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Description	P37676
Date	Thu Jan 5 11:56:50 GMT 2012
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Protein structure prediction results for the protein sequence: MKLRSVTYALFIAGLAAFSTSSLAAQSLRF GYET SQTDSQHI AAKKFNDLLQERTKGELK.

The figure displays six panels showing the sequence, secondary structure, SS confidence, Disorder, Disorder confidence, and the full sequence and structure.

Panel 1 (Residues 1-60):

- Sequence:** MKLRSVTYALFIAGLAAFSTSSLAAQSLRF GYET SQTDSQHI AAKKFNDLLQERTKGELK
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.

Panel 2 (Residues 70-120):

- Sequence:** LKLPDSTLGN AQAMISGVRGGTIDMEMSGSNNFAGLSPVMNLLDVPFLFRDTAHAKHTL
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.

Panel 3 (Residues 130-180):

- Sequence:** DGKVGDDLKASLEGKGLKVLAYWENGWRDVTNSRAPVKTPADLKGLKIRTNNSPMNIAAF
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.

Panel 4 (Residues 190-240):

- Sequence:** KVFGANPIPMPPAEVYTGLETRTIDAQEHPI NVVWSAKFFE VQKFLSLTHHAYSPLL VVI
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.


Panel 5 (Residues 250-300):

- Sequence:** NKAKFDGLSP EFQQALVSSAQEAGNYQRKLVAEDQKKI I DGMKEAGVEVI TDLDRKAFSD
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.


Panel 6 (Residues 310-320):


- Sequence:** ALGNQVRDMFVKDVPQGADLLKAVDEVQ
- Secondary structure:** Shows several alpha-helices (green cylinders) and beta-strands (blue arrows).
- SS confidence:** High confidence (red) for most regions.
- Disorder:** Shows some disordered regions (grey) and high confidence (red) for others.
- Disorder confidence:** High confidence (red) for most regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand