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pUC18-human-RmGFP

Blue is the pUC18 vector sequence
Underlined are the key restriction sites that were inserted with the
PCR product
Green is the humanized RmGFP sequence

CTACTCTAGAGGATCCCCCCAGATCTATGAGCAAGCAGATCCTGAAGAACACCTGCCTGCAGGAGGTGAT
GAGCTACAAGGTGAACCTGGAGGGCATCGTTAACAACCACGTGTTACCATGGAGGGCTGCGGCAAGGGCA
ACATCCTGTTTCGGCAACCAATTGGTGCAGATCCGCGTGACCAAGGGCGCCCCCTGCCCTTCGCTTCGAC
ATCGTGAGCCCCGCTTCCAGTACGGCAACCGTACGTTACCAAGTACCCCAACGACATCAGCGACTACTT
CATCCAGAGCTTCCCCGCCGGCTTCATGTACGAGCGCACCCCTGCGCTACGAGGACGGCGGCCTGGTGGAGA
TCCGCAGCGACATCAACCTGATCGAGGACAAGTTTCGTGTACCGCGTGGAGTACAAGGGCAGCAACTTCCCC
GACGACGGGCCCCGTGATGCAGAAGACCATCCTGGGCATCGAGCCCAGCTTCGAGGCCATGTACATGAACAA
CGGCGTGCTGGTGGGCGAGGTGATCCTGGTGTACAAGCTTAACAGCGGCAAGTACTACAGCTGCCACATGA
AGACCCTGATGAAGAGCAAGGGCGTGGTGAAGGAGTTCCCCAGCTACCATTTCATCCAGCACCGCCTCGAG
AAGACCTACGTGGAGGACGGCGGCTTCGTGGAGCAGCACGAGACCGCCATCGCCCAGATGACCAGCATCGG
CAAGCCCCCTGGGATCCCTGCACGAGTGGGTGTGATACTAGTGGGGGTACCGAGCTCGAATTTCGTAATCAT
GTCATAGCTGTTTTCTGTGTGAAATTGTTATCCGCTCACAAATCCACACAACATACGAGCCGGAAGCATAA
AGTGTAAGCCTGGGGTGCCTNATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC
CAGTCGGNAAACCTGTCTGCCAGCTGCATTAATGAATCG

7 atgagcaagcagatcctgaagaacacctgcctgcaggaggtgatg
M S K Q I L K N T C L Q E V M
52 agctacaaggtgaacctggagggcatcgttaacaaccacgtgttc
S Y K V N L E G I V N N H V F
97 accatggagggctgaggcaagggcaacatcctgttcggcaaccaa
T M E G C G K G N I L F G N Q
142 ttggtgcagatccgctgacccaagggcgccccctgcccttcgcc
L V Q I R V T K G A P L P F A
187 ttcgacatcgtgagccccgccttccagtacggcaaccgtacgttc
F D I V S P A F Q Y G N R T F
232 accaagtacccaacgacatcagcgactacttcatccagagcttc
T K Y P N D I S D Y F I Q S F
277 cccgccggcttcatgtacgagcgcaccctgcgctacgaggacggc
P A G F M Y E R T L R Y E D G
322 ggctgggtggagatccgcagcgacatcaacctgatcgaggacaag
G L V E I R S D I N L I E D K
367 ttctgtaccgcgtggagtacaagggcagcaacttccccgacgac
F V Y R V E Y K G S N F P D D
412 gggcccgatgcagaagaccatcctgggcatcgagcccagcttc
G P V M Q K T I L G I E P S F

457 gaggccatgtacatgaacaacggcgtgctggtgggcgaggtgatc
E A M Y M N N G V L V G E V I
502 ctggtgtacaagcttaacagcggcaagtactacagctgccacatg
L V Y K L N S G K Y Y S C H M
547 aagaccctgatgaagagcaagggcgtggtgaaggagttcccagc
K T L M K S K G V V K E F P S
592 taccacttcatccagcaccgcctcgagaagacctacgtggaggac
Y H F I Q H R L E K T Y V E D
637 ggcggcttcgtggagcagcagagaccgccatcgcccagatgacc
G G F V E Q H E T A I A Q M T
682 agcatcggcaagccctgggatccctgcacgagtgggtgtga
S I G K P L G S L H E W V *