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Description	Q46811
Date	Wed Jan 25 15:21:12 GMT 2012
Unique Job ID	49666942a3972321

Protein structure visualization of the full-length protein (1-480) in five segments. Each segment shows the amino acid sequence, secondary structure (alpha-helices in green, beta-strands in blue), and disorder predictions (SS confidence, Disorder, Disorder confidence).

Segment 1 (1-60): Sequence: MGDIMRPIPF EELLTRIFDEYQQQRSIFGIPEQQFYSPVK GKTVSVFGET CATPVGPAAG. Secondary structure: Alpha-helices at positions 10-25 and 35-40. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 2 (70-120): Sequence: PHTQLAQNI V TSWLTGGRFI ELKTVQILDRLELEKPCIDA EDECFNTEWS TEFTLLKAWD. Secondary structure: Alpha-helices at positions 70-80 and 110-120. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 3 (130-180): Sequence: EYLKAWFALH LLEAMFQPSDSGKSFI FNM SVGYNLEGI KQPPMQQFI DNMDASDHPKFA. Secondary structure: Alpha-helices at positions 130-140 and 170-180. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 4 (190-240): Sequence: QYRDTLNKLL QDDAFLARHGLQEKRESLQALPARIPTSMV HGVTLSTMHG C PPHEIEAIC. Secondary structure: Alpha-helices at positions 190-200 and 230-240. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

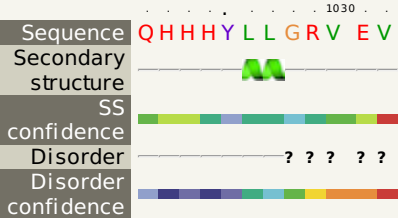
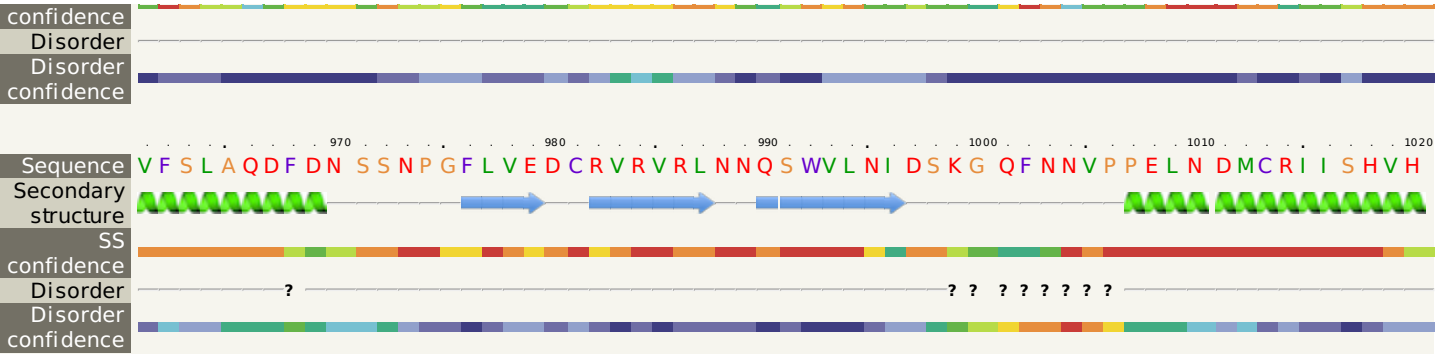
Segment 5 (250-300): Sequence: RYMLEEKGLN T FVKLNPTLLGYARVREILDVCGFYI GLKEESFDHDLKL TQALEMLERL. Secondary structure: Alpha-helices at positions 250-260 and 290-300. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 6 (310-360): Sequence: MALAKEKSLG FGVKLTNTLTGINNKGALPGEEMYMSGRAL FPLSINVAAVLSRAFDGKLP. Secondary structure: Alpha-helices at positions 310-320 and 350-360. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 7 (370-420): Sequence: ISYSGGASQL TIRDFDTGIRPITMATDLLKPGGYLRLSA CMRELEGS DA WGLDHVDVER. Secondary structure: Alpha-helices at positions 370-380 and 410-420. Disorder: High confidence disorder regions at the N-terminus and C-terminus.

Segment 8 (430-480): Sequence: (Continuation of the previous segment). Secondary structure: Alpha-helices at positions 430-440 and 470-480. Disorder: High confidence disorder regions at the N-terminus and C-terminus.





Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand