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Description	P76057
Date	Thu Jan 5 12:17:58 GMT 2012
Unique Job ID	1daeb78281d49536

Protein structure and analysis for the full-length protein (1-60) and a fragment (1-10).


Full-length protein (1-60):

- Sequence:** MAQVIFNEEWMVEYGLMLRTGLGARQIEAYRQNCWVEGFHFKRVSPLGKPD SKRGIIWY
- Secondary structure:** Shows a series of alpha-helices (green) and loops (blue). A large blue arrow indicates a long loop region between residues 35 and 45.
- SS confidence:** High confidence (red) for most regions, with some lower confidence (yellow, green, blue) in the loop regions.
- Disorder:** Most of the protein is predicted to be ordered (red), with some disorder (yellow, green, blue) in the loop regions.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow, green, blue) in the loop regions.


Fragment (1-10):


- Sequence:** YPKINQFIKDS
- Secondary structure:** Shows a single alpha-helix (green).
- SS confidence:** High confidence (red) for the entire fragment.
- Disorder:** The fragment is predicted to be ordered (red).
- Disorder confidence:** High confidence (red) for the entire fragment.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand