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Protein structure and disorder analysis of the C-terminal region (residues 1 to 350). The figure displays the amino acid sequence, secondary structure, solvent accessibility (SS), confidence, and disorder predictions for this region. The sequence is color-coded by physicochemical properties. Secondary structure is shown as blue arrows. Solvent accessibility is shown as a red and green bar. Confidence is shown as a green bar. Disorder is shown as a grey bar with question marks. The C-terminal region (residues 1-350) shows a high degree of disorder, with many residues marked as '?' in the disorder prediction.

Residue	Sequence	Secondary structure	SS	confidence	Disorder	Disorder confidence
1	M	α	High	High	?	High
10	L	α	High	High	?	High
20	V	α	High	High	?	High
30	K	α	High	High	?	High
40	A	α	High	High	?	High
50	S	α	High	High	?	High
60	K	α	High	High	?	High
70	N	α	High	High	?	High
80	E	α	High	High	?	High
90	A	α	High	High	?	High
100	S	α	High	High	?	High
110	D	α	High	High	?	High
120	N	α	High	High	?	High
130	A	α	High	High	?	High
140	S	α	High	High	?	High
150	S	α	High	High	?	High
160	A	α	High	High	?	High
170	Q	α	High	High	?	High
180	T	α	High	High	?	High
190	N	α	High	High	?	High
200	S	α	High	High	?	High
210	D	α	High	High	?	High
220	F	α	High	High	?	High
230	G	α	High	High	?	High
240	V	α	High	High	?	High
250	N	α	High	High	?	High
260	I	α	High	High	?	High
270	L	α	High	High	?	High
280	S	α	High	High	?	High
290	E	α	High	High	?	High
300	T	α	High	High	?	High
310	I	α	High	High	?	High
320	F	α	High	High	?	High
330	N	α	High	High	?	High
340	V	α	High	High	?	High
350	F	α	High	High	?	High

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand