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pUC19-P-Luc

Pleuromamma sp. Luciferase- coding sequence in green, start codon in **bold**
C-terminal His-tag in red
Key restriction enzyme site are underlined
pUC19 sequences in blue

CGGATAACAATTTACACAGGAAACAGCT**ATG**ACCATGATTACGCCAAGCTTGCATGCCTGCAGGTCGACTCTAGATTA
GTGATGGTGATGGTGATGTGTGAGGCACCTTCTTCTGGTGAACCTTCTCCTGGTCAGGAATATGAACAGTGACTGGGCTGC
AGTCTTCTTGGGGCTTCATGCTGCATTTCGTGGTACTCGACCGTTGCACACTTCTTGGTCTTAACAGGCCGGCAGTCCAAT
GAACTCTTGACCTGACAATTGGTTCTCATAGACAAAGAGTGGGAAGGTCCCTCTATGAAGTCTGCATACTTAAGGTGAGA
CAGGATGCCGCATTCCGTCTTGACAGTTGGAAAATCTACATCTTTCTCCACGATATTACATTCTTCCCAAGTGACAGGAG
TGCATTTCTCGGTACCACCCCAAACCTTGTGGCATTGGCGTCAACTTCCCAATCAGTAACGCAGTTATCTTTAGTGACT
TGTTTGCCTCTGGAACCTTGCTTCTGTGCGGTACAGTGTAACTTCCACGCAGGACTTGTACGCGTAGTCTTTGTA
TTGAACTTGGCATCTATTCTGCCAGTGGAAATCAAATCTGGGTCCACAGTCGGCCCAAGCAACTGCTTGGCATTTCATCT
CGGTACATCGGCGCAAACCTTGCTTCTGCTTCTAGCCGAATTTCTAAG**CAT**TTTGAATTCACTGGCCGTGCTTTTACAA
CGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAG
CGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATGGCGAATGGCGCCTGATGCGGTATTTTCTCC
TTACGCATCTGTGCGGTATTTACACCGCATATGGTGCCTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAG
CCCCGAGACCCGCCAACACCCGCTGA

Coding sequence:

615 atgcttagaaattcggctaggaagcaagagcaagtttgccgat
M L R N S A R K Q E Q V C A D
570 gtgaccgagatgaaatgccaagcagttgcttgggcccactgtgga
V T E M K C Q A V A W A D C G
525 cccagatttgattccactggcaggaatagatgccaagttcaatac
P R F D S T G R N R C Q V Q Y
480 aaggactacgcgtacaagtccctgcgtggaagttgattacactgta
K D Y A Y K S C V E V D Y T V
435 ccgcacaggaagcaagttccagagtgcaaacaagtcactaaagat
P H R K Q V P E C K Q V T K D
390 aactgcgttactgattgggaagttgacgccaatggcaacaaggtt
N C V T D W E V D A N G N K V
345 tggggtggtaccgagaaatgcactcctgtcacttgggaagaatgt
W G G T E K C T P V T W E E C
300 aatatcgtggagaaagatgtagatTTTCCAactgtcaagacggaa
N I V E K D V D F P T V K T E
255 tgcggcatcctgtctcaccttaagtatgcagacttcatagagggga
C G I L S H L K Y A D F I E G
210 cttccactcttTgtctatgagaaccaattgtcaggtcaagagt
P S H S L S M R T N C Q V K S
165 tcattggactgccggcctgttaagaccaggaagtgcaacggctc
S L D C R P V K T R K C A T V
120 gagtaccacgaatgcagcatgaagccccagaagactgcagccca

E Y H E C S M K P Q E D C S P
75 gtcactgttcatattcctgaccaggagaaagttcaccagaagaag
V T V H I P D Q E K V H Q K K
30 tgcctcacacatcaccatcaccatcactaa 1
C L T H H H H H H *