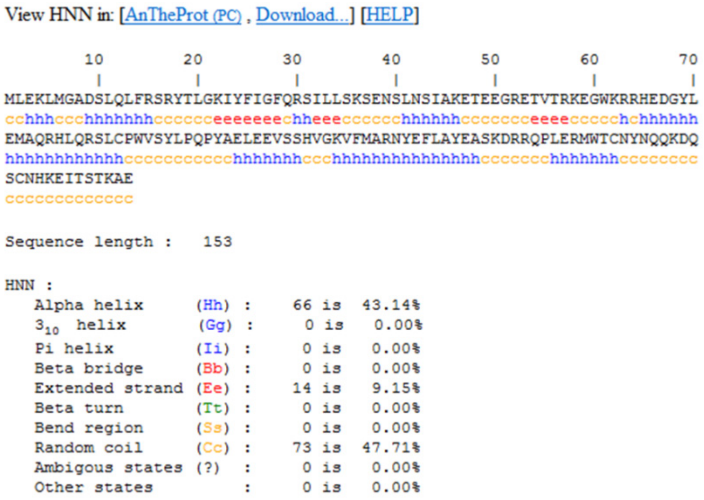
Supplementary Information

Figure S1. Prediction of the G72 secondary structure. The secondary structure of G72 was predicted using Hierarchical Neural Network at the ExPASy proteomics server. h, e and c: Residues predicted to have an -helical, -strand, or coil conformation, respectively.



View HNN in: [AnTheProt (PC) , Download...] [HELP]

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          10        20        30        40        50        60        70
           |         |         |         |         |         |         |
MLEKLMGADSLQLFRSRYTLGKIYFIGFQRSILLSKSENSLNSIAKETEEGRETVTRKEGWKRRHEDGYL
cchhhccchhhhhhhcccccceeeeeeechheeeccccccchhhhhhccccccceeeecccccchchhhhhh
EMAQRHLQRSLCPWVSYLPQPYAELEEVSSHVGKVFMARNYEFLAYEASKDRRQPLERMWTCNYNQQKDQ
hhhhhhhhhhhhccccccccccchhhhhhhccchhhhhhhhhhhhhhhccccccchhhhhhhcccccccc
SCNHKEITSTKAE
ccccccccccccc

Sequence length :   153

HNN :
   Alpha helix     (Hh) :    66 is  43.14%
   3_{10}  helix   (Gg) :     0 is   0.00%
   Pi helix        (Ii) :     0 is   0.00%
   Beta bridge     (Bb) :     0 is   0.00%
   Extended strand (Ee) :    14 is   9.15%
   Beta turn       (Tt) :     0 is   0.00%
   Bend region     (Ss) :     0 is   0.00%
   Random coil     (Cc) :    73 is  47.71%
   Ambigous states (?)  :     0 is   0.00%
   Other states         :     0 is   0.00%
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