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The figure displays protein structure and disorder analysis for the full-length protein (1-240) and a fragment (EGNARL). The analysis includes sequence, secondary structure, confidence, and disorder predictions.

Full-length protein (1-240):

- Sequence:** MF FNTKHTTALCFVTCMAFSSSSSIADI V I S GTRVI YKSDQKSVNVRL ENKGNP LLLVQS W
- Secondary structure:** Alpha helix (residues 1-20), Beta strand (residues 25-30), Beta strand (residues 35-40), Beta strand (residues 45-50), Beta strand (residues 55-60), Beta strand (residues 65-70), Beta strand (residues 75-80), Beta strand (residues 85-90), Beta strand (residues 95-100), Beta strand (residues 105-110), Beta strand (residues 115-120), Beta strand (residues 125-130), Beta strand (residues 135-140), Beta strand (residues 145-150), Beta strand (residues 155-160), Beta strand (residues 165-170), Beta strand (residues 175-180), Beta strand (residues 185-190), Beta strand (residues 195-200), Beta strand (residues 205-210), Beta strand (residues 215-220), Beta strand (residues 225-230), Beta strand (residues 235-240).
- SS confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) in the N-terminal region.
- Disorder:** Predicted disordered regions (indicated by ?) are located at the N-terminus (residues 1-10), between residues 20-30, between residues 30-40, between residues 40-50, between residues 50-60, between residues 60-70, between residues 70-80, between residues 80-90, between residues 90-100, between residues 100-110, between residues 110-120, between residues 120-130, between residues 130-140, between residues 140-150, between residues 150-160, between residues 160-170, between residues 170-180, between residues 180-190, between residues 190-200, between residues 200-210, between residues 210-220, between residues 220-230, between residues 230-240.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) in the N-terminal region.

Fragment (EGNARL):

- Sequence:** EGNARL
- Secondary structure:** Alpha helix (residues 1-6).
- SS confidence:** High confidence (red) for the entire fragment.
- Disorder:** Predicted disordered regions (indicated by ?) are located at the N-terminus (residues 1-1), between residues 1-2, between residues 2-3, between residues 3-4, between residues 4-5, between residues 5-6, between residues 6-7.
- Disorder confidence:** High confidence (red) for most regions, with some lower confidence (yellow/green) in the N-terminal region.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand