



2501 TTTTCTGCCAGGTTGGCTACCCAGGCTACTGCTAAGACTCGTACTTCCAGTTTGGTGTGGGCGAGCTTTCAGACTCCATCCTCCTTACAGTCCATGTCCC
647▶ F S A Q V A T Q A T A K T R T S Q F G V G S F Q T P S S F S S M S
2601 TCCTGGTGCCCCAATGCATCGCCTGGTGTCTGCTACCCTAGTCTACCAATCGTGGATCTAACTTTGCTCCTGAGACTGGACAGACTGCAGGACA
680▶ L P G A P T A S P G A A A Y P S L T N R G S N F A P E T G Q T A G Q
BspLU11I (2787)
2701 ATTCCAGACACGGACAGCAGAGGGTGTGGTGTCTGGCCACAGTGGCAGGGCCAGCAGCCTCATCATCGTTCAAGTTCTAGTGAGCAACATGTTCAACAA
713▶ F Q T R T A E G V G V W P Q W Q G Q Q P H H R S S S S E Q H V Q Q
Bsu36I (2824)
2801 CCGCCAGCACAGCAACCTGGCCAGCCTGAGGTCTCCAGGAGATGCTGTCCATGCTGGGAGATCAGAGCAACAGCTACAACAATGAAGAATCCCTGATC
747▶ P P A Q Q P G Q P E V F Q E M L S M L G D Q S N S Y N N E E F P D
NheI (2954)
2901 TAACTATGTTTCCCCCTTTTCCAGAATAGAATATTGGGGTGAGGATAAGGGGTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAA
780▶ L T M F P P F S E • N
HpaI (3092)
3001 CCACAAC TAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAACAA
MfeI (3103)
3101 CAACAATTGCATTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAAT
3201 ACAGCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTGCCAATGTGCA
SapI (3370)
3301 TTAGCTGTTTGCAGCCTCACCTCTTTTCATGGAGTTAAGATATAGTGATTTTCCCAAGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCAC
SspI (3427) SwaI (3441)
3401 TGACCTCCACATTCCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAAATAATGTTTTTTATTAGGCAGAATCCAGATGCT
EcoO109I (3502)
3501 CAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTA
141 ◀ •
3601 GTTCTGGTGTACTTGTAGGGGATGAGTTCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAG
140◀ 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 A Y D S
BstXI (3731)
3701 ATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCT
106◀ 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 D F D K
StuI (3866)
3801 TCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCC
73◀ 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 I I E G
3901 AGTCTTGGTCTGATGGCCGCCCGACATGGTGTCTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGA
40◀ 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 L D Q Q
XmnI (4008) AseI (4074)
4001 GAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGG
6◀ S I N F T K M ◀
4101 CGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGT
SpeI (4229)
4201 TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCGTGAGTCAAACCGCTA
SnaBI (4357)
4301 TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATG
NdeI (4462)
4401 TACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGTACTGCCAAGTGGGCAGTTT
4501 ACCGTAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCTGTTGGG
PacI (4648)
4601 CGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAA
SdaI (4640) BspLU11I (4658)
4701 AGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA
4801 AAGATACCAGGCGTTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGC
ApaLI (4972)
4901 GTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGCTCCAGCTGGGCTGTGTGCACGAACCCCGTTTCAGCCCGACC
5001 GCTGCGCCTTATCCGGTAACTATCGTCTTGTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG

5101 GTATGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC

5201 TTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAG

5301 GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATT

EagI (5408)

NotI (5407)

5401 TAAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAA

5501 CGAAACAAAACAAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA