predicted signal sequence | G-X-S-X-G motif | His$_6$ tag | stop codon

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1         10        20        30        40        50        60        70        80        90
GTGAAAGCTGCAACACGTAATTATCTAGCGCTTGTGGCTTCAGGGGTTCTCATGACTGCCGCTTCCCCTGTCGCCGGCGCTATCGATTCCGCCGA
V  K  A  A  T  R  N  Y  L  A  L  V  A  S  G  V  L  M  T  A  A  S  P  V  A  G  A  I  D  S  A  E

100       110       120       130       140       150       160       170       180       190
ATCGGCTCCACCAGTTGAAGAGCATTCAGAACTTCCAGAATCCTCTTTTATTGACGAGGAACTTAAAGGCGCAGGATCCGCTGAAGATTCACAAG
S  A  P  P  V  E  E  H  S  E  L  P  E  S  S  F  I  D  E  E  L  K  G  A  G  S  A  E  D  S  Q

200       210       220       230       240       250       260       270       280
AGGCGAAATCAATGGCCGAAGAAGCCTCCAAACTCCCTCCCCTTTCATCAGGGCTCTTGGGCCCAGGTGACCATATCGGAGATCAATACACCGCT
E  A  K  S  M  A  E  E  A  S  K  L  P  P  L  S  S  G  L  L  G  P  G  D  H  I  G  D  Q  Y  T  A

290       300       310       320       330       340       350       360       370       380
TTCTACCACGATCCAGTAGAACTCGACTCCTCGGAGCCTGGACAGCTCTTCCGATCAGAATCTGTGCGCAACTCCAAAAATCCACTTGGCATCAG
F  Y  H  D  P  V  E  L  D  S  S  E  P  G  Q  L  F  R  S  E  S  V  R  N  S  K  N  P  L  G  I  S

390       400       410       420       430       440       450       460       470
CAACGTCGGCCCTTATAAGGCAGACCGCATACTCTATTCTTCCACCAACCGTTCTGGAGAAAAGATCCAAGTAAGCGGGATGGTCATTGAACCTA
N  V  G  P  Y  K  A  D  R  I  L  Y  S  S  T  N  R  S  G  E  K  I  Q  V  S  G  M  V  I  E  P

480       490       500       510       520       530       540       550       560       570
AAACCGAGTGGGGCGGAGAAGGCCCACGCCCTGTCGTGGCATTTGCACCGGGTACTCAAGGATTAGCGGACCGTTGTGCCGCCTCCCGTAAAATT
K  T  E  W  G  G  E  G  P  R  P  V  V  A  F  A  P  G  T  Q  G  L  A  D  R  C  A  A  S  R  K  I

580       590       600       610       620       630       640       650       660
GCAGACGGGGTTGGAGACTACGAGCAGTTCTATTTCCATCAGTACCTTAAGAAGGGCTATGCTGTAGTACTCACCGACTACGAGGGCCTTGGCAC
A  D  G  V  G  D  Y  E  Q  F  Y  F  H  Q  Y  L  K  K  G  Y  A  V  V  L  T  D  Y  E  G  L  G  T

670       680       690       700       710       720       730       740       750       760
CCCTGGCATGCACACGTACATGGATCGCGCATCCCAAGGCCATACAGTCCTCGACAGTATTCGAGCTGCGCAGCAACTAGAAGGCTGGGACATTA
P  G  M  H  T  Y  M  D  R  A  S  Q  G  H  T  V  L  D  S  I  R  A  A  Q  Q  L  E  G  W  D  I

770       780       790       800       810       820       830       840       850
ACGAAACCAACCCAGTATTTATCAATGGCTACTCCCAAGGCGGTGGAGCTGCTGCCGCTGCTGCCGAGCTATATGATGACTATGCTCCGGAGCTC
N  E  T  N  P  V  F  I  N  G  Y  S  Q  G  G  G  A  A  A  A  A  A  E  L  Y  D  D  Y  A  P  E  L

860       870       880       890       900       910       920       930       940       950
AACATCAAGCTTGCGACTATCGGTGCTGCGCCAACAGACCTTACGCTGTTGCCTTCTACCCTCGACGGCTCCTCGTATTTCCTCTTCGAGTCGTA
N  I  K  L  A  T  I  G  A  A  P  T  D  L  T  L  L  P  S  T  L  D  G  S  S  Y  F  L  F  E  S  Y

960       970       980       990       1,000     1,010     1,020     1,030     1,040
TGCCCTTCTAGGGCTAAGCAACTCCTATGGCGAGGATCTGTACTCGCATCTCAATGACCGGGGCGCAAGAAAGCTACAGGATGCGACGAATACTT
A  L  L  G  L  S  N  S  Y  G  E  D  L  Y  S  H  L  N  D  R  G  A  R  K  L  Q  D  A  T  N  T

1,050     1,060     1,070     1,080     1,090     1,100     1,110     1,120     1,130     1,140
GTACTATGGGGCTCCTTAAGACCGCCGGCACTACCGTTGAGCGGATCAGCAACGATGGCAGAACCGTGCAAGACTTCATTGACAGTGAGCCTTTC
C  T  M  G  L  L  K  T  A  G  T  T  V  E  R  I  S  N  D  G  R  T  V  Q  D  F  I  D  S  E  P  F

1,150     1,160     1,170     1,180     1,190     1,200     1,210     1,220     1,230
AAATCGATGCTGGCAGAGCAGCATATTGGCTACGCTGCTCCCGCGATTCCAGTCGTCATTACGCATGGCCGCGGTGATGACGTGATTCCGTACTC
K  S  M  L  A  E  Q  H  I  G  Y  A  A  P  A  I  P  V  V  I  T  H  G  R  G  D  D  V  I  P  Y  S

1,240     1,250     1,260     1,270     1,280     1,290     1,300     1,310     1,320     1,330
TACTGCTGAACAGCTCGTAAATGAATGGACTGAGCGCGGCGCCGATGTCACTTTCATCCCAAATAACGCCCACACTCACCCGACCGGCACTATTC
T  A  E  Q  L  V  N  E  W  T  E  R  G  A  D  V  T  F  I  P  N  N  A  H  T  H  P  T  G  T  I

1,340     1,350     1,360     1,370     1,380     1,390     1,400     1,413
CGCACATCATCGAATCAGTAAAAGCTATTGACGCTGCGCTACAGCACGAGGAGGGAAGCCAGCACCATCACCATCACCATTAA
P  H  I  I  E  S  V  K  A  I  D  A  A  L  Q  H  E  E  G  S  Q  H  H  H  H  H  H  *
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