



BstEII (2604) SalI (2638) SfiI (2697)
2601 GGCTGGTCACCCTACCGGAGCCGGGAGCCGGGGCGGCTCGACTACCAGCTGCTGACCTTGGCCCTGCTGACGGTCAACCGCTGCTGGTGCTCCTGGC
680▶ G L V T L P E A G S R G G V D Y Q L L T L A L L T V N A L L V L L A
BspLU11I (2780)
2701 CTTGGCGGCTGGGCGTCTCGCTGGCTGCGTAGAACTGCGGGCTAGCGGAAAGGGCGGGCCCCGGTCCACGTTCCGGCACATGACTCCACCCGACGG
713▶ L A A W A S R W L R R K L R A R R K G G A P V H V R H M Y S T R R
NcoI (2810) SgrAI (2817) DraIII (2868)
2801 CCCCTGCGCTCCATGGGACCGGCGTGTCCGCCGACTTCTCGGGATTCCAGTCGCACCGGCCACGCACCACCGTGTGCGCGCTCAGTGAGGCGGACCTCA
747▶ P L R S M G T G V S A D F S G F Q S H R P R T T V C A L S E A D L
EcoRI (2902) Tth111I (2992)
2901 TCGAATTCCTCCGACCGCTTTCATGGACAGTCGCGGGCGGCGCGGGCGGCGAGCCTGAGACGGGAGACCGTCTCCTGCAGCGATTTCGCCGACTAGGT
780▶ I E F P C D R F M D S A G G G A G G S L R R E D R L L Q R F A D •
MseI (3025) NheI (3019)
3001 CCAGGGCATATAGAGACCAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATT
HpaI (3157) MfeI (3168)
3101 TGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACCAATTGCATTCATTTTATGTTTCAGGTTTCAGG
EcoRI (3253)
3201 GGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTTAACTCCAAATCAAGCC
3301 TCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGT
SspI (3492)
3401 TTAAGATATAGTGTATTTTCCCAAGTTTGAAGTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATAGTAAATATTCA
SwaI (3506)
3501 GAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTT
3601 GGACTTAGGGAACAAAGGAACCTTTAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGGAGGGGATGAGTTCCTCAA
141▶ • N R T Y K L P I L E E I
3701 TGGTGGTTTTGACCAGTTGCCATTCTCAATGAGCACAAAGCAGTCAGGACATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGACCC
128▶ T T K V L K 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
3801 CCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATG
95▶ 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 S V A S G I A I
3901 GCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGT
61▶ 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 R I A A G V H H K
XmnI (4073) BspHI (4081)
4001 TGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGATGGCCCTCCTATA
28▶ N D E Y L M T I K E T A V E V L E L D Q Q S I N F T K M
AseI (4139)
4101 GTGAGTCGTATTATACTATGCGGATATACTATGCGGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCCTAAACGAG
SpeI (4294)
4200 CTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTA
4299 G TCAAAACAAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGTATCCACGCCATTGATGTACTGCCAAAACCGCA
SnaBI (4422)
4398 TCATCATGGTAATAGCGATGACTAATACGTAGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACC
NdeI (4527)
4498 GTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGG
4598 AAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTT
SdaI (4705) PacI (4713) BspLU11I (4723)
4698 ATGTAACGCCCTG CAG G TT AA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGC
4796 TCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTTTTCCCTGGAAAGCTC
4896 CCTCGTGGCTCTCTGTTCCGACCCTGCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGG
ApaLI (5037)
4996 TATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCAGCAACCCCGTTTCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTG
5096 AGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTTGAA
5196 GTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCC
5296 GGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTA
PacI (5453) SwaI (5462) NotI (5472)
5396 CGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTT
5495 ATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCT
5595 GTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA