


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Description	P76559
Date	Thu Jan 5 12:24:37 GMT 2012
Unique Job ID	358b8adb569fc7a1

Figure 1 displays the protein structure and disorder analysis of the human protein encoded by the LOC101929 gene. The figure shows the full-length protein sequence (600 amino acids) and its predicted secondary structure (SS) and disorder.


The protein sequence is shown in a color-coded format, with residues grouped into blocks. The secondary structure is represented by blue arrows (alpha-helices) and green cylinders (beta-strands). The disorder analysis is shown as a bar chart below the sequence, with colors indicating different levels of disorder confidence.


The protein is predicted to be disordered, with several regions of high confidence disorder (red) and some regions of low confidence disorder (green).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand