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Description	P0AE63
Date	Wed Jan 25 15:20:30 GMT 2012
Unique Job ID	f95df9c17c4e4530

The figure displays protein structure and disorder analysis for two proteins. The top protein is 60 residues long, and the bottom protein is 14 residues long. Both show sequence, secondary structure, and disorder predictions.

**Top Protein (60 residues):**

- Sequence:** M P Y K T K S D L P E S V K H V L P S H A Q D I Y K E A F N S A W D Q Y K D K E D R R D D A S R E E T A H K V A W A A V
- Secondary structure:** Alpha helices (green) are predicted at residues 10-15, 16-25, 26-35, 36-45, and 51-60.
- SS confidence:** High confidence (red) is shown for most of the protein, with some lower confidence (yellow and green) at the N-terminus and C-terminus.
- Disorder:** Disordered regions (grey) are predicted at residues 1-9, 26-27, and 46-50.
- Disorder confidence:** High confidence (red) is shown for most of the protein, with some lower confidence (yellow and green) at the N-terminus and C-terminus.

**Bottom Protein (14 residues):**

- Sequence:** K H E Y A K G D D K W H K K S
- Secondary structure:** Alpha helices (green) are predicted at residues 1-6.
- SS confidence:** High confidence (red) is shown for most of the protein, with some lower confidence (yellow and green) at the N-terminus and C-terminus.
- Disorder:** Disordered regions (grey) are predicted at residues 7-10 and 11-14.
- Disorder confidence:** High confidence (red) is shown for most of the protein, with some lower confidence (yellow and green) at the N-terminus and C-terminus.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

➡ Beta strand