



Sgfl (11) **EcoRI (16)**
1 GGATCTGCGATCGCTGAATTC**TGGGACTTTCCACTGGGACTTTCCACTGGGACTTTCCACTGGGACTTTCCACTCCTGCAGC**

101 AGTGGATATTTCCAGAAA**ACTTTTTGGATGCAGTTGGGGATTCTCTTTACTGGATGTGGACAATATCTCTCTATTATTCACAGGAAGCAATCCCTCCT**

201 **ATAAAAGGGCCTCAGCAGAAGTAGTGTTCAGCTGTTCTTGGCTGACTTCACATCAAAGCTTCTATACTGACCTGAGACAGAGC** **HindIII (256)** **NcoI (283)**
1▶ **M A S K V**

301 **ACGACCCCGAGCAACGCAAACGCATGATCACTGGGCCTCAGTGGTGGGCTCGCTGCAAGCAAATGAACGTGCTGGACTCCTTCATCAACTACTATGATTC**
6▶ **Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S**

401 **CGAGAAGCACGCCGAGAACGCCGTGATTTTTCTGCATGGTAACGCTGCCTCCAGCTACCTGTGGAGGCACGCTGCTGCCTCACATCGAGCCCGTGGCTAGA**
39▶ **E K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R**

501 **TGCATCATCCCTGATCTGATCGGAATGGTAAGTCCGGCAAGAGCGGAATGGCTCATATCGCTCCTGGATCACTACAAGTACCTCACCGCTTGGTTG**
73▶ **C I I P D L I G M G K S G K S G N G S Y R L L D H Y K Y L T A W F**

601 **AGCTGCTGAACCTTCAAAGAAAATCATCTTTGTGGCCACGACTGGGGGCTTGTCTGGCCTTCTACTACTCTACGAGCACCAAGACAAGTCAAGGC**
106▶ **E L L N L P K K I I F V G H D W G A C L A F H Y S Y E H Q D K I K A**

EcoRV (770)
701 **CATCGTCCATGCTGAGAGTGTCTGGACGTGATCGAGTCTGGGACGAGTGGCCTGACATCGAGGAGGATATCGCCCTGATCAAGAGCGAAGAGGGCGAG**
139▶ **I V H A E S V V D V I E S W D E W P D I E E D I A L I K S E E G E**

801 **AAAATGGTGTGAGAATAACTTCTTCGTCGAGACCATGCTCCAAGCAAGATCATCGGAAACTGGAGCCTGAGGAGTTCGCTGCCTACCTGGAGCCAT**
173▶ **K M V L E N N F F V E T M L P S K I M R K L E P E E F A A Y L E P**

901 **TCAAGGAGAAGGGCGAGGTTAGACGGCTACCTCTCTGGCTCGCGAGATCCCTCTCGTTAAGGGAGGCAAGCCCGACGCTCGTCCAGATTGTCCGCAA**
206▶ **F K E K G E V R P T L S W P R E I P L V K G G K P D V V Q I V R N**

1001 **CTACAACGCTACCTTCGGCCAGCGACGATCTGCTAAGATGTTTCATCGAGTCCGACCTGGGTTCTTTTCCAACGCTATTGTGAGGGAGCTAAGAAG**
239▶ **Y N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K**

1101 **TTCCCTAACACCGAGTTCGTGAAGGTGAAGGGCCTCCACTTCAGCCAGGAGGACGCTCCAGATGAAATGGTAAGTACATCAAGAGCTTCGTGGAGCGCG**
273▶ **F P N T E F V K V K G L H F S Q E D A P D E M G K Y I K S F V E R**

1201 **TGCTGAAGAACGAGCAGTAATCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTA**
306▶ **V L K N E Q •**

HpaI (1362)
1301 **TTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAATTGCATTATTTTATGTTTCAGGTTCA**

EcoRI (1456)
1401 **GGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTCATAAAATACAGCATAGCAAACCTTAACCTCCAATCAAG**

1501 **CCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGA**

SapI (1645)
1601 **GTTAAGATATAGTGTATTTTCCAAGTTTGAAGTACTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTTTTATGTAATAAT**

1701 **CAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAG**

1801 **TTGGACTTAGGGAACAAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTC**
141▶ **N R T Y K L P I L E E**

SacI (1974)
1901 **AATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAAGGAGCATAGTCAAGATGAGCTCTCTGCACATGCCACAGGGGCTGACC**
129▶ **I 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**

2001 **ACCTGATGGATCTGTCCACCTCATCAGAGTAGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCAATGGCAA**
95▶ **V 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**

StuI (2136)
2101 **TGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTG**
62▶ **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**

2201 **CTTGTGTCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCCTA**
29▶ **K 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**

Asel (2343)
2301 **TAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGCAACTACTGTTTGTAGGCGCCGGTCCACAGCTTG** **GATCTGTAACGGCGCAG**

2401 **AACAGAAAACGAAACAAGACGTAGAGTTGAGCAAGCAGGGTCAAGGAAAGCGTGAGAGCCGGCTGAGTCTAGGTAGGCTCAAGGGAGCGCCGGACAA**

2501 **AGGCCCGGTCTCGACCTGAGCTTTAAACTTACCTAGACGGCGGACGCGAGTTCAAGGAGCCACAGGCGGGAGGCGGAGGAGGCGGAGGCGGACTCAACCGCGGTG**

HindIII (2656) **Psp1406I (2699)**
2601 **GATGGCGGCTCAGGTAGGGCGGGCGCGTGAAGGAGAGATGCGAGCCCTCGAAGCTTCAGCTGTGTTCTGGCGGCAACCCGTTGCGAAAAAGAAC**

2701 **GTTACGGCGACTACTGCACTTATATACGGTCTCCCCACCCTCGGAAAAAGGCGGAGCCAGTACACGACATCACTTTCCAGTTTACCCCGGCCAC**

2801 **AgeI (2812)** CTTCTCTAGGCACCGGTTCAATTGCCGACCCCTCCCCCAACTTCTCGGGGACTGTGGGCGATGTGCGCTCTGCCACTGAC **SpeI (2881)** TAGTGGGCCCTGCAGGTT

2901 **BspLU11I (2909)** AATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGTGCGCTTTTTCCATAGGCTCCGCCCCCTGACGAGCAT

3001 CACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTC

3101 CGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT

3201 CGTTCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC

3301 GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT

3401 AACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGG

3501 TAGCGGTGGTTTTTTTGTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGG

3601 **NotI (3659)** AACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGAATAAAATATCTTTATTTTCATTACATCTGTGTGT

3701 TGGTTTTTGTGTGAATCGTAACATAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGT

3801 GCCAGAACATTTCTCTATCGAA