



2601 **StuI (2646)**
GACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCG
66 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 T K T R I A A

2701 **BspHI (2796)**
BbsI (2792)
XmnI (2788)
CCCCGACATGGTGTCTTGTCTCATAGAGCATGGTGTCTTCTCAGTGGGACCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCAT
33 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 S I N F T K M

2801 **AseI (2854)**
GATGGCCCTCTATAGTGAAGTCTATTATACTATGCGCATATACTATGCGGATGATTAATTGTCAAACACGCGTGGATGGCGTCTCCAGCTATCTGAC
←

2900 **SacI (2911)**
GGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCCTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTC

3000 **SpeI (3009)**
CCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTA
←

3099 **SnaBI (3137)**
CTGCCAAAACCGCATCATCATGGTAATAGCGGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCTACTGGGCATAATGCCAG

3199 **NdeI (3242)**
GCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCC

3299
ATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGACCCAGGCGGGCC

3399 **SdaI (3420)** **PacI (3428)** **BspLU11I (3438)**
ATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTCTGCGG
←

3497
GTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT

3597
CCCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATA

3697 **ApaLI (3752)**
GCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGG

3797
TAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCT

3897
ACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTG

3997
GTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCC

4097 **EagI (4188)**
PacI (4168) **SwaI (4177)** **NotI (4187)**
TTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGA

4197
ATAAAATATCTTTATTTTTCATTACATCTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAACGAAACAAACAAACT

4297
AGCAAATAGGCTGTCCCAGTGAAGTGACGGTGCCAGAACATTTCTCTATCGAA