

Email	l.a.kelley@imperial.ac.uk
Description	P45800
Date	Wed Jan 25 15:20:55 GMT 2012
Unique Job ID	c4f2eb709e6db4f5

Sequence: MSTIVIFLAALLACSLLAGWLIKVRSRRRQLPWTNAFADAQTRKLTPEERSAVENYLES

Secondary structure: 1-10: alpha-helix, 11-20: alpha-helix, 21-30: alpha-helix, 31-40: alpha-helix, 41-50: alpha-helix, 51-60: alpha-helix, 61-70: alpha-helix, 71-80: alpha-helix, 81-90: alpha-helix, 91-100: alpha-helix, 101-110: alpha-helix, 111-120: alpha-helix, 121-130: alpha-helix, 131-140: alpha-helix, 141-150: alpha-helix, 151-160: alpha-helix, 161-170: alpha-helix, 171-180: alpha-helix, 181-190: alpha-helix, 191-200: alpha-helix, 201-210: alpha-helix, 211-220: alpha-helix, 221-230: alpha-helix, 231-240: alpha-helix, 241-250: alpha-helix, 251-260: alpha-helix, 261-270: alpha-helix, 271-280: alpha-helix, 281-290: alpha-helix, 291-300: alpha-helix, 301-310: alpha-helix, 311-320: alpha-helix, 321-330: alpha-helix, 331-340: alpha-helix, 341-350: alpha-helix, 351-360: alpha-helix, 361-370: alpha-helix, 371-380: alpha-helix, 381-390: alpha-helix, 391-400: alpha-helix, 401-410: alpha-helix, 411-420: alpha-helix.

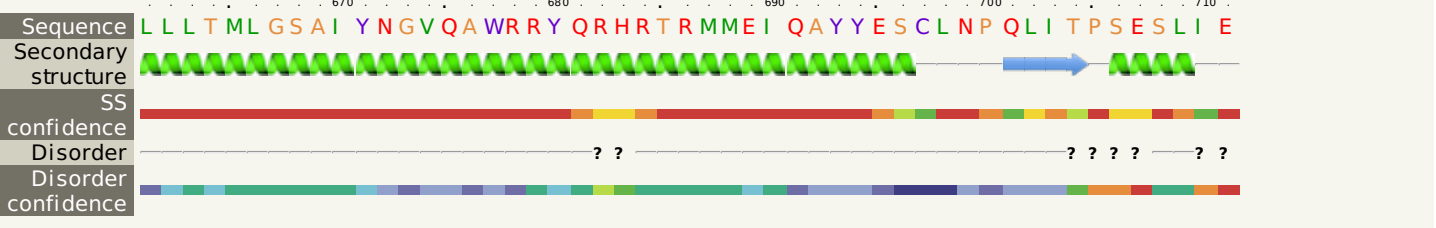
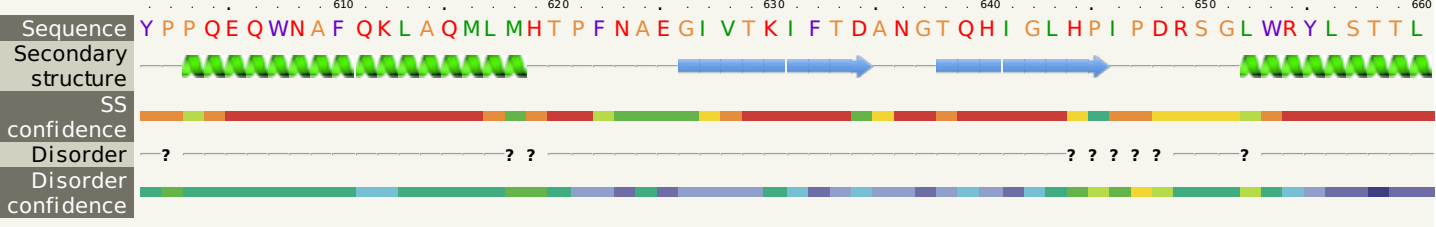
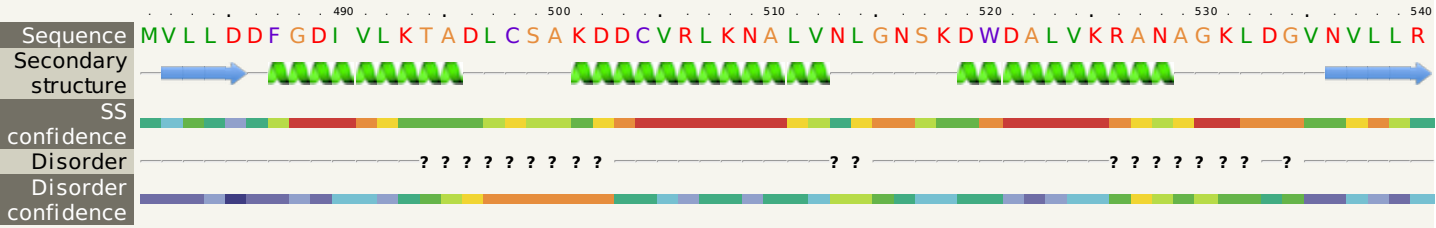
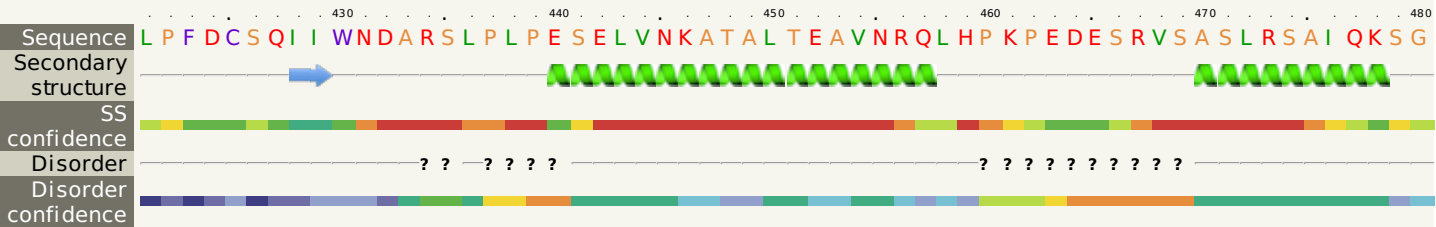
SS confidence: 1-10: 0.9, 11-20: 0.9, 21-30: 0.9, 31-40: 0.9, 41-50: 0.9, 51-60: 0.9, 61-70: 0.9, 71-80: 0.9, 81-90: 0.9, 91-100: 0.9, 101-110: 0.9, 111-120: 0.9, 121-130: 0.9, 131-140: 0.9, 141-150: 0.9, 151-160: 0.9, 161-170: 0.9, 171-180: 0.9, 181-190: 0.9, 191-200: 0.9, 201-210: 0.9, 211-220: 0.9, 221-230: 0.9, 231-240: 0.9, 241-250: 0.9, 251-260: 0.9, 261-270: 0.9, 271-280: 0.9, 281-290: 0.9, 291-300: 0.9, 301-310: 0.9, 311-320: 0.9, 321-330: 0.9, 331-340: 0.9, 341-350: 0.9, 351-360: 0.9, 361-370: 0.9, 371-380: 0.9, 381-390: 0.9, 391-400: 0.9, 401-410: 0.9, 411-420: 0.9.

Disorder: 1-10: 0.0, 11-20: 0.0, 21-30: 0.0, 31-40: 0.0, 41-50: 0.0, 51-60: 0.0, 61-70: 0.0, 71-80: 0.0, 81-90: 0.0, 91-100: 0.0, 101-110: 0.0, 111-120: 0.0, 121-130: 0.0, 131-140: 0.0, 141-150: 0.0, 151-160: 0.0, 161-170: 0.0, 171-180: 0.0, 181-190: 0.0, 191-200: 0.0, 201-210: 0.0, 211-220: 0.0, 221-230: 0.0, 231-240: 0.0, 241-250: 0.0, 251-260: 0.0, 261-270: 0.0, 271-280: 0.0, 281-290: 0.0, 291-300: 0.0, 301-310: 0.0, 311-320: 0.0, 321-330: 0.0, 331-340: 0.0, 341-350: 0.0, 351-360: 0.0, 361-370: 0.0, 371-380: 0.0, 381-390: 0.0, 391-400: 0.0, 401-410: 0.0, 411-420: 0.0.

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Sequence: TQVLQVP GPTGASAPI SLALNAESNNVMM LTHAI TRYGI STDDPNK WRYLDSVEVHLR

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Confidence Key  
High(9) [Color bar] Low (0)  
? Disordered  
Alpha helix  
Beta strand