



1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

BspLU11I (560)

Agel (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTTTTCCCTGGCCAGGAGGAACACTGCGCCCCAA
137 M F S P G Q E E H C A P N
601 TAAGGAGCCAGTAAATACGGGAGCTGGTGGTGTCTCGGTACAATGGTGCTTTACCAATGGAGATAGAGGACGGAGAAAAGTAGATTTGCCCTCTAC
137 K E P V K Y G E L V V L G Y N G A L P N G D R G R R K S R F A L Y
701 AAGCGCCCAAGGCAAATGGTGTCAAACCCAGCACCGTCCATGTGATATCCACGCCCCAGGCATCAAAGGCTATCAGCTGCAAAGGTCAACACAGTATAT
47 K R P K A N G V K P S T V H V I S T P Q A S K A I S C K G Q H S I
801 CCTACACTTTGTAAGGAATCAGACTGTGGTGGTGGAGTACACACATGATAAGGATACGGATATGTTTCAGGTGGGAGATCAACAGAAAAGCCCTATCGA
80 S Y T L S R N Q T V V V E Y T H D K D T D M F Q V G R S T E S P I D
901 CTTGTTGTACAGACACGATTTCTGGCAGCCAGAACACGGACGAAGCCAGATCACACAGAGCACCATATCCAGGTTTCGCTGCAGGATCGTGTGCGAC
113 F V V T D T I S G S Q N T D E A Q I T Q S T I S R F A C R I V C D
1001 AGGAATGAACCTTACACAGCAGGATATTCGCCGCCGATTGACTCTCCAAAAACATATTTCTGGAGAAAAGGCAGCAAAGTGGAAAAACCCCGACG
147 R N E P Y T A R I F A A G F D S S K N I F L G E K A A K W K N P D
1101 GCCACATGGATGGGCTACTACTAATGGCGTCTGGTGTGATCCACGAGGGGGTTCACCGAGGAGTCCCAGCCGGGGTCTGGCGCGAGATCTCTGT
180 G H M D G L T T N G V L V M H P R G G F T E E S Q P G V W R E I S V
1201 CTGTGGAGATGTGTACACCTTGCAGAAACAGGTCCGCCAGCAACGAGGAAAGTGGTGGAAAGTGAGACCAACGCTCTGCAGGACGGCTCCCTCATT
213 C G D V Y T L R E T R S A Q Q R G K L V E S E T N V L Q D G S L I
1301 GACCTGTGTGGGCCACTCTCTCTGGAGAACAGCAGATGGGCTTTTTCACTCCAAGTCAAGACATAGAAGCCCTCCGGCAGGAGATTAACGCCG
247 D L C G A T L L W R T A D G L F H T P T Q K H I E A L R Q E I N A
1401 CCCGGCTCAGTGTCTGTGGGCTCAACACCTGGCCTTCCCGAGCATCAACAGGAAAGAGTGGTGGAGGAGAAGCAGCCCTGGGCATATCTCAGTTG
280 A R P Q C P V G L N T L A F P S I N R K E V V E E K Q P W A Y L S C
1501 TGGCCACGTGCACGGGTACCACAACCTGGGGCCATCGGAGTGACACGGAGGCAACGAGAGGGAGTGTCCCATGTGCAGGACTGTGGGCCCTATGTGCT
313 G H V H G Y H N W G H R S D T E A N E R E C P M C R T V G G P Y P
1601 CTCTGGCTGGTGTGAGGACGATTTATGTAGACGAGACCGCAACTCATGCTTTCACTCCCTGTGGACAGTGTCTCGGAGAAAGTGTGCAAAAT
347 L W L G C E A G F Y V D A G P P T H A F T P C G H V C S E K S A K
1701 ACTGGTCTCAGATCCCGTTCCTCATGAACTCATGCATTTACGCTGCTTCCCTTTCTGTGCTACACAGCTGGTGGGGAGCAAACCTGCATCAAAT
380 Y W S Q I P L P H G T H A F H A A C P F C A T Q L V G E Q N C I K L

NheI (1845)

1801 AATTTTCCAAGGTCCAATTGACTGACGCCCTTGACAGCCATCTACGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACA
413 I F Q G P I D •
1901 GAATGCAGTGAACAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGTCGAATAACAAGTTAACAAACA
2001 CATTCAATTTATGTTTCAGGTTCAAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAG
2101 CAAAACTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCATTAGCTGTT
2201 TGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCAAAGTTTGAAGTCTTTCATTTCTTTATGTTTTAAATGCAGTACCTCCC
2301 ACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCT
2401 TCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTCTGGT
141 • N R T
2501 GACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCT
137 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 A Y D S I L E
2601 CTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGT
103 R C M G C P S V R I S R D V E D S Y P H R V A V I T D F D K Q G N
2701 TGCTCACAGCAGCCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCGCTTGGT
70 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 I I E G T K T
2801 CCTGATGGCCGCCCGACATGGTGTGTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGCAGCTCCACCAGTCCAGATCCTGCTGAGAGATGTTG
37 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 L D Q Q S I N
2901 AAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCTCTCCAG
3 F T K M
3001 CTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATT
3101 TTGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGGAGTCAAACCGCTATCCACGCC

3201 ATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAAAACCGCATCATGTACTGGGCA
3301 TAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAAT
3401 ACTCCACCCATTGACGTCAATGGAAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCC
BspLU11I (3549)
3501 AGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGCT
3601 TGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCA
3701 GCGGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTT
3801 TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCT
3901 TATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAACAGGATTAGCAGAGCGAGGTATGTAGG
4001 CCGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAA
4101 AGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAG
4201 AAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGC
4301 GCGCGCAATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAA
4401 ACAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA