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Figure 1 displays the protein structure and disorder analysis of the C-terminal region of the protein. The top panel shows the full sequence (1-60) with secondary structure (SS) and disorder confidence. The bottom panel shows a zoomed-in view of the C-terminal region (70-100) with SS and disorder confidence.

Top Panel (Full Sequence):

- Sequence:** M C R H S L R S D G A G F Y Q L A G C E Y S F S A I K I A A G G Q F L P V I C A M A M K S H F F L I S V L N R R L T L T
- Secondary structure (SS):** The structure is shown as a ribbon diagram. The first 10 residues (MCHSLRSD) form a small alpha-helix. Residues 11-15 (GAGFY) form a loop. Residues 16-25 (QLAGCEYS) form a long alpha-helix. Residues 26-35 (FSAIKI) form a short alpha-helix. Residues 36-60 (AAGGQFLPVICAMAMKSHFFLISVLRRLTLT) form a long alpha-helix.
- Disorder confidence:** The disorder confidence is shown as a bar chart. The first 10 residues (MCHSLRSD) have a high disorder confidence (red). Residues 11-15 (GAGFY) have a low disorder confidence (blue). Residues 16-60 (QLAGCEYSFSAIKI AAGGQFLPVICAMAMKSHFFLISVLRRLTLT) have a high disorder confidence (red).

Bottom Panel (Zoomed-in View):

- Sequence:** A V Q G I L G R F S L F
- Secondary structure (SS):** The structure is shown as a ribbon diagram. The first 10 residues (AVQGLGR) form a long alpha-helix. Residues 11-15 (FSLF) form a short alpha-helix.
- Disorder confidence:** The disorder confidence is shown as a bar chart. The first 10 residues (AVQGLGR) have a high disorder confidence (red). Residues 11-15 (FSLF) have a low disorder confidence (blue).

Confidence Key

High(9)  Low (0)

The confidence key is a horizontal bar with 10 colored segments. From left to right, the colors are: red, orange, yellow, light green, green, teal, light blue, medium blue, dark blue, and purple. The bar is labeled 'High(9)' on the left and 'Low (0)' on the right.

? Disordered

 Alpha helix

→ Beta strand