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Description	P77288
Date	Thu Jan 5 12:27:16 GMT 2012
Unique Job ID	ec0a19cbc18fd33a

Sequence: MSKFVKTAIAAAMVVGAF... (residues 1-120)

Secondary structure: [Alpha-helix (1-25), Beta-strand (30-35), Beta-strand (40-45), Beta-strand (50-55), Beta-strand (60-65)]

SS confidence: [High confidence for helix, lower for strands]

Disorder: [Disordered regions at 1-5, 25-30, 35-40, 45-50, 55-60, 65-70]

Disorder confidence: [High confidence for disordered regions]

Sequence: AEKLKNGTTTPKNFQIRLQDCVFDTQETMTTTFGTVSSANSNGNYTIFNTDTGAAFNN (residues 70-120)

Secondary structure: [Alpha-helix (70-75), Beta-strand (80-85), Beta-strand (90-95), Beta-strand (100-105), Beta-strand (110-115)]

SS confidence: [High confidence for helix, lower for strands]

Disorder: [Disordered regions at 75-80, 85-90, 95-100, 105-110, 115-120]

Disorder confidence: [High confidence for disordered regions]

Sequence: VSLAIGDSLGTSYKSGMGI DQKI VKDTATNKGKAKQTLNFKAWLVGAADAPDLGNF EANT (residues 130-180)

Secondary structure: [Alpha-helix (130-135), Beta-strand (140-145), Beta-strand (150-155), Beta-strand (160-165), Beta-strand (170-175)]

SS confidence: [High confidence for helix, lower for strands]

Disorder: [Disordered regions at 135-140, 145-150, 155-160, 165-170, 175-180]

Disorder confidence: [High confidence for disordered regions]

Sequence: TFQITYL (residues 1-6)


Secondary structure: [Alpha-helix (1-3)]

SS confidence: [High confidence for helix]


Disorder: [Disordered regions at 4-6]


Disorder confidence: [High confidence for disordered regions]

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand