

Gene barK

ATGTAGAGGACCGACGGGGAAACCCCTGGACATAGGGGAATCCCGTCTGTTCCGGACTAGCTATTAAAGC
M * R T D G E T L D I G N P V V R T S Y * S

1,800 1,808 1,816 1,824 1,832 1,840 1,848 1,856 1,864

AGACCCACCTCGTTACGTCCACGGCACGAGGAATGATCTCGAGTTGCTTTGCTCGTGCCAAATACG
R P T S L R P R

1,872 1,880 1,888 1,896 1,904 1,912 1,920 1,928

AGGCCGGCTCAGCAACCTGGTTTAAAGTGGAACATACACCGGCAGCTAACCAACGGTGACGAGAGT
R P A Q Q P G L

1,936 1,944 1,952 1,960 1,968 1,976 1,984 1,992

GACTCTATGTCGCTGGACCGGCAGTGGCTTCGTTTCTAACGCGATCATACCGCTGCCACCGGTTGG

2,000 2,008 2,016 2,024 2,032 2,040 2,048 2,056 2,064

TACGAAGGAACCCAGCGATCTCAAACCATGTCATTGTCGTCTTGAATTATGCCTTTATGGAAACCA

2,064 2,072 2,080 2,088 2,096 2,104 2,112 2,120 2,128

BamHI site

AACTAAGAGTCTGTAATAGACATCAATCGACCACGGAGGAGGCCGTCGTAGTGGCCGGGCTTTATT

2,136 2,144 2,152 2,160 2,168 2,176 2,184 2,192

ACCGGAAAGGGTACCTTATCGAGTCATGAGGTATGGAGAAATAGGTCTCAAATGGCCTAAAAGCA

2,200 2,208 2,216 2,224 2,232 2,240 2,248 2,256

Gene kanR

GAACATCATGTGATTCACTTCATTTATAAGGAATTGCCGAACACCGCCTAAGCTAGCTATGCTGAA

2,264 2,272 2,280 2,288 2,296 2,304 2,312 2,320 2,328

Gene kanR

TGCGACTCACCATAACACGCTGTCTATTTGATGATGCGTCGTGTGACTCGGGCCGCGCGCACCAA

2,328 2,336 2,344 2,352 2,360 2,368 2,376 2,384 2,392

Gene kanR

GGACGGACAAATTCGACAATCCTGTTGATCGCCGGGGCGCAATACATGTTGACGAATTGGCTTGAC

2,400 2,408 2,416 2,424 2,432 2,440 2,448 2,456

Gene kanR

AAGACCCATCGATTAGAGAAAGGAGGTAGCGGAATAACATAAGCCGACGTATCTGTGCACGGTAA

2,464 2,472 2,480 2,488 2,496 2,504 2,512 2,520

Gene kanR

CATCTGAAAGCGTTGTTCTGTAGGCCAACCCAGGGTAAAATGACATGATAAACCACTACCATCG

2,528 2,536 2,544 2,552 2,560 2,568 2,576 2,584 2,592

ATGTTCGAAGACAGGTTAATATATACTTTCTGCGGCTTAGTCAGCTGCGGCAGACAGTGCTATGGG

2,592 2,600 2,608 2,616 2,624 2,632 2,640 2,648 2,656

CGTACATTCTATGACACCTAACAAACACGCGCCATAATGCGCTGGCACCGGTCAAATCTGAAACG

2,664 2,672 2,680 2,688 2,696 2,704 2,712 2,720

CACGGCGTCCATCCACGCTGCCGCT

2,728

2,736

2,744