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Protein structure and disorder analysis of the C-terminal region (residues 1-420). The figure displays the amino acid sequence, secondary structure (SS), confidence scores, and disorder predictions for the C-terminal region. The sequence is color-coded by physicochemical properties. Secondary structure is shown as green cylinders (alpha-helices) and blue arrows (beta-strands). Disorder is indicated by a red line with question marks. Confidence scores are shown as a bar chart below the disorder line.

Residue	Sequence	SS	Confidence	Disorder
1-60	MNRDSFYPAIACFPLLLMLLAGCAPMHETRQALSQQTPAAQVDTALPTALKMVGQT XQWWL	Alpha-helices	High	Disordered
61-120	EYHDNQLTSLINNALQNAPDMQVAEQRIQLAEAQAQAVATQDGPQIDFSADMERQKMSAE	Alpha-helices, Beta-strand	High	Disordered
121-180	GLMGPFALNDPAAGTTGPWYTNGT FGLTAGVHLDI WGNRAEVTARLGTVKARAAEREQT	Beta-strand, Alpha-helices	High	Disordered
181-240	RQLLAGSVARLYWEWQTQAALNTVLQQIEKEQNTIIATDRQLYQNGITSSVEGVETDINA	Alpha-helices	High	Disordered
241-300	SKTRQQ LNDVAGKMKIIEARLSALTNNQTKSLKLKPVALPKVASQLPDELGYSL LARRAD	Alpha-helices	High	Disordered
301-360	LQAAHWYVSSLSTIDAAKA AFYPDINLMAFLQQDALHLSDLFRHSAQQMGV TAGLTLPI	Alpha-helices, Beta-strand	High	Disordered
361-420	FDSGRLNANLDIAKAESNLSIASYNKAVVEAVNDVARAASQVQTLAEKNQHQAQIERDAL	Alpha-helices	High	Disordered

