
1 10 20 30 40 50 60
GELK01048600.1 GCAGGTTGTTTGTTTCTTTGACCAACGATGGCTTTGAAGAGGCCATCAGGGAAAGCAGCA
DVNP1_sequenced ....
70 80 90 100 110 120
GELK01048600.1 CCAGCAATGAAGGACAGTTCCAAGGCGGCCATGAAACCCAGCATGAAGGGGAAGAAACCG
DVNP1_sequenced ....TGAAGGGGAAGAAACCG
130 140 150 160 170 180
GELK01048600.1 AGCGCAATTGCCAGAGGAAGCCGCATGTACGCGGCTGTGTTCTCGGGCAGGAAGGAGAAG
DVNP1_sequenced AGCGTCATCGCCAGAGGAAGTCGCATGTACGCGGTTGTGTTCTCGGGCAGGAAGGAGAAA
190 200 210 220 230 240
GELK01048600.1 ACGTACACGGGCTTGACCAAGTCGGACCTCCAACGCAATTCCTACAACCGTATTGTTTCG
DVNP1_sequenced ACGTACACGGGCTTGACCAAGTCTGACCTTCAACGCAATTCCTACAACCGCATTGTTTCG
250 260 270 280 290 300
GELK01048600.1 AAACGGCGATCGGCGCTCGCCAAGAAGCGGTACCAGGGGAGCCGGTTCCAACGGTGGATC
DVNP1_sequenced AAACGTCGATCGGCGATTTCCAAGAAGCGGTACCAGGGGAGCCAGTTCCAACGGTGGATC
310 320 330 340 350 360
GELK01048600.1 CAGGCGGCTGCTGTTGCGCGGAAGGAGCTCAATGTGACCGGCTTCGTGGCGGTGAATTCG
DVNP1_sequenced CAGGCGCTTGCAGTTGCGCGGAAAGAGCTCAATTTGACCAGCTTCGTGGCGGTGAATTCG
370 380 390
GELK01048600.1 TCCAGTGTTCAGGGGAGGGCTTTGTTCTCGAAAGCCC
DVNP1_sequenced TCGACTGTGCAGGGGAGGGCTTTGTTCTCGAA.....