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Protein structure prediction results for the protein sequence MSVQQIDWDLALIQKYNYSGRPYTSYPTALFESEDFGEQAFLLQAVARYPERPLSLYVHIP. The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence across the entire length of the protein (1-420 residues).

**Sequence:** MSVQQIDWDLALIQKYNYSGRPYTSYPTALFESEDFGEQAFLLQAVARYPERPLSLYVHIP

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 10 to 30, a beta-strand at residue 35, and a large alpha-helix from residue 38 to 110. A beta-strand is also present at residue 115.

**SS confidence:** The confidence is generally high, with a notable dip around residue 35.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 35 and 115.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 35.

**Sequence:** FCHKLCYFCGCKNIVTRQQHKADQYLDALDAQEIVHRAPLFAGRHVSQLHWGGGTPPTLYLNK

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 70 to 110, a beta-strand at residue 115, and a large alpha-helix from residue 118 to 180. A beta-strand is also present at residue 185.

**SS confidence:** The confidence is generally high, with a notable dip around residue 115.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 115 and 185.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 115.

**Sequence:** AQISRLMKLLRENFQFNADAEISIEVDPREIELDVL DHLRAEGFNRLSMGVQDFNKEVQR

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 130 to 180, a beta-strand at residue 185, and a large alpha-helix from residue 190 to 240. A beta-strand is also present at residue 245.

**SS confidence:** The confidence is generally high, with a notable dip around residue 185.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 185 and 245.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 185.

**Sequence:** LVNREQDEEFI FALLNHAREIGFTSTNIDL IYGLPKQTPESFAFTLKRVAELNPDRLSVF

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 190 to 240, a beta-strand at residue 245, and a large alpha-helix from residue 250 to 300. A beta-strand is also present at residue 305.

**SS confidence:** The confidence is generally high, with a notable dip around residue 245.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 245 and 305.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 245.

**Sequence:** NYAHLPTIFAAQRKIKDADLPSPQQKL DILQETIAFLTQSGYQFIMGDMHFARPDDDELAVA

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 250 to 300, a beta-strand at residue 305, and a large alpha-helix from residue 310 to 360. A beta-strand is also present at residue 365.

**SS confidence:** The confidence is generally high, with a notable dip around residue 305.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 305 and 365.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 305.

**Sequence:** QREGVLHRNFQGYTTQGD TLLGMGVSAISMI GDCYAQNQKELKQYYQQVDEQGNALWRG

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 310 to 360, a beta-strand at residue 365, and a large alpha-helix from residue 370 to 420. A beta-strand is also present at residue 425.

**SS confidence:** The confidence is generally high, with a notable dip around residue 365.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 365 and 425.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 365.

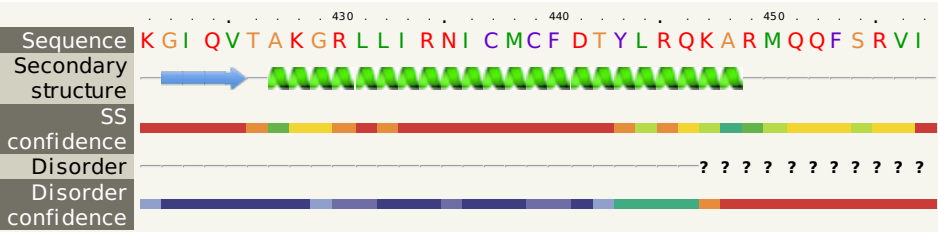
**Sequence:** IALTRDDCIRRDVIKSLICNFRLDYAPIEKQWDLHFADYFAEDL KLLAPLAKDGLVDVDE

**Secondary structure:** The structure is primarily composed of alpha-helices (green cylinders) and beta-strands (blue arrows). Key features include a long alpha-helix from residue 370 to 420, a beta-strand at residue 425, and a large alpha-helix from residue 430 to 480. A beta-strand is also present at residue 485.

**SS confidence:** The confidence is generally high, with a notable dip around residue 425.

**Disorder:** The protein is mostly ordered, with a few regions of low confidence (indicated by question marks) around residues 425 and 485.

**Disorder confidence:** The confidence is generally high, with a notable dip around residue 425.



Confidence Key

High(9) [red bar] [orange bar] [yellow bar] [green bar] [light blue bar] [dark blue bar] Low (0)

? Disordered

Alpha helix

Beta strand