

Email	l.a.kelley@imperial.ac.uk
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Figure 1 displays the protein structure and disorder analysis of the 608 amino acid protein. The top panel shows the full sequence (1-608) with secondary structure (SS) and disorder confidence. The bottom panel shows a zoomed-in view of the C-terminal region (70-100) with secondary structure and disorder confidence.

**Top Panel (Full Sequence):**

- Sequence:** M K H K L S A I L M A F M L T T P A A F A A P E A T N G T E A T T G T T G T T T T T T G A T T A T T T G G V A A G A V
- Secondary structure:** The structure is shown as a green ribbon model. It features several alpha-helices and beta-strands, with a large blue arrow indicating a long loop or disordered region.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction, with colors ranging from red (low) to green (high).
- Disorder:** A bar chart showing the disorder confidence, with colors ranging from red (low) to green (high).
- Disorder confidence:** A bar chart showing the confidence of the disorder prediction, with colors ranging from red (low) to green (high).

**Bottom Panel (Zoomed-in View):**

- Sequence:** G T A T V V G V A T A V G V A T L A V V A A N D S G D G G S H N T S T T T S T T R
- Secondary structure:** The structure is shown as a green ribbon model. It features several alpha-helices and beta-strands, with a large blue arrow indicating a long loop or disordered region.
- SS confidence:** A bar chart showing the confidence of the secondary structure prediction, with colors ranging from red (low) to green (high).
- Disorder:** A bar chart showing the disorder confidence, with colors ranging from red (low) to green (high).
- Disorder confidence:** A bar chart showing the confidence of the disorder prediction, with colors ranging from red (low) to green (high).

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand