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Job GOR4 (ID: 16fe3de40cfa) is running on NPS@ server (started on 20250714-064953).  
Results will be shown below. Please wait and don't go back.

In your publication cite :

NPS@: Network Protein Sequence Analysis  
TIBS 2000 March Vol. 25, No 3 [291]:147-150  
Combet C., Blanchet C., Geourjon C. and Deléage G.

Running-

## GOR4 result for : UNK 121920

Abstract ([/NPSA/npsa\\_references.html#gor4](#)) GOR secondary structure prediction method version IV, J. Garnier, J.-F. Gibrat, B. Robson, Methods in Enzymology, R.F. Doolittle Ed., vol 266, 540-553, (1996)

View GOR4 in: [AnTheProt (PC) ([http://npsa-pbil.ibcp.fr/cgi-bin/npsa\\_mpsaview.pl?fn=/tmp/16fe3de40cfa.gor4.mpsa.mpsa&gui=antheprot](http://npsa-pbil.ibcp.fr/cgi-bin/npsa_mpsaview.pl?fn=/tmp/16fe3de40cfa.gor4.mpsa.mpsa&gui=antheprot)) , Download... (<http://antheprot-pbil.ibcp.fr>)] [HELP ([http://npsa-pbil.ibcp.fr/cgi-bin/npsa\\_automat.pl?page=/NPSAHLP/npsahlp\\_locsoft.html](http://npsa-pbil.ibcp.fr/cgi-bin/npsa_automat.pl?page=/NPSAHLP/npsahlp_locsoft.html))]

The sequence logo displays the conservation of amino acids at specific positions. The x-axis represents positions 10, 20, 30, 40, and 50. The y-axis shows the frequency of each amino acid (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y) at each position. The most conserved amino acids are I, K, F, N, and V across all positions.

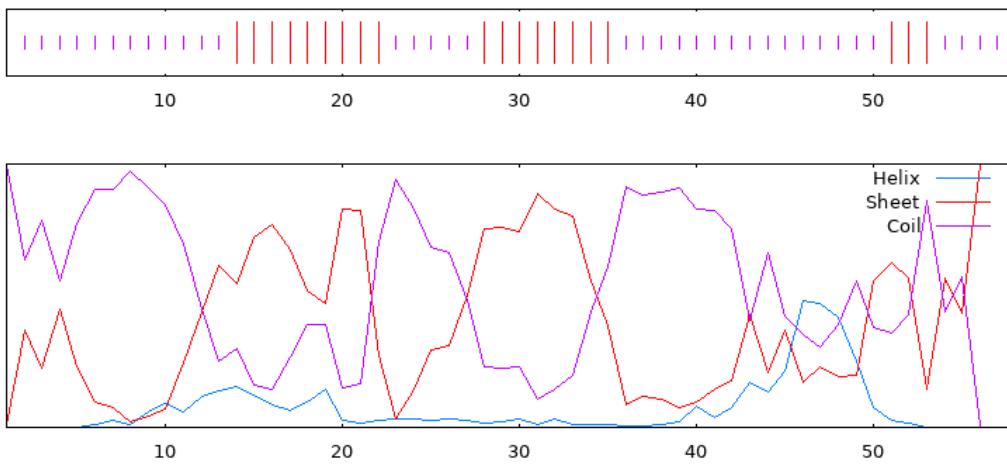
Sequence length : 58

60B4 :

```

K4 :
Alpha helix      (Hh) :    0 is   0.00%
 $\beta_{10}$  helix     (Gg) :    0 is   0.00%
Pi helix        (Ii) :    0 is   0.00%
Beta bridge      (Bb) :    0 is   0.00%
Extended strand  (Ee) :   20 is  34.48%
Beta turn         (Tt) :    0 is   0.00%
Bend region       (Ss) :    0 is   0.00%
Random coil       (Cc) :   38 is  65.52%
Ambiguous states (?) :    0 is   0.00%
Other states      :    0 is   0.00%

```



Prediction result file (text): [GOR4 (/tmp/16fe3de40cfa.gor4.mpsa)]

User : public Last modification time : Mon Jul 14 06:49:55 2025. Current time : Mon Jul 14 06:49:55 2025



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