

Product Information

pVQAd RSV K-NpA Shuttle Plasmid

Overview

This shuttle plasmid contains the Rous Sarcoma Virus LTR. Expression levels are very high in most tissues and this promoter is an alternative to the CMV promoter. The multiple cloning site contains 10 unique restriction sites to facilitate subcloning you cDNA of interest.

MCS

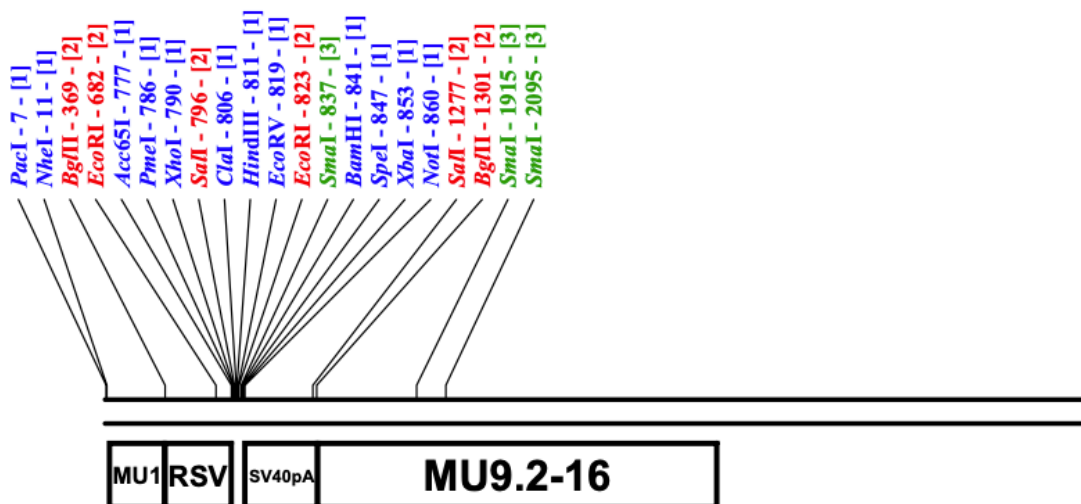
KpnI PmeI XhoI Sall* ClaI HindIII

ACCACATTGGTGTGCACCTCCAAGCTGGTACCGTTTAAACTCGAGGTCGACGGTATCGATAAGCTT

EcoRV EcoRI* PstI* SmaI* BamHI SpeI XbaI NotI SacII*

GATATCGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGAGCGGCCCCACCGCG

Map



pVQAd RSV K-N pA
6081 bp

Sequence

1 AATTAATTAA GCTAGCATCA TCAATAATAT ACCTTATTTT GGATTGAAGC
 51 CAATATGATA ATGAGGGGGT GGAGTTTGTG ACGTGCGCG GGGCGTGGGA

101 ACGGGGCGGG TGACGTAGTA GTGTGGCGGA AGTGTGATGT TGCAAGTGTG
151 GCGGAACACA TGTAAGCGAC GGATGTGGCA AAAGTGACGT TTTTGGTGTG
201 CGCCGGTGTA CACAGGAAGT GACAATTTTC GCGCGTTTT AGGCGGATGT
251 TG TAGTAAAT TTGGGCGTAA CCGAGTAAGA TTTGGCCATT TTCGCGGGAA
301 AACTGAATAA GAGGAAGTGA AATCTGAATA ATTTTGTGTT ACTCATAGCG
351 CGTAATATTT GTCTAGGGAG ATCTGCGATG TACGGGCCAG ATATACGCGT
401 ATCTGAGGGG ACTAGGGTGT GTTTAGGCGA AAAGCGGGGC TTCGGTTGTA
451 GCGGTTAGG AGTCCCCTCA GGATATAGTA GTTTCGCTTT TGCATAGGGA
501 GGGGGAAATG TAGTCTTATG CAATACTCTT GTAGTCTTGC AACATGGTAA
551 CGATGAGTTA GCAACATGCC TTACAAGGAG AGAAAAAGCA CCGTGCATGC
601 CGATTGGTGG AAGTAAGGTG GTACGATCGT GCCTTATTAG GAAGGCAACA
651 GACGGGTCTG ACATGGATTG GACGAACCAC TGAATTCCGC ATTGCAGAGA
701 TATTGTATTT AAGTGCCTAG CTCGATACAA TAAACGCCAT TTGACCATTC
751 ACCACATTGG TGTGCACCTC CAAGCTGGTA CCGTTTAAAC TCGAGGTCGA
801 CGGTATCGAT AAGCTTGATA TCGAATTCCT GCAGCCCGGG GGATCCACTA
851 GTTCTAGAGC GGCCGCCACC GCGGGGAGAT CCAGACATGA TAAGATACAT
901 TGATGAGTTT GGACAAACCA CACTAGAAT GCAGTAAAA AAATGCTTTA
951 TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT TATAAGCTGC
1001 AATAACAAG TTAACAACAA CAATTGCATT CTTTTATGT TTCAGGTTCA
1051 SGGGGAGGTG TGGGAGGTTT TTTAAAGCAA GTAAACCTC TACAAATGTG
1101 GTATGGCTGA TTATGATCCC GGCTGCCTCG CGCGTTTCGG TGATGACGGT
1151 GAAAACCTCT TGACACATGC AGCTCCCGGA GACGGTCACA GCTTGTCTGT
1201 AAGCGGATGC CGGGAGCAGA CAAGCCCGTC AGGGCGCGTC AGCGGGTGT
1251 GCGGGGTGTC GGGGCGCAGC CATGAGGTCG ACTCTAGTCC CCGCGGTGGC
1301 AGATCTGGAA GGTGCTGAGG TACGATGAGA CCCGCACCAG GTGCAGACCC
1351 TGCGAGTGTG GCGGTAACA TATTAGGAAC CAGCCTGTGA TGCTGGATGT
1401 GACCGAGGAG CTGAGGCCCG ATCACTTGGT GCTGGCCTGC ACCCGCGCTG
1451 AGTTTGGCTC TAGCGATGAA GATACAGATT GAGGACTGA AATGTGTGGG
1501 CGTGGCTTAA GGGTGGGAAA GAATATATAA GGTGGGGGTC TTATGTAGTT
1551 TTGTATCTGT TTTGCAGCAG CCGCCGCCGC CATGAGCACC AACTCGTTG
1601 ATGGAAGCAT TGTGAGCTCA TATTTGACAA CGCGCATGCC CCCATGGGCC
1651 GGGGTGCGTC AGAATGTGAT GGGCTCCAGC ATTGATGGTC GCCCGTCTCT
1701 GCCCGCAAAC TCTACTACCT TGACCTACGA GACCGTGTCT GGAACGCCGT
1751 TGGAGACTGC AGCCTCCGCC GCCGTTTCCAG CCGCTGCAGC CACCGCCCGC
1801 GGGATTGTGA CTGACTTTGC TTTCTGAGC CCGTTGCAA GCAGTGCAGC
1851 TTCCCGTTCA TCCGCCCGCG ATGACAAGTT GACGGCTCTT TTGGCAAA
1901 TGGATTCTTT GACCCGGGAA CTTAATGTG TTTCTCAGCA GCTGTTGGAT
1951 CTGCGCCAGC AGGTTTCTGC CCTGAAGGCT TCCTCCCTC CCAATGCGGT
2001 TTAACAATA AATAAAAAAC CAGACTCTGT TTGGATTTGG ATCAAGCAAG
2051 TGTCTTGCTG TCTTATTTA GGGGTTTTGC GCGCGCGGTA GGCCCGGGAC
2101 CAGCGGTCTC GGTGTTGAG GGTCTGTGT ATTTTTTCCA GGACGTGGTA
2151 AAGGTGACTC TGGATGTTCA GATACATGGG CATAAGCCCG TCTCTGGGGT
2201 GGAGGTAGCA CACTGCAGA GCTTCATGCT GCGGGGTGGT GTTGTAGATG
2251 ATCCAGTCGT AGCAGGAGCG CTGGGCGTGG TGCCTAAAAA TGTCTTTCAG
2301 TAGCAAGCTG ATTGCCAGGG GCAGGCCCTT GGTGTAAGTG TTTACAAAGC
2351 GGTTAAGCTG GGATGGGTGC ATACGTGGGG ATATGAGATG CATCTTGGAC
2401 TGTATTTTGA GTTTGGCTAT GTTCCAGCC ATATCCCTCC GGGGATTCAT
2451 GTTGTGCAGA ACCACCAGCA CAGTGTATCC GGTGCACTTG GGAAATTTGT
2501 CATGTAGCTT AGAAGGAAAT GCGTGGAAGA ACTTGAGAC GCCCTGTGA
2551 CCTCAAGAT TTTCCATGCA TTCGTCCATA ATGATGGCAA TGGGCCACG
2601 GCGGCGGCC TGGGCGAAGA TATTTCTGGG ATCACTAACG TCATAGTTGT
2651 GTTCCAGGAT GAGATCGTCA TAGGCCATTT TTACAAAGCG CGGGCGGAGG
2701 GTGCCAGACT GCGGTATAAT GGTTCATCC GGCCAGGGG CGTAGTTACC
2751 CTCACAGATT TGCATTTCCC ACGTTTGGT TTCAGATGGG GGGATCATGT
2801 CTACCTGCGG GCGGATGAAG AAAACGGTTT CCGGGGTAGG GGAGATCAGC
2851 TGGGAAGAAA GCAGTTTCT GAGCAGCTGC GACTTACCGC AGCCGGTGGG
2901 CCCGTAAATC ACACCTATTA CCGGGTCAA CTGGTAGTTA AGAGAGCTGC
2951 AGCTGCCGTC ATCCCTGAGC AGGGGGGCCA CTCGTTAAG CATGTCCTG

3001 ACTCGCATGT TTTCCCTGAC CAAATCCGCC AGAAGGCGCT CGCCGCCAG
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3101 CCGCCGTAGG CATGCTTTTG AGCGTTTGAC CAAGCAGTTC CAGGCGGTCC
3151 CACAGCTCGG TCACCTGCTC TACGGCATCT CGATCCAGCA TATCTCCTCG
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3351 GTGCGCTTGA GGCTGGTCTT GCTGGTGCTG AAGCGCTGCC GGTCTTCGCC
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