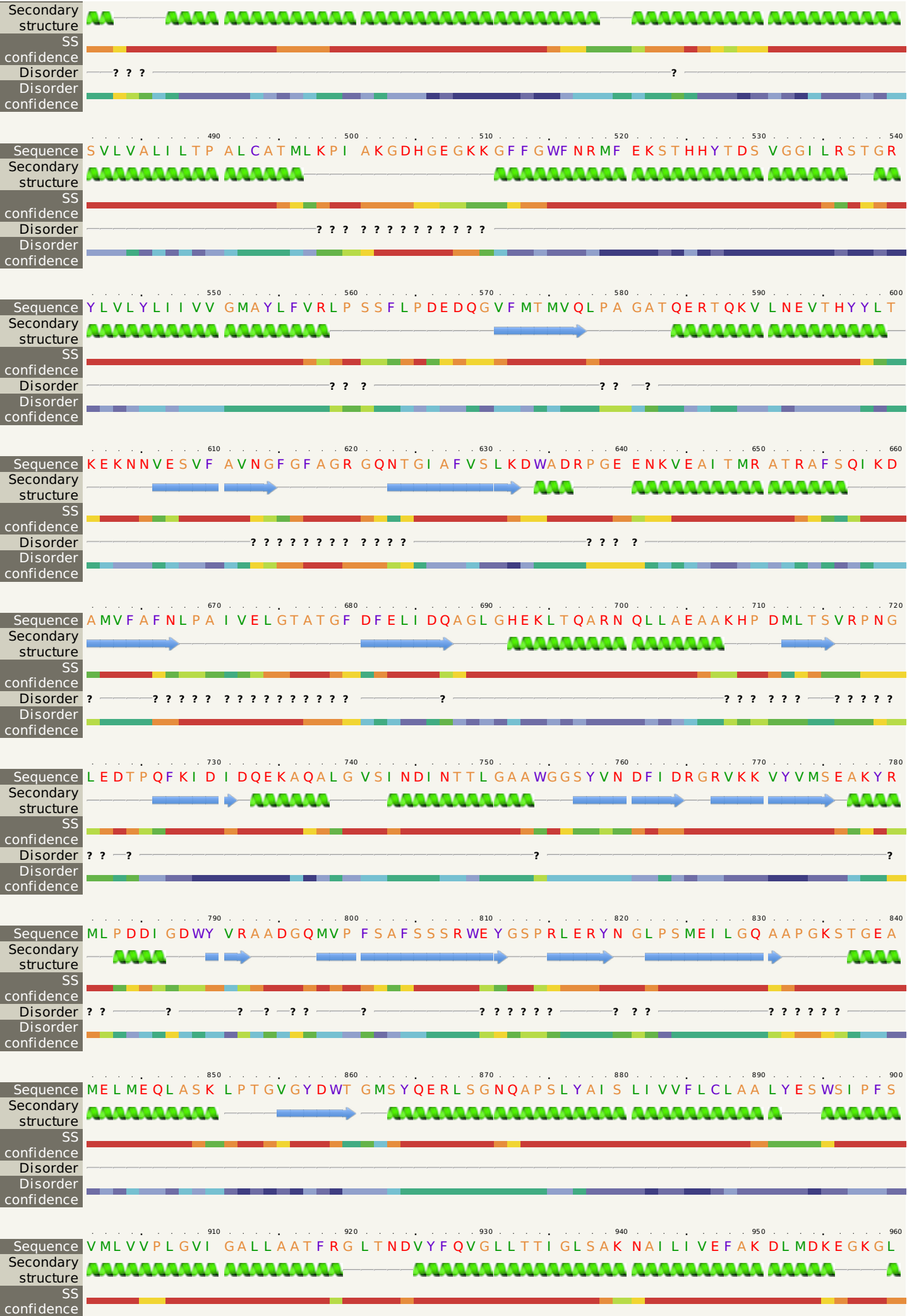
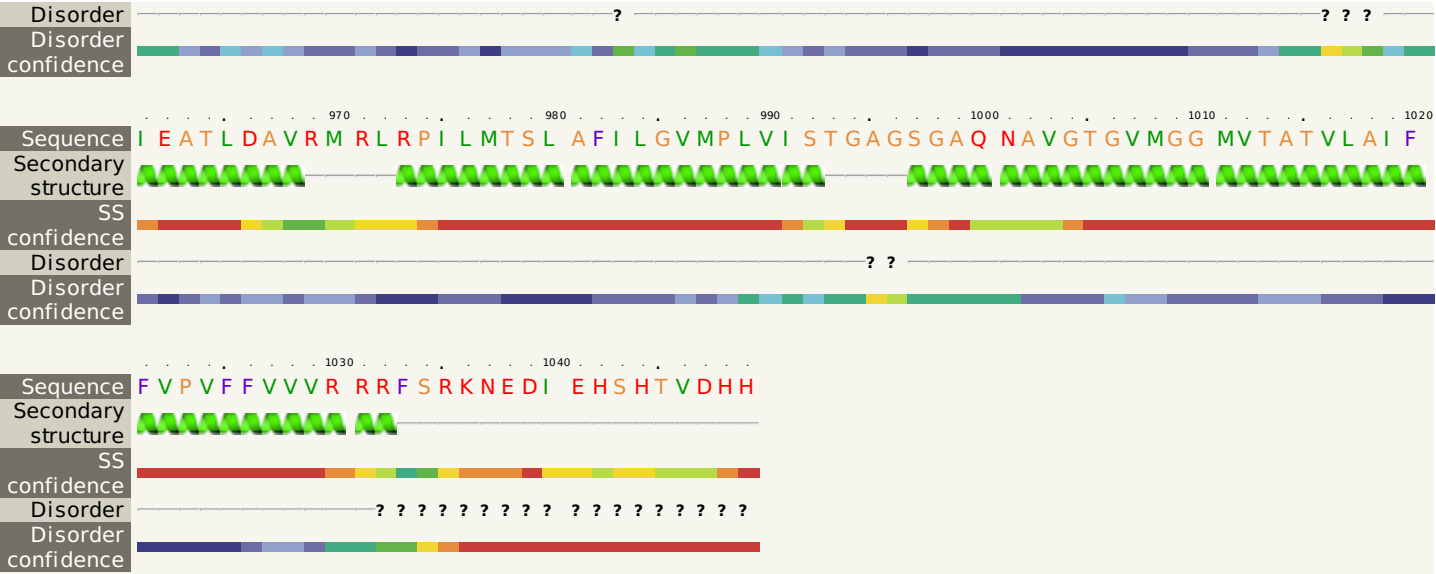


Email	l.a.kelley@imperial.ac.uk
Description	P31224
Date	Thu Jan 5 11:47:22 GMT 2012
Unique Job ID	6b373747e88d0410

Protein structure prediction results for the protein sequence: MPNFFIDRPIFAWVIAIIIMLAGGLAIIKLKPVAQYPTIAPPAVTISASYPGADAKTVQDTVTQVIEQNMNGIDNLMYMSNSSDSTGTVQITLTFESGTDADI AQVQVQNK LQLAMPLLPQEVQQQGVSV EKSSSFLMVVGVI NT DGTMT QEDI SDYVAA NMKDAI SRTS GVG DVQLFGSQYAMRIWMNP NELNKFQLTP VDVITAI KAQNAQVAAGQLG GTPPVKGQQL NASII AQTRLTSTEEFGKIL LKVNQDGSRV LLRDVAKIEL GGENYDII AE FNGQPASGLG I KLATGANALDTAAAIRAEL AKMEPFFPSG LKIVYPYDTTP FVKI SI HEV VKTLVEAII L VFLVMYLF LQNF RATLIPTI AVPVVLLGT F AVLAAFGFSI NT LTMFGMVL AIGLLVDDAI VVVENVERVMAEEGLPPKEA TRKSMGOIQG ALVGI AMVLSAVFVPMAFFG GSTGAIYROF SITIVSAMAL.

The figure displays the sequence, secondary structure, SS confidence, disorder, and disorder confidence for each residue.





Confidence Key
High(9) [red bar] [orange bar] [yellow bar] [light green bar] [green bar] [dark green bar] [blue bar] Low (0)
? Disordered
[green cylinder] Alpha helix
[blue arrow] Beta strand