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Description	P0ACY3
Date	Thu Jan 5 11:19:25 GMT 2012
Unique Job ID	409e9b5324026365

Protein structure prediction results for a protein of 420 residues. The image displays six blocks of analysis, each corresponding to a 60-residue segment. Each block includes the amino acid sequence, secondary structure prediction (SS) with helices and strands shown as green cylinders and blue arrows, confidence scores for SS, disorder, and disorder confidence, and disorder predictions.

Block 1 (Residues 1-60): Sequence: MNI F DHY RQR YEA AKDEE FT LQE FLT TCR QDRS AY ANAA ER LLMAI GE PV MV DTA QE PR L. SS: Helices at 1-10, 15-20, 25-30, 35-40, 45-50, 55-60. Disorder: 1-10, 15-20, 25-30, 35-40, 45-50, 55-60.

Block 2 (Residues 61-120): Sequence: SRL F S NRVI AR YPA FEE FYG MEDAI EQI VSY LKHAA QGLE EKKQI LY LL GPV GGGKSS LA. SS: Helices at 61-70, 75-85, 90-100, 105-115, 120-125. Disorder: 61-70, 75-85, 90-100, 105-115, 120-125.

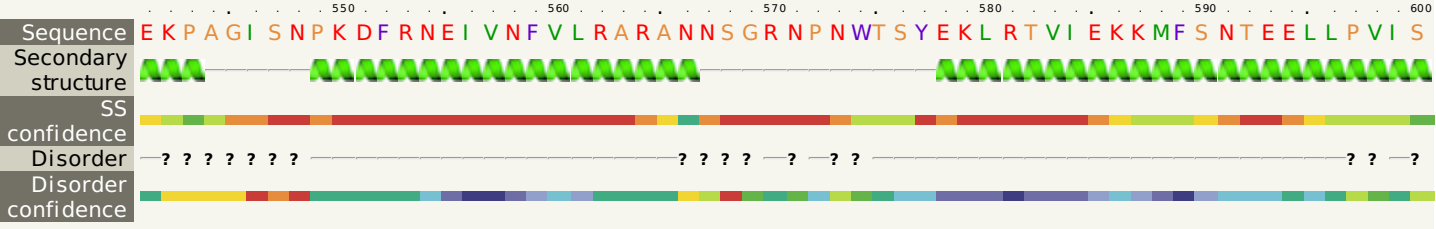
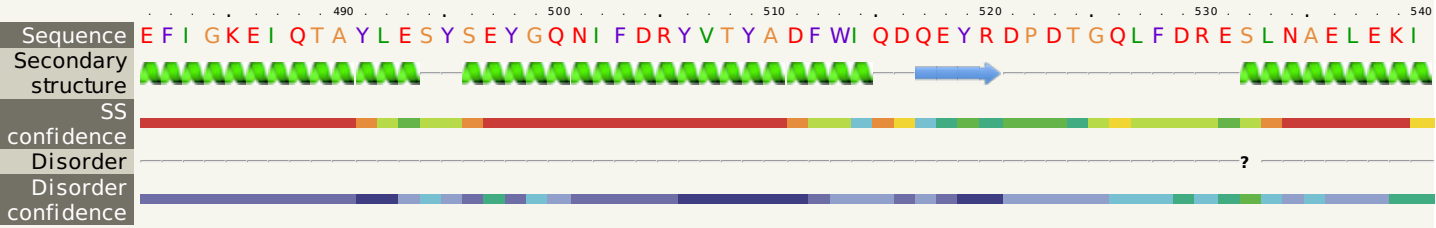
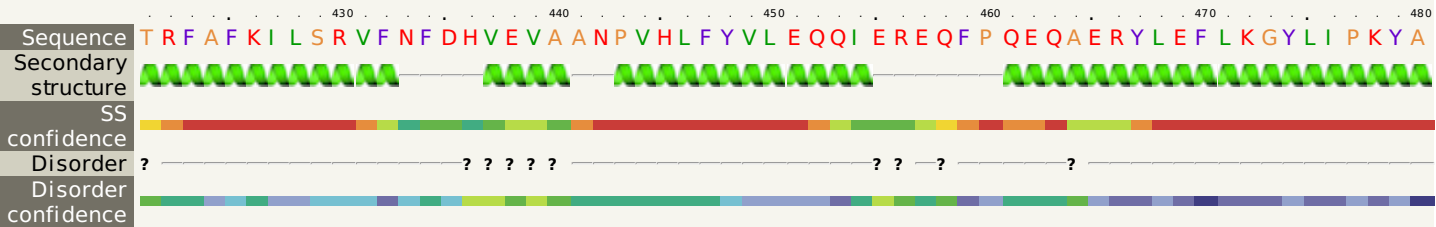
Block 3 (Residues 121-180): Sequence: ERL KSL MQL VPI YVL SANGER SPV NDHP FCL FNP QEDA QI LEKEY GI PRR YLGTI MSP WA. SS: Helices at 121-130, 135-145, 150-160, 165-175, 180-185. Disorder: 121-130, 135-145, 150-160, 165-175, 180-185.

Block 4 (Residues 181-240): Sequence: AKRL HEF GGD I TKFR VVKV WPSI LQQI AIA KTE PGDEN NQDI SAL VGKV DI RKLE HYAQ N. SS: Helices at 181-190, 195-205, 210-220, 225-235, 240-245. Disorder: 181-190, 195-205, 210-220, 225-235, 240-245.

Block 5 (Residues 241-300): Sequence: DPDA YGY SGA LCR ANQGI ME FVEM FKA PI KVL HPLL TATQ EGN YNGTE GI SAL PFNGI IL. SS: Helices at 241-250, 255-265, 270-280, 285-295, 300-305. Disorder: 241-250, 255-265, 270-280, 285-295, 300-305.

Block 6 (Residues 301-360): Sequence: AHS NESE WVT FRNN KNNEA FLDR VYI VKVP YCLRI SEEI K IYE KLLNH SELTH APCAP GT. SS: Helices at 301-310, 315-325, 330-340, 345-355, 360-365. Disorder: 301-310, 315-325, 330-340, 345-355, 360-365.

Block 7 (Residues 361-420): Sequence: LETLS RFSI LSRL KEPEN SSI YSKMR VYD GESL KDTDP KAKSY QEY RDY AGV DEGMNGL S. SS: Helices at 361-370, 375-385, 390-400, 405-415, 420-425. Disorder: 361-370, 375-385, 390-400, 405-415, 420-425.



Confidence Key
High(9) Low (0)
? Disordered
Alpha helix
Beta strand