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Description	P0A993
Date	Thu Jan 5 11:09:40 GMT 2012
Unique Job ID	1ab4cf22e9b8d7fc

Protein structure visualization of the human protein (UniProt ID: P05125). The figure displays the protein sequence, secondary structure, and disorder predictions across six segments.

Segment 1 (Residues 1-60): Sequence: MKT LGE F I V E K Q H E F S H A T G E L T A L L S A I K L G A K I I H R D I N K A G L V D I L G A S G A E N V Q G E. Secondary structure shows several alpha-helices. Disorder is predicted in the first 10 residues and between residues 25 and 35.

Segment 2 (Residues 70-120): Sequence: V Q Q K L D L F A N E K L K A A L K A R D I V A G I A S E E E D E I V V F E G C E H A K Y V V L M D P L D G S S N I D V. Secondary structure shows a long alpha-helix followed by a beta-strand. Disorder is predicted between residues 100 and 110.


Segment 3 (Residues 130-180): Sequence: N V S V G T I F S I Y R R V T P V G T P V T E E D F L Q P G N K Q V A A G Y V V Y G S S T M L V Y T T G C G V H A F T Y. Secondary structure shows a long alpha-helix followed by a beta-strand. Disorder is predicted between residues 140 and 150.

Segment 4 (Residues 190-240): Sequence: D P S L G V F C L C Q E R M R F P E K G K T Y S I N E G N Y I K F P N G V K K Y I K F C Q E E D K S T N R P Y T S R Y I. Secondary structure shows a long alpha-helix followed by a beta-strand. Disorder is predicted between residues 210 and 220, and between residues 230 and 240.


Segment 5 (Residues 250-300): Sequence: G S L V A D F H R N L L K G G I Y L Y P S T A S H P D G K L R L L Y E C N P M A F L A E Q A G G K A S D G K E R I L D I. Secondary structure shows a long alpha-helix followed by a beta-strand. Disorder is predicted between residues 270 and 280, and between residues 290 and 300.


Segment 6 (Residues 310-330): Sequence: I P E T L H Q R R S F V G N D H M V E D V E R F I R E F P D A. Secondary structure shows a long alpha-helix followed by a beta-strand. Disorder is predicted between residues 320 and 330.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand