

Email	l.a.kelley@imperial.ac.uk
Description	Q46808
Date	Thu Jan 5 12:34:35 GMT 2012
Unique Job ID	5ea91f1b9f173ca3

1 10 20 30 40 50 60

Sequence MNI FTEAAKL EEQNCP FAMAQI VDSRGSTP RHSAQMLV RADGSI VGTI GGGMVERKVI EE

Secondary structure

SS

confidence

Disorder

Disorder confidence

70 80 90 100 110 120

Sequence SLQALQERKPR LFHGRMARN GADAVGSDCG GAMS VFI SVHGMRPRLV LI GAGHVNRAI AQ

Secondary structure

SS

confidence

Disorder

Disorder confidence

130 140 150 160 170 180

Sequence SAALLGF DI AVADI YRES LNPEL FPPSTTL LHAES FGAAVEALDI RPDNF VLI ATNNQDR

Secondary structure

SS

confidence

Disorder

Disorder confidence

190 200 210 220 230 240

Sequence EALDKLI EQPI A WLGLLASRR KVKQL FLRQL REKGV AEEHI ARLHAPVGY NI GAETPQE I A

Secondary structure

SS

confidence

Disorder

Disorder confidence

250 260 270 280 290 300

Sequence ISVLA EI LQVKNNAP GGLMMKPS HPSGHQL VVI RGAGDI ASGV ALRLYHAG FKVI MLEVE

Secondary structure

SS

confidence

Disorder

Disorder confidence

310 320 330 340 350 360

Sequence KPTVI RCTVAF AQA VF DGE MTEGV TARLATSSAEAMKLT ERGFI PVMVDPACSL LDELK

Secondary structure

SS

confidence

Disorder

Disorder confidence

370 380 390 400 410 420

Sequence PLCVVDAI LAKQNLG TRADMAPVTI ALGPG FTAGKDCHAVI ETNRGHWL GQVI YSGCAQE

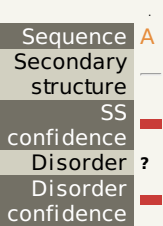
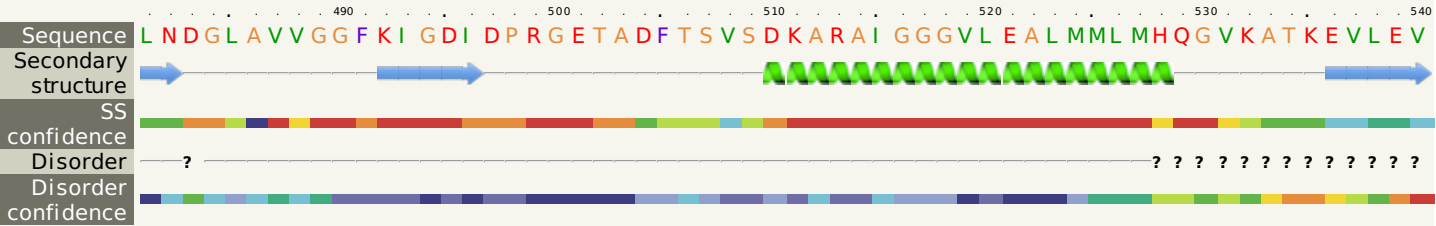
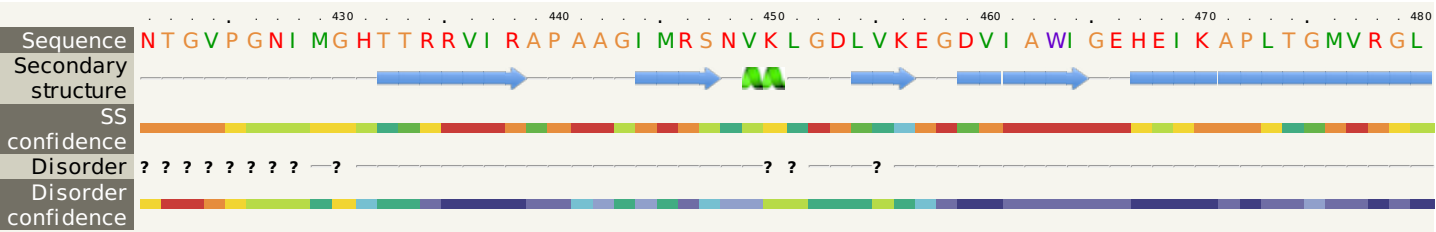
Secondary structure

SS

confidence

Disorder

Disorder confidence



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