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Description	P0A940
Date	Thu Jan 5 11:09:19 GMT 2012
Unique Job ID	a52ee0e5b33074ab

Protein structure and disorder analysis of the full-length protein (1-420). The figure displays the amino acid sequence, secondary structure, solvent accessibility (SS), confidence, and disorder predictions across the entire protein length.

**Sequence:** MAMKLLI ASLLFSSATVYGAEGFVVKDIHFEGLQRVAVGAALLSMPVVRTGDTVNDEDI S

**Secondary structure:** [Alpha-helix] [Coiled-coil] [Alpha-helix] [Alpha-helix] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

**Sequence:** NTIRALFATGNFEDVRVLRDGD TLLVQVKERPTIASITFSGNKSVKDDMLKQNL EASGVR

**Secondary structure:** [Alpha-helix] [Coiled-coil] [Coiled-coil] [Coiled-coil] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

**Sequence:** VGESLDRTTI ADIEKGLDFYYSVGKYSASVKA VVTP LPRNRVDLKL V FQEGVSAEI QQI

**Secondary structure:** [Alpha-helix] [Coiled-coil] [Coiled-coil] [Coiled-coil] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

**Sequence:** NIVGNHAF TTDELI SHFQLRDEVPW WNVVGDRKYQKQKL AGDLETLRSY LDRGYARFNI

**Secondary structure:** [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

**Sequence:** DSTQVSLTPDKKGI VVTVNI TEGDQYKLSGVEVSGNL AGHSAEI EQLTKI EPGE L YNGTK

**Secondary structure:** [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

**Sequence:** VTKMEDDI KKLGRYGYA YPRVQSMPEI NDADKTVKLRV NV DAGNR FYVRKI RFEGNDTS

**Secondary structure:** [Alpha-helix] [Coiled-coil] [Coiled-coil] [Coiled-coil] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]

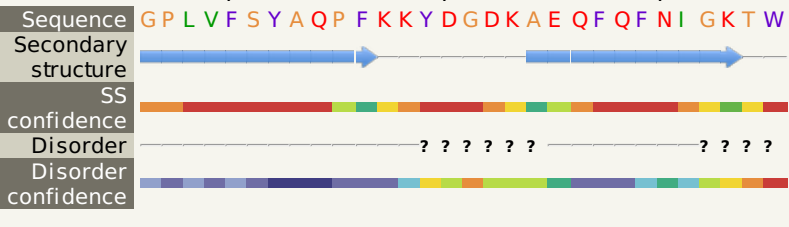
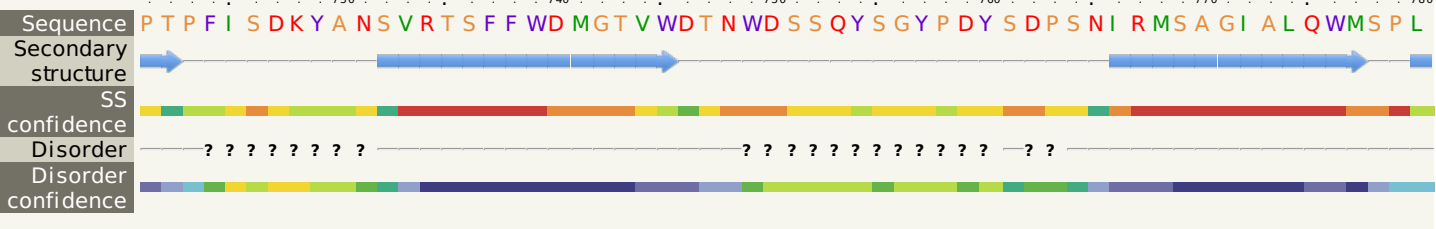
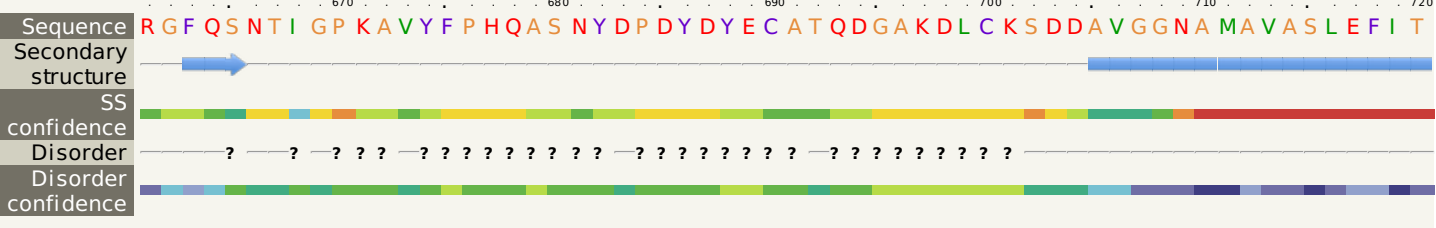
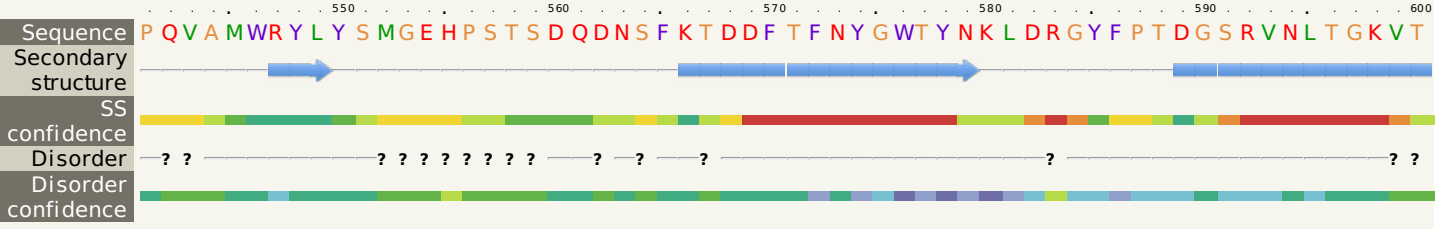
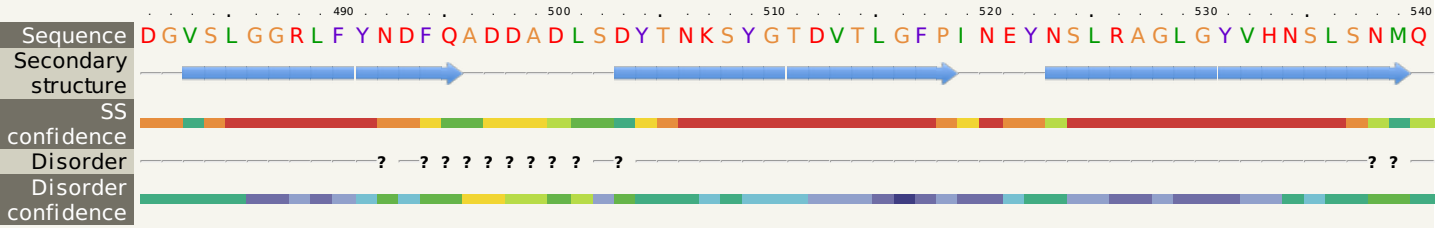
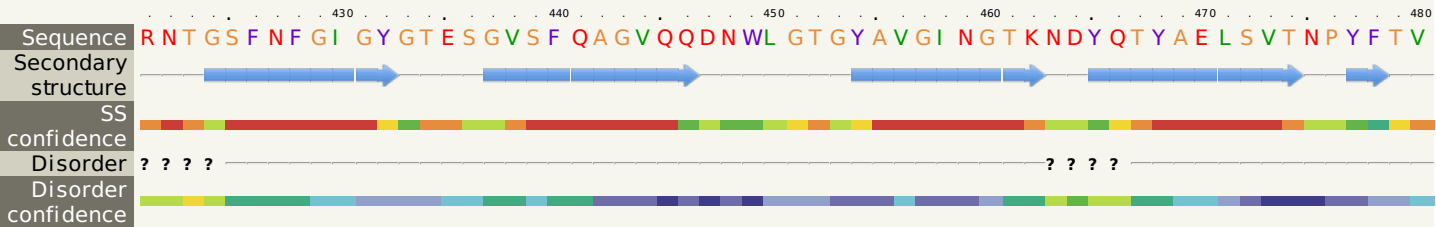
**Sequence:** KDAVLRREMRQMEGAWLGS DLDV DQGKERL NRLGFFETVDTDTQRVP GSPDQVDV VYKVKE

**Secondary structure:** [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix] [Alpha-helix]

**SS confidence:** [High] [High] [High] [High] [High]

**Disorder:** [Disordered] [Disordered] [Disordered] [Disordered] [Disordered]

**Disorder confidence:** [High] [High] [High] [High] [High]



Confidence Key

High(9) [Color scale from red to blue] Low (0)

? Disordered

Alpha helix

Beta strand