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Description	P39387
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The figure displays the C-terminal region of the protein, showing sequence, secondary structure, and disorder predictions for residues 1-300. The protein is composed of several alpha-helices and beta-strands, with a disordered region at the C-terminus.

Sequence: MTNFTTSTPHDALFKTFLTHPDTARDFMEIHLPKDLRELCDLDSLKLESASFVDEKLRLALHSDILWSVKTRREGDGYIYVVIEHQSRREDIHMAFRLMRYSMAMVQRHIEHDKRQPLPLVIPMLFYHGSRSPPYPSLWLCWLDEFADPTTARKLYNAAFPLVDVTVVPDDEIVQHRRVALLLELIQKHIRQRDLMLGLIDQLVVLVTECANDSQITALLNYILLTGDEARFNEFISELTRRMPQHRERIMTIAERIHNDGYIKGEQRILRLLLQNGADPEWIKITGLSAEQMQALRQPLPERERYSWLKSY


Secondary structure: The structure is composed of several alpha-helices (green cylinders) and beta-strands (blue arrows). The C-terminal region (residues 1-300) shows a disordered region (red) and a structured region (green).

SS confidence: The confidence of the secondary structure prediction is shown as a bar chart, with values ranging from 0.0 to 1.0.


Disorder: The disorder prediction is shown as a bar chart, with values ranging from 0.0 to 1.0. The C-terminal region (residues 1-300) is predicted to be disordered.


Disorder confidence: The confidence of the disorder prediction is shown as a bar chart, with values ranging from 0.0 to 1.0.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand