGAG 21/19      2     Hae I       WGG|CCW           6
Hae II      R,GCGC`Y          6     Hae III     GG|CC             15
Hga I       GACGC 9/14        4     HgiA I      G,WGCW`C          6
HgiE II     ACCNNNNNNGGT -1/132      Hha I       G,CG`C            22
HinC II     GTY|RAC           2     Hind II     GTY|RAC           2
HinD III    A`AGCT,T          1     Hinf I      G`ANT,C           8
HinI I      GR`CG,YC          3     HinP I      G`CG,C            22
Hpa I       GTT|AAC           1     Hpa II      C`CG,G            20
Hph I       GGTGA 12/11       5     Kas I       G`GCGC,C          2
Kpn I       G,GTAC`C          1     Mae I       C`TA,G            6
Mae II      A`CG,T            11    Mae III     `GTNAC,           12
Mbo I       `GATC,            17    Mbo II      GAAGA 12/11       7
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Mlu I      A`CGCG,T         1     Mme I      TCCRAC 25/23     2         Rsr II     CG`GWC,CG        1     Sac I      G,AGCT`C         1
Mnl I      CCTC 10/10       18    Msc I      TGG|CCA          2         Sac II     CC,GC`GG         1     Sal I      G`TCGA,C         1
Mse I      T`TA,A           14    Msl I      CAYNN|NNRTG      1         Sap I      GCTCTTC 8/11     3     Sau3A I    `GATC,           17
Msp I      C`CG,G           20    MspA1 I    CMG|CKG          7         Sau96 I    G`GNC,C          6     Sca I      AGT|ACT          1
Mun I      C`AATT,G         1     Nae I      GCC|GGC          2         ScrF I     CC`N,GG          13    Sec I      C`CNNG,G         7
Nar I      GG`CG,CC         2     Nci I      CC`S,GG          9         SfaN I     GCATC 9/13       17    Sfc I      C`TRYA,G         5
Nco I      C`CATG,G         2     Nde I      CA`TA,TG         2         Sfi I      GGCCN,NNN`NGGCC  1     Sma I      CCC|GGG          1
NgoM I     G`CCGG,C         2     Nhe I      G`CTAG,C         1         SnaB I     TAC|GTA          1     Spe I      A`CTAG,T         1
Nla III    ,CATG`           19    Nla IV     GGN|NCC          11        Sph I      G,CATG`C         2     Spl I      C`GTAC,G         1
Not I      GC`GGCC,GC       1     Nru I      TCG|CGA          1         Srf I      GCCC|GGGC        -     Ssp I      AAT|ATT          1
Nsi I      A,TGCA`T         1     Nsp7524 I  R`CATG,Y         6         Stu I      AGG|CCT          1     Sty I      C`CWWG,G         3
NspB II    CMG|CKG          7     NspH I     R,CATG`Y         6         Taq I      T`CG,A           12    Tfi I      G`AWT,C          4
Pac I      TTA,AT`TAA       -     PaeR7 I    C`TCGA,G         1         Tsp45 I    `GTSAC,          6     Tth111 I   GACN`N,NGTC      3
Pal I      GG|CC            15    PflM I     CCAN,NNN`NTGG    1         Tth111 II  CAARCA 16/14     5     Vsp I      AT`TA,AT         1
Ple I      GAGTC 9/10       2     Pme I      CTTT|AAAC        -         Xba I      T`CTAG,A         1     Xca I      GTA|TAC          2
Pml I      CAC|GTG          1     PpuM I     RG`GWC,CY        -         Xcm I      CCANNNN,N`NNNNTGG-     Xho I      C`TCGA,G         1
Psp1406 I  AA`CG,TT         2     PspA I     C`CCGG,G         1         Xho II     R`GATC,Y         9     Xma I      C`CCGG,G         1
Pst I      C,TGCA`G         1     Pvu I      CG,AT`CG         1         Xma III    C`GGCC,G         2     Xmn I      GAANN|NNTTC      2
Pvu II     CAG|CTG          3     Rsa I      GT|AC            7
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