

Email	l.a.kelley@imperial.ac.uk
Description	Q46835
Date	Thu Jan 5 12:35:01 GMT 2012
Unique Job ID	e22a522bdc7d23fa

The figure displays protein structure and disorder analysis for the full-length protein (1-120) and two fragments (1-60 and 70-120). The analysis includes the amino acid sequence, secondary structure (SS), confidence, and disorder predictions.

Full-length protein (1-120):

- Sequence:** MSIKQMPGRVLI SLLLSVTGLLSGCASHNENASLLAKKQAQNI SQNLPI KSAGYTLVLAQ
- Secondary structure:** The protein is predominantly alpha-helical, with several long alpha-helices and a few beta-strands (indicated by blue arrows).
- SS confidence:** High confidence (red) is observed throughout the protein, with some lower confidence regions (yellow and green).
- Disorder:** The protein is mostly ordered, with some disordered regions (indicated by question marks) at the N-terminus and C-terminus.
- Disorder confidence:** High confidence (red) is observed throughout the protein, with some lower confidence regions (yellow and green).

Fragment 1-60:

- Sequence:** MSIKQMPGRVLI SLLLSVTGLLSGCASHNENASLLAKKQAQNI
- Secondary structure:** The fragment is predominantly alpha-helical.
- SS confidence:** High confidence (red) is observed throughout the fragment.
- Disorder:** The fragment is mostly ordered, with some disordered regions (indicated by question marks) at the N-terminus.
- Disorder confidence:** High confidence (red) is observed throughout the fragment.

Fragment 70-120:

- Sequence:** SQNLPI KSAGYTLVLAQ
- Secondary structure:** The fragment is predominantly alpha-helical, with a few beta-strands (indicated by blue arrows).
- SS confidence:** High confidence (red) is observed throughout the fragment.
- Disorder:** The fragment is mostly ordered, with some disordered regions (indicated by question marks) at the C-terminus.
- Disorder confidence:** High confidence (red) is observed throughout the fragment.

➔ Beta strand