

Email	l.a.kelley@imperial.ac.uk
Description	P25714
Date	Thu Jan 5 11:42:16 GMT 2012
Unique Job ID	6153acb633a4f4cf

Sequence: MDSQRNLLVLIALLFVSFMIWQAWEQDKNPQPQAQQTQTQTTTAAGSAADQGVPAASGQGKL

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: ISVKTDVLDLTI NTRGGDVEQALLPAYPKE LNSTQPFQLLETSPQFIYQAQSGLTGRDGP

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: DNPANGPRPLYNVEKDAYVLAEQNELQVPMTYTDAAGNTFTKTFVLKRGDYAVNVNYNV

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: QNAGEKPLEISSFGQLKQSI TLPPLDTGSSNFALHTFRGAAYSTPDEKYEKFKFDTIAD

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: NENLNISSKGGVWAMLQQYFATAWI PHNDGTNNFYTANLGNGLAAIGYKSKPVLVQPGQT

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: GAMNSTLWVGPEIQDKMAAVAPHLDLTVDYGWLWFI SQPLFKLLKWIHSFVGNWGFSSII

Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]

Sequence: ITFIVRGI MYPLTKAQYTSMAKMRMLQPKI QAMRERLGDGDKQRI SQEMMALYKAEKVNPL

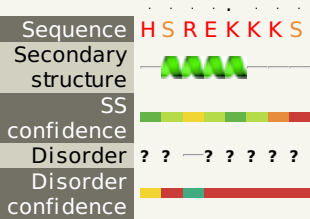
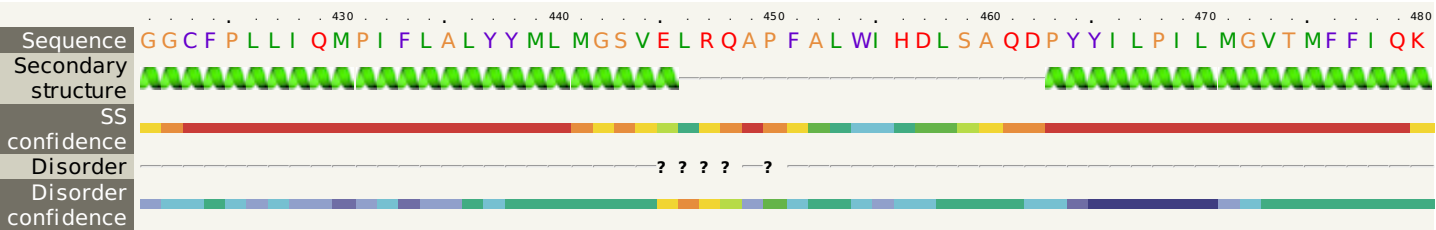
Secondary structure: [Alpha-helices and loops represented by blue arrows and cylinders]

SS: [Solvent accessibility scale from 0 to 100]

confidence: [Confidence score scale from 0 to 100]

Disorder: [Disorder prediction scale from 0 to 100]

Disorder confidence: [Disorder confidence scale from 0 to 100]



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