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Protein structure and disorder analysis of the C-terminal region (residues 1 to 420). The figure displays the amino acid sequence, secondary structure, solvent accessibility (SS), confidence, and disorder for each residue.

**Sequence:** MRKI VAMAVI CLTAASGLTSA YAAQLADDE AGLRI RLKNE LRRADKPSAGAGRDI YAVVQ

**Secondary structure:** [Alpha-helices and loops represented by blue arrows]

**SS (Solvent Accessibility):** [Bar chart showing accessibility levels]

**confidence:** [Bar chart showing confidence levels]


**Disorder:** [Bar chart showing disorder predictions with question marks]

**Disorder confidence:** [Bar chart showing confidence in disorder predictions]


Residue numbers: 1, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420.


Sequence	K
Secondary structure	—
SS confidence	■
Disorder	?
Disorder confidence	■

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand