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The figure displays protein structure and disorder analysis for three segments of a protein. The top segment (1-60) shows a protein with a high degree of disorder, indicated by the 'Disorder' track. The middle segment (70-120) shows a protein with a high degree of disorder, indicated by the 'Disorder' track. The bottom segment (1-60) shows a protein with a high degree of disorder, indicated by the 'Disorder' track.

Protein 1 (1-60):

- Sequence: M E G E L I E N N G L D I Y D T S E T P K K R G R P A K Y N E K I A T Q I V L L V S E G Y S L R K I S M M P G M P S H R
- Secondary structure: Alpha helix (residues 1-10), Alpha helix (residues 11-20), Alpha helix (residues 21-30), Alpha helix (residues 31-40), Alpha helix (residues 41-50), Alpha helix (residues 51-60)
- SS confidence: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder confidence: High (red) for most regions, lower (yellow/green) for some regions.


Protein 2 (70-120):

- Sequence: Q M M R W Q L E H M D F R E G I A W M S W L W C A E A G R R A V E I I D E V D I N A E D G P K Q L R K A E A K A K A L L
- Secondary structure: Alpha helix (residues 70-80), Alpha helix (residues 81-90), Alpha helix (residues 91-100), Alpha helix (residues 101-110), Alpha helix (residues 111-120)
- SS confidence: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder confidence: High (red) for most regions, lower (yellow/green) for some regions.


Protein 3 (1-60):


- Sequence: A A A K L N S L K H S P F G D D K Q
- Secondary structure: Alpha helix (residues 1-10), Alpha helix (residues 11-20), Alpha helix (residues 21-30), Alpha helix (residues 31-40), Alpha helix (residues 41-50), Alpha helix (residues 51-60)
- SS confidence: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder: High (red) for most regions, lower (yellow/green) for some regions.
- Disorder confidence: High (red) for most regions, lower (yellow/green) for some regions.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand