

Translation of huPlg.seq(1-786)

Universal code

Total amino acid number: 261, MW=28580

Max ORF starts at AA pos 1(may be DNA pos 1) for 261 AA(783 bases), MW=28580

```

      10      20      30      40      50      60
1      AAAC TTTACGACTACTGTGATGTCCCTCAGTGTGCGGCCCTTCATTTGATTGTGGGAAG
1      K  L  Y  D  Y  C  D  V  P  Q  C  A  A  P  S  F  D  C  G  K

      70      80      90      100     110     120
61     CCTCAAGTGGAGCCGAAGAAATGTCCCTGGAAGGGTTGTGGGGGGGTGTGTGGCCCACCCA
21     P  Q  V  E  P  K  K  C  P  G  R  V  V  G  G  C  V  A  H  P

      130     140     150     160     170     180
121    CATTCTGGCCCTGGCAAGTCAGTCTTAGAACAAAGTTTGGAAATGCACCTTCTGTGGAGGC
41     H  S  W  P  W  Q  V  S  L  R  T  R  F  G  M  H  F  C  G  G

      190     200     210     220     230     240
181    ACCTTGATATCCCCAGAGTGGGTGTTGACTGCTGCCCACTGCTTGGAGAAGTCCCCAAGG
61     T  L  I  S  P  E  W  V  L  T  A  A  H  C  L  E  K  S  P  R

      250     260     270     280     290     300
241    CCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAGTGAATCTCGAACCGCATGTT
81     P  S  S  Y  K  V  I  L  G  A  H  Q  E  V  N  L  E  P  H  V

      310     320     330     340     350     360
301    CAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCACACGAAAAGATATTGCCTTGCTA
101    Q  E  I  E  V  S  R  L  F  L  E  P  T  R  K  D  I  A  L  L

      370     380     390     400     410     420
361    AAGCTAAGCAGTCCCTGCCGTCACTGACAAAGTAATCCCAGCTTGTCTGCCATCCCCA
121    K  L  S  S  P  A  V  I  T  D  K  V  I  P  A  C  L  P  S  P

      430     440     450     460     470     480
421    AATTATGTGGTCGCTGACCGGACCGAATGTTTCATCACTGGCTGGGGAGAAAACCCAAGGT
141    N  Y  V  V  A  D  R  T  E  C  F  I  T  G  W  G  E  T  Q  G

      490     500     510     520     530     540
481    ACTTTTGGAGCTGGCCTTCTCAAGGAAGCCCAGCTCCCTGTGATTGAGAATAAAGTGTGC
161    T  F  G  A  G  L  L  K  E  A  Q  L  P  V  I  E  N  K  V  C

      550     560     570     580     590     600
541    AATCGCTATGAGTTTCTGAATGGAAGAGTCCAATCCACCGAACTCTGTGCTGGGCATTTG
181    N  R  Y  E  F  L  N  G  R  V  Q  S  T  E  L  C  A  G  H  L

      610     620     630     640     650     660
601    GCCGGAGGCACTGACAGTTGCCAGGGTGACAGTGGAGGTCCTCTGGTTTGCTTCGAGAAG
201    A  G  G  T  D  S  C  Q  G  D  S  G  G  P  L  V  C  F  E  K

      670     680     690     700     710     720
661    GACAAATACATTTTACAAGGAGTCACTTCTTGGGGTCTTGGCTGTGCACGCCCAATAAG
221    D  K  Y  I  L  Q  G  V  T  S  W  G  L  G  C  A  R  P  N  K

      730     740     750     760     770     780
721    CCTGGTGTCTATGTTTCGTGTTTCAAGGTTTGTACTTGGATTGAGGGAGTGATGAGAAAT
241    P  G  V  Y  V  R  V  S  R  F  V  T  W  I  E  G  V  M  R  N

781    AATTAA
261    N  *
```