





2401 AATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAG

2501 CTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGA  
141 • N R T Y K L P I L E E I T T K V L K G N M E I L V F C D P

2601 GCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGG  
110 A Y D S I L E R C M G C P S V V R I S R D V E D S Y P H R V A V I T

2701 TGTCAAAGTCCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGA  
77 D F D K Q G N S V A S G I A I A E A C V T V R G I Y A E I H V A S

2801 GATGATCTCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCC  
44 I I E G T K T R I A A G V H H K N D E Y L M T I K E T A V E V L E

2901 AGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAAA  
10 L D Q Q S I N F T K M

3001 CAGCGTGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATG

3101 GGGCGGAGTTGTTACGACATTTTGAAAGTCCCCTGATTACTAGTCAAAACAACTCCCATGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGA  
SpeI (3141)

3201 GTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCC  
SnaBI (3269)

3301 CATAAGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCA  
NdeI (3374)

3401 AGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACGTCAATGGGG

3501 GGGGTCGTTGGGCGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA  
SdaI (3552) BspLU11I (3570)

3601 GGAACCGTAAAAAGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAGAGGTGGCGAAACCC  
PacI (3560)

3701 GACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTTCTC  
BspLU11I (3570)

3801 CCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCCG

3901 TTCAGCCCAGCGCTGCGCTTATCCGTAACATATCGTCTTGAGTCCAACCCGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGAT

4001 TAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTG

4101 AAGCCAGTTACCTTCGGAAGAGTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGC

4201 GCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCATGGCTAG

EagI (4320)

PacI (4300) SwaI (4309) NotI (4319)

4301 TTAATTAACATTTAATCAGCGCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACATAACGCTCTCC

4401 ATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTATCGAA