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The figure displays the protein structure and disorder analysis for the C-terminal region of the protein, residues 1-420. The analysis is presented in a series of horizontal tracks corresponding to the residue numbers (1 to 420).

Sequence: The amino acid sequence is shown in a color-coded format. The sequence is: MSADLSI GNEI KDSFKETHK WVQNNLKWLKDI EQFYRERAKLEKDYSERLSRLSAEYFNK (residues 1-60), KSSTSVPI SVGDTPTTTPGSI EAAGVVAWNEILSQTDMS KDHDQLSTD FENHVANQLSC (residues 70-120), LFTKLDMTLSKINGFNNDMVNKKDNIYHEL EKAKKDYDEACSTMEMARNRYTKASNDRNK (residues 130-180), KKLDEKEMEMNKCKNEYLIKINQANRTKDKYFQDVP EVDLLQDVNEAKTLFLNDLWLK (residues 190-240), AASVENDLGANVSKRLQAANSVVKQNKPSLNTAIFIKHNLKNWKEPQDFVYKPSPVWHDD (residues 250-300), EKFAVPSSLEVEDLRIKLAKAENDYNSLQDKTQNELSKLSTLNKIKHEMKTNEDNINATK (residues 310-360), FYDTLKEYLNVVSPFTSHETLKLQAEVQIESIQNNVP EEDLDSTDNIDLSKTKKKSGIF S (residues 370-420).

Secondary structure: The secondary structure is represented by green bars indicating alpha-helices and loops. The structure shows a complex arrangement of helices and loops throughout the protein.

SS confidence: The confidence in the secondary structure prediction is shown as a red bar. The confidence is generally high, with some lower confidence regions (yellow/green) around residues 10-20 and 30-40.

Disorder: The disorder analysis is shown as a series of question marks (?) indicating regions of predicted disorder. Disordered regions are primarily located at the N-terminus (residues 1-20), around residues 70-120, and at the C-terminus (residues 370-420).

Disorder confidence: The confidence in the disorder prediction is shown as a series of colored bars (green, yellow, orange, red) indicating the level of confidence. Higher confidence (red) is seen in the N-terminal region and around residues 370-420.

