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Description	P40120
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Protein structure and disorder analysis of the full-length protein (1-420 aa). The figure displays the amino acid sequence, secondary structure (SS), confidence scores, and disorder predictions across the entire protein length. The sequence is color-coded by physicochemical properties. Secondary structure elements are shown as blue arrows (alpha-helices) and green cylinders (beta-strands). Disorder is indicated by a red line with confidence scores below it.

Sequence: MDRRRFIKGSMAAAVCGTSGIASLFSQAAF AADSDIADGQTQRFDFSLQSM AHDLAQT
Secondary structure: [SS elements: 1-28, 31-34, 51-60]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 1-28, 31-34, 51-60]
Disorder confidence: [Disorder confidence scores]

Sequence: AWRGAPRPLPDTLATMTPQAYNSIQYDAEKSLWHNVENRQLDAQFFHMGMGFRRRVRMFS
Secondary structure: [SS elements: 71-78, 81-88, 91-98, 101-108, 111-118, 121-128]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 71-78, 81-88, 91-98, 101-108, 111-118, 121-128]
Disorder confidence: [Disorder confidence scores]

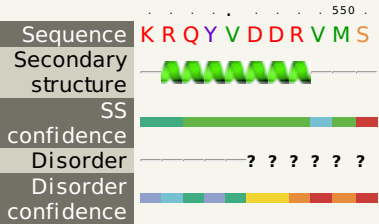
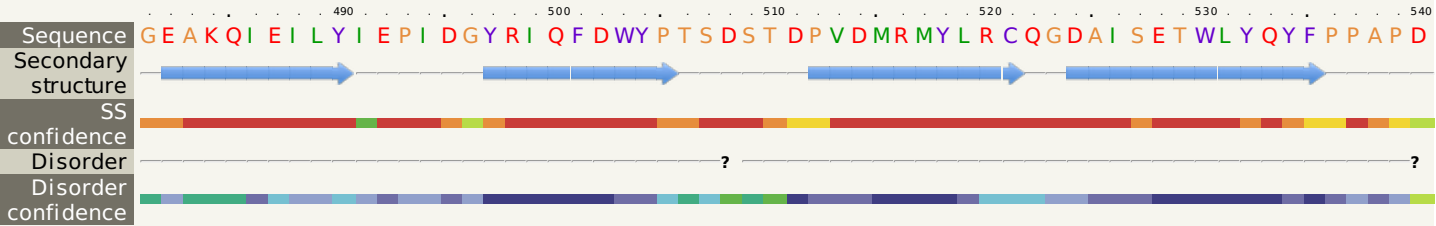
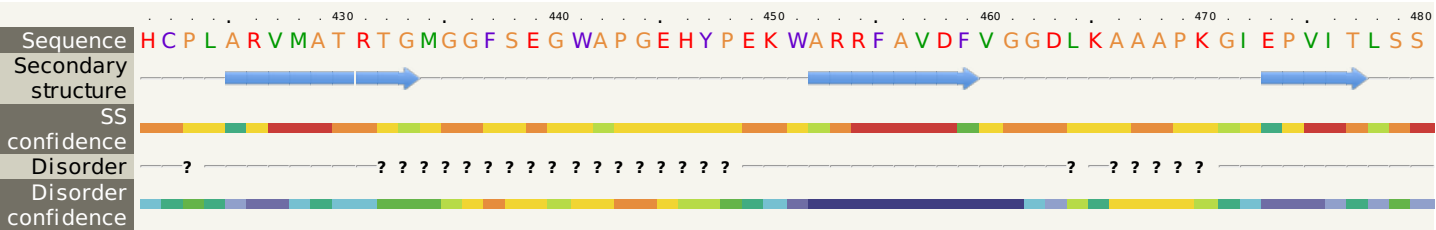
Sequence: VDPATHLAREIHFRPELKFYNDAGVDTKQLEGSDDLGFAGFRVFKAPELARRDVVSFLGA
Secondary structure: [SS elements: 131-138, 141-148, 151-158, 161-168, 171-178, 181-188]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 131-138, 141-148, 151-158, 161-168, 171-178, 181-188]
Disorder confidence: [Disorder confidence scores]

Sequence: SYFRAVDDTYQYGLSARGLAIDTYTDSKEEFPDFTAFWFDTVKPGATTFTVYALLDSASI
Secondary structure: [SS elements: 191-198, 201-208, 211-218, 221-228, 231-238, 241-248]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 191-198, 201-208, 211-218, 221-228, 231-238, 241-248]
Disorder confidence: [Disorder confidence scores]

Sequence: TGAYKFTIHCEKSQVIMDVENHLYARKDIKQLGIA PMTSMFSCGTNERRMCDTIHPQIHD
Secondary structure: [SS elements: 251-258, 261-268, 271-278, 281-288, 291-298, 301-308]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 251-258, 261-268, 271-278, 281-288, 291-298, 301-308]
Disorder confidence: [Disorder confidence scores]

Sequence: SDRLSMWRGNGEWICRPLNPNQKLQFNAYTDNNPKGFGLLQLDRDFS HYQDI MGWYNKRP
Secondary structure: [SS elements: 311-318, 321-328, 331-338, 341-348, 351-358, 361-368]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 311-318, 321-328, 331-338, 341-348, 351-358, 361-368]
Disorder confidence: [Disorder confidence scores]

Sequence: SLWVEPRNKVGKGTIGLMEIPTTG ETL DNI VCFWQPEKAVKAGDEF AFQYRLYWSAQPPV
Secondary structure: [SS elements: 371-378, 381-388, 391-398, 401-408, 411-418, 421-428]
SS confidence: [Confidence scores for SS elements]
Disorder: [Disorder prediction: 371-378, 381-388, 391-398, 401-408, 411-418, 421-428]
Disorder confidence: [Disorder confidence scores]



Confidence Key

High(9) Low (0)

? Disordered

Alpha helix

Beta strand