



100
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1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
 101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
 301 GCCATCCACGCCGTTGAGTCCGCTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
 401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

SphI (560)
AgeI (552)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGTCAGCATGCAGAGCTCCACAGCGTCTTATTCTGTGCTCAC
 601 GGTCACTTCTTACCTCCAGGTGCTGGCTCACCCAGGCTCCATCCCAACTCTGTGCTTATCATGACCAGTAAGAAGATCCCCAACACACTACTG
 13▶ V T S F T S Q V L A H P G S I P T S C C F I M T S K K I P N T L L
 701 AAGAGCTACAAAAGAATCACCAACAACAGATGCACCCTGAAAGCCATAGTCTTCAAGACCAGTTGGGCAAAGAGATCTGTGCTGACCCCAAGAAGAAGT
 47▶ K S Y K R I T N N R C T L K A I V F K T R L G K E I C A D P K K K

NheI (888)

801 GGTCCAGGATGCCACAAAGCACCTGGACAAAACTCAAACCTCAAACACCATAAACCAACCTCCTCTTGTGACTAACCCAGAGCCCTAGCTGGCCA
 80▶ W V Q D A T K H L D Q K L Q T P K P •
 901 GACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTG

1001 TAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTA
 1101 AAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATA
 1201 AGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGATTTTCCCAAGGTTTGA
 1301 ACTAGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAA
 1401 ATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTAAATAGA
 1501 AATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTC

1601 AATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAG
 118▶ 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 E D S Y
 1701 GGGTCCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTCAGCACAGACAGTACCCTGCCAATGT
 84▶ 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 V R G I Y
 1801 AGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTGGTCTGTGCGCCCGGACATGGTGTCTGTTGCTCCTCATAGAGCATGGTATCTTCTC
 51▶ A E I H V A S 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
 1901 AGTGGCGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTTCATGGTGGCCCTCTATAGTGAGTCTATTATACTATGCCGATATACTA
 18▶ T A V E V L E L D Q Q S I N F T K M

2001 TGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGC
 2101 CTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGT

2201 GGAGACTTGAAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGAT
 2301 GTACTGCCAAGTAGGAAAGTCCCATAGGTCATGACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATA
 2401 TGATACACTTGATGACTGCCAAGTGGGCGATTACCGTAAATACTCCACCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACG
 2501 TCATTATTGACGTCAATGGGCGGGGCTGTTGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGA
 2601 GCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCT

2701 CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCGTGAAGCTCCCTCGTGGCTCTCTGTTCCGACCCTGCCGCTTAC
 2801 CGGATACCTGTCCGCTTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTGCTCCAAGCTG
 2901 GGCTGTGTGCACGAACCCCGTTCCAGCCGACCGTGGCGCTTATCCGGTAACTATCGTCTTGTGAGTCAACCCGGTAAGACACGACTTATCGCCACTGG
 3001 CAGCAGCCACTGTTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGT
 3101 ATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAACAACCCACCGTGGTAGCGGTGGTTTTTTT

3201 GTTTGAAGCAGCAGATTACGCCGAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAACTCACGTT
3301 AAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAA
3401 TCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCT
3501 ATCGAA