





I M T H L G P H L N I V N L L G A C T K S G P I Y I I T E Y C F Y

**BspHI (2639)**

2601 GGGATTTGGTCAACTACTTGCATAAAGAACAGAGATAGCTTCATGAGCCAACCCAGAGAAGCCGAAGAAAGACCTGGACATCTTTGGATTGAATCCTGC  
680▶ G D L V N Y L H K N R D S F M S Q H P E K P K K D L D I F G L N P A  
2701 AGACGAGAGCACAAAGAAGTTATGTGATTTTGTCTTTGAAAATAACGGCGACTACATGGACATGAAGCAAGCTGATACCACACAGTATGTCCCATGCTT  
713▶ D E S T R S Y V I L S F E N N G D Y M D M K Q A D T T Q Y V P M L  
2801 GAAAGGAAAGAGGTTTCTAAATACTCTGACATCCAGAGATCGCTGTACGATCGGCCAGCTCCTACAAGAAGAAATCCATGCTAGACTCAGAAGTCAAAA  
747▶ E R K E V S K Y S D I Q R S L Y D R P A S Y K K K S M L D S E V K

**XhoI (2969)**

**BstBI (2991)**

2901 ACCTCCTTTCCGGACGATGACTCCGAGGGTCTGACTTTGCTGGATCTATTGAGCTTCACCTATCAAGTTGCTCGAGGAATGGAATTTTTGGCTTCGAAAAA  
780▶ N L L S D D D S E G L T L L D L L S F T Y Q V A R G M E F L A S K N

**BglIII (3059)**

3001 TTGTGTCCACCGGACCTGGCTGCCCGCAACGCTCCTCCTGGCGCAAGGAAAAATTGTGAAGATCTGTGATTTTGGCCTGGCCAGACATCATGCACGAT  
813▶ C V H R D L A A R N V L L A Q G K I V K I C D F G L A R D I M H D

**ScaI (3121)**

3101 TCCAACACTCGTGTCAAAAGGCGACTTTTCTGCTGTGAAGTGGATGGCACCCGAGAGCATCTTCGACAACCTCTACACCACGCTGAGTGACGTCTGGT  
847▶ S N Y V S K G S T F L P V K W M A P E S I F D N L Y T T L S D V W  
3201 CCTATGGCATTCTGCTCTGGAAATCTTTCCCTTGGTGGCACACCCATCTGCGCATGATGGTGCATTCTACTTTCTACAATAAGATCAAGAGTGGATA  
880▶ S Y G I L L W E I F S L G G T P Y P G M M V D S T F Y N K I K S G Y  
3301 CCGGATGGCCAAACCTGACCATGCCACCAGTGAAGTCTATGAGATCATGGTGCAGTGTGAAACAGTGAAGCCGAGAAGAGACCCTCCTTCTACCACCTC  
913▶ R M A K P D H A T S E V Y E I M V Q C W N S E P E K R P S F Y H L

**SphI (3497)**

3401 AGCGAGATAGTGGAGAACCTGTTGCCGGGACAATAAGAAGATTGAAAAGATTCACCTGGACTTCTAAAGAGTGACCATCCAGCCGTGGCACGCA  
947▶ S E I V E N L L P G Q Y K K S Y E K I H L D F L K S D H P A V A R

**Eco47III (3598)**

3501 TCGGGTGGACTCTGATAATGCGTACATCGGTGTCACTTACAAAAATGAAGAGATAAGCTGAAGACTGGGAAAGTGGCCTGGACGAACAGAGACTGAG  
980▶ M R V D S D N A Y I G V T Y K N E E D K L K D W E S G L D E Q R L S  
3601 CGCTGACAGTGGCTACATCATCCCCCTGCCAGACATTGACCTGTTCCAGAGGAGGAAGACCTGGGCAAGAGGAACAGACACAGCTCACAGACTTCGGAA  
1013▶ A D S G Y I I P L P D I D P V P E E E D L G K R N R H S S Q T S E  
3701 GAGAGTCCATCGAGACAGGTTCCAGTAGTTCACCTTCATCAAGAGAGAGGACGAGACCATCGAGGACATCGACATGATGGATGACATTGGTATAGATT  
1047▶ E S A I E T G S S S S T F I K R E D E T I E D I D M M D D I G I D  
3801 CCTCGGACCTGGTGGAGGACAGCTTCTGTAAGTACACGCTCCGGGTATCATCTTCTCCGGGAGCCTCCTCGGGATAACCTTAAGAAAACCACTTCATT  
1080▶ S S D L V E D S F L •

**NheI (3937)**

3901 GCAATGCAAAAGTTGAGAAGAGGACTTGGGTGATGTGGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAG

**HpaI (4075) MfeI (4086)**

4001 TGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAATGCATTCATT

4101 TTATGTTTCAGGTTCCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAAACTT

4201 TAACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCT

**SapI (4353)**

4301 CACCTTCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAACAGTCTTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCC

**SspI (4410) SwaI (4424)**

4401 TTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATA

4501 TCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTTCTGGTGTACTTGA

4601 GGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACAT

4701 GCCACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCTGACAGCCACAATGGTGTCAAAGTCCCTCTGCCGTTGCTCACA

**StuI (4849)**

4801 GCAGACCAATGGCAATGGCTTCAGCACAGACAGTACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGG

4901 CCGCCCCGACATGGTCTTGTTCCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTT

**AseI (5057)**

5001 CATGGTGGCCCTCTATAGTGTGATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTG

5101 ACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTACCGCCATTTCGCTCAATGGGCGGAGTTGTTACGACATTTTGGAAAG

**SpeI (5212)**

5201 TCCCGTTGATTTACTAGTCAAAACAACTCCATTGACGTCAATGGGTGGAGACTTGAAATCCCGTGAGTCAAACCGCTATCCACGCCATTGATGT

**SnaBI (5340)**

5301 ACTGCCAAACCGCATCATCATGTAATAGCGATGACTAATACGTAGATGACTGCCAAGTAGGAAAGTCCCATAGGTCATGTAAGTGGGCATAATGCCA

**NdeI (5445)**

5401 GGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACC

5501 CATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGC

**PacI (5631)**

**SdaI (5623)**

**BspLU11I (5641)**

5601 CATTACCGTAAGTTATGTAACGCTGCAGGTTAATAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCG

5701 TTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTC

5801 CCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAG

**ApaLI (5955)**

5901 CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTTATCCGGT

6001 AACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA

6101 CAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACCTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGG

6201 TAGCTCTTGATCCGGCAAACAACCCAGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCT

**EagI (6391)**

**PacI (6371) SwaI (6380) NotI (6390)**

6301 TTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAA

6401 TAAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTA

6501 GCAAAATAGGCTGTCCCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA