



1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTTCACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BspLU111 (560)

Agel (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCAACATGTTGAAACTATTATTGTACCTAGATCCTTCTTAGT  
1 M L K L L L S P R S F L V  
601 CCTTCAGTGCTCCTGCTGAGGGCAGGGTGGAGCTCCAAGTCTCATGTCCAGTGCAGTGAAGACATCAAAGCTGATTTGATCCTGACTTCTACAGCC  
13 L Q L L L L R A G W S S K V L M S S A N E D I K A D L I L T S T A  
701 CCTGAACACCTCAGTGCTCCTACTCTGCCCTTCCAGAGGTTCAAGTGTCTTGTGTTCAACATAGAGTACATGAATTGCACTTGAATAGCAGTTCTGAGC  
47 P E H L S A P T L P L P E V Q C F V F N I E Y M N C T W N S S S E  
801 CTCAGGCAACCAACCTCAGCTGCACATAGGTACAAGTATCTGATAATAATACATTCAGGAGTGCAGTCACTATTTGTTCTCAAAGAGATTACTTC  
80 P Q A T N L T L H Y R Y K V S D N N T F Q E C S H Y L F S K E I T S  
901 TGGCTGTGAGATACAAAAAGAAGATATCCAGCTCTACCAGACATTTGTTGTCCAGCTCCAGGACCCCCAGAAAACCCAGAGGCGAGCTGTACAGAAGCTA  
113 G C Q I Q K E D I Q L Y Q T F V V Q L Q D P Q K P Q R R A V Q K L  
1001 AACCTACAGAATCTTGATCCCACGGGCTCCAGAAAATCTAACACTCAGCAATCTGAGTGAATCCCAGCTAGAGTGTGAGTGAAGGAGCAGACATATTA  
147 N L Q N L V I P R A P E N L T L S N L S E S Q L E L R W K S R H I  
1101 AAGAACGCTGTTTACAATACTTGGTGCAGTACCGGAGCAACAGAGATCGAAGCTGGACGGAACATAAGTGAATCATGAACCTAGATTTCTCCCTGCCTAG  
180 K E R C L Q Y L V Q Y R S N R D R S W T E L I V N H E P R F S L P S  
1201 TGTGGATGAGTGAACGGTACACATTTCCGGTTCGGAGCCGCTATAACCAATCTGTGGAAGTTCTCAACAGTGGAGTAAATGGAGCCAGCCTGTCCAC  
213 V D E L K R Y T F R V R S R Y N P I C G S S Q Q W S K W S Q P V H  
1301 TGGGGGAGTCATACTGTAGAGGAGAATCCTTCTTGTGTTGCACTGGAAGCTGTGCTTATCCCTGTTGGCACCATGGGGTTGATTATTACCCTGATCTTTG  
247 W G S H T V E E N P S L F A L E A V L I P V G T M G L I I T L I F  
1401 TGTAAGTGTGGTGAACGAATGCTCCAATCCCCCATCAAGAATCTAGAGGATCTGGTACTGAATACCAAGGGAACCTTTCCGCTGGAGTGGTGT  
280 V Y C W L E R M P P I P P I K N L E D L V T E Y Q G N F S A W S G V  
1501 GTCTAAAGGGCTGACTGAGAGTCTGCAGCCAGACTACAGTGAACGGTCTGCCACGTGAGGAGATTTCCCCCAAAGGAGGGGCCCTAGGAGAGGGGCCCT  
313 S K G L T E S L Q P D Y S E R F C H V S E I P P K G G A L G E G P  
1601 GGAGTTCTCCTCAGCCTGCATAGCCCTTACTGGCTCCCCATGTTATTCTCTGAAGCCGGAAGCCTGAACATCAATCCTTTGATGGAACCTGAAAG  
347 G G S P C S L H S P Y W P P P C Y S L K P E A •

NheI (1701)

1701 TGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCT  
1801 ATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGGAGGTGTGGGAGGTTT  
1901 TTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTC  
2001 TGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTT  
2101 TCCAAGTGTGAACTAGCTCTTCATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCTTTTATGTAATAATTCAGAAATAATTTAAATACAT  
2201 CATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGG  
2301 AACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTTCTCAATGGTGGTTTTGACCAGCT  
141 • N R T Y K L P I L E E I T T K V L K  
2401 TGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGCCAC  
122 G N M E I L V F C D P A Y D S I L E R C M G C P S V V R I S R D V  
2501 CTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACAGACAGTG  
89 E D S Y P H R V A V I T D F D K Q G N S V A S G I A I A E A C V T  
2601 ACCCTGCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGCTCATAGAGCA  
55 V R G I Y A E I H V A S I E G T K T R I A A G V H H K N D E Y L M  
2701 TGGTATCTTCTCAGTGGCAGCTCCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGATTATACTA  
22 T I K E T A V E V L E L D Q Q S I N F T K M  
2801 TGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAACGAGCTCTGCTTATATAGACCTC  
2901 CCACCGTACACGCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGTTTACTAGTCAAAACAAACTCCCATTG  
3001 ACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGA  
3101 CTAATACGTAGATGTAAGTGGAAAGTCCATAAGGTCATGTAAGTGGCATAATGCCAGGCGGGCCATTTACCGTCAATTGACGTCAATAGGGGG

3201 CGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACT  
3301 ATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCCTGCAGGTTAAT  
BspLU11I (3405)  
3401 TAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAC  
3501 AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGA  
3601 CCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGGTAGGTCGT  
3701 TCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC  
3801 TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACA  
3901 CTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAG  
4001 CGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA  
4101 GAAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTATTACATCTGTGTGTTGG  
4201 TTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGAAGTGCAGGTGCC  
4301 AGAACATTTCTCTATCGAA