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## pUC18-Rr-GFP

*Renilla reniformis* GFP - coding sequence in green, ATG start codon **bold**  
Key restriction enzyme sites are underlined  
pUC18 sequences in blue

ATGACCATGATTACGAATTCGAGCTCGGTACCCGGGCTGCAGGAATTCGGCACGAGGCTGACACAATAAAAAACCTTTCA  
AATTGTTTCTCTGTAGCAGGAAGT**ATGGATCTCGCAAAACTTGGTTTGAAGGAAGTGATGCCTACTAAAATCAACTTAGA**  
**AGGACTGGTTGGCGACCACGCTTTTCTCAATGGAAGGAGTTGGCGAAGGCAACATATTGGAAGGAACTCAAGAGGTGAAGA**  
**TATCGGTAACAAAAGGCGCACCCTCCATTTCGCATTTGATATCGTATCTGTTGCTTTCTCATATGGGAACAGAGCTTAT**  
**ACTGGTTACCCAGAAGAAATTTCCGACTACTTCCCTCCAGTCGTTTCCAGAAGGCTTTACTTACGAGAGAAACATTCGTTA**  
**TCAAGATGGAGGAACTGCAATTGTTAAATCTGATATAAGCTTGGAAAGATGGTAAATTCATAGTGAATGTAGACTTCAAAG**  
**CGAAGGATCTACGTCGCATGGGACCAGTCATGCAGCAAGACATCGTGGGTATGCAGCCATCGTATGAGTCAATGTACACC**  
**AATGTCATTTCAAGTTATAGGGGAATGTATAATAGCATTCAAACCTCAAACCTGGCAAACATTTCACTTACCACATGAGGAC**  
**AGTTTACAAATCAAAGAAGCCAGTGAAACTATGCCATTGTATCATTTTCATCCAGCATCGCCTCGTTAAGACCAATGTGG**  
**ACACAGCCAGTGGTTACGTTGTGCAACACGAGACAGCAATTGCAGCGCATTCTACAATCAAAAAAATTGAAGGCTCTTTA**  
**CCATAGATATCTATACACAATTATTCTATGCACGTAGCATTTTTTTTGGAAATATAAGTGGTATTGTTCAATAAAATATTA**  
AATATAAAAAAAAAAAAAAAAAAACTCGACCTGCAGGCAT

Coding Sequence:

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1 atggatctcgcaaaacttggtttgaaggaagtgatgcctactaaa
  M D L A K L G L K E V M P T K
46 atcaacttagaaggactggttggcgaccacgctttctcaatggaa
  I N L E G L V G D H A F S M E
91 ggagttggcgaaggcaacatattggaaggaactcaagaggtgaag
  G V G E G N I L E G T Q E V K
136 atatcggtaacaaaaggcgcaccactcccattcgcatttgatatac
  I S V T K G A P L P F A F D I
181 gtatctgttgctttctcatatgggaacagagccttataactggttac
  V S V A F S Y G N R A Y T G Y
226 ccagaagaaatttccgactacttccctccagtcgtttccagaaggc
  P E E I S D Y F L Q S F P E G
271 tttacttacgagagaaacattcgttatcaagatggaggaactgca
  F T Y E R N I R Y Q D G G T A
316 attgttaaactctgatataagccttgggaagatggtaaattcatagtg
  I V K S D I S L E D G K F I V
361 aatgtagacttcaaagcgaaggatctacgtcgcacatgggaccagtc
  N V D F K A K D L R R M G P V
406 atgcagcaagacatcgtgggtatgcagccatcgtatgagtcaatg
  M Q Q D I V G M Q P S Y E S M
451 tacaccaatgtcattcagttataggggaatgtataatagcattc
  Y T N V T S V I G E C I I A F
496 aaacttcaaactggcaaacatttcaattaccacatgaggacagtt
  K L Q T G K H F T Y H M R T V
541 taaaaatcaaagaagccagtggaactatgccattgtatcatttc
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Y K S K K P V E T M P L Y H F  
586 atccagcatcgcctcgttaagaccaatgtggacacagccagtggt  
I Q H R L V K T N V D T A S G  
631 tacgttgtgcaacacgagacagcaattgcagcgcattctacaatc  
Y V V Q H E T A I A A H S T I  
676 aaaaaaattgaaggctctttacatag 702  
K K I E G S L P \*