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The figure displays protein structure and disorder analysis for the full-length protein (residues 1-240) and a fragment (residues 191-204). The analysis includes sequence, secondary structure, solvent accessibility (SS), confidence, and disorder predictions.


Full-length protein (1-240):

- Sequence:** MI KQTIVALLLSVGASSVFAAGTVKVFSSNGSSEAKTTLTGA EHLI DLVGQPRRLANS WWP GA
- Secondary structure:** Alpha helices (green) and beta strands (blue) are shown. Helices are located at residues 1-10, 11-15, 16-20, 21-25, 26-30, 31-35, 36-40, 41-45, 46-50, 51-55, 56-60, 61-65, 66-70, 71-75, 76-80, 81-85, 86-90, 91-95, 96-100, 101-105, 106-110, 111-115, 116-120, 121-125, 126-130, 131-135, 136-140, 141-145, 146-150, 151-155, 156-160, 161-165, 166-170, 171-175, 176-180, 181-185, 186-190, 191-195, 196-200, 201-205, 206-210, 211-215, 216-220, 221-225, 226-230, 231-235, 236-240.
- SS confidence:** A bar chart showing confidence levels for each residue.
- Disorder:** A bar chart showing disorder predictions. Residues 1-10, 11-15, 16-20, 21-25, 26-30, 31-35, 36-40, 41-45, 46-50, 51-55, 56-60, 61-65, 66-70, 71-75, 76-80, 81-85, 86-90, 91-95, 96-100, 101-105, 106-110, 111-115, 116-120, 121-125, 126-130, 131-135, 136-140, 141-145, 146-150, 151-155, 156-160, 161-165, 166-170, 171-175, 176-180, 181-185, 186-190, 191-195, 196-200, 201-205, 206-210, 211-215, 216-220, 221-225, 226-230, 231-235, 236-240 are predicted to be disordered.
- Disorder confidence:** A bar chart showing confidence levels for each residue.


Fragment (191-204):


- Sequence:** QRI P Q
- Secondary structure:** Alpha helix (green) is shown at residues 191-195.
- SS confidence:** A bar chart showing confidence levels for each residue.
- Disorder:** A bar chart showing disorder predictions. Residues 191-195 are predicted to be disordered.
- Disorder confidence:** A bar chart showing confidence levels for each residue.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand