

Email	l.a.kelley@imperial.ac.uk
Description	P0A855
Date	Thu Jan 5 11:06:56 GMT 2012
Unique Job ID	6b37b73bed2f7f2b

Protein structure and disorder analysis of the human protein sequence. The figure displays the full sequence (1-420 residues) with secondary structure elements (SSEs) and disorder predictions. The sequence is color-coded by residue type: basic (blue), acidic (red), polar (green), and non-polar (yellow). SSEs are shown as blue arrows. Disorder is indicated by a red line with green segments representing predicted disorder confidence. The sequence is: MKQALRVAFGFLILWASVLHAEVRIVIDSGVDSGRPIGVVPFQWAGPGAAPEDI GGI VAA DL RNS GK F NP L DRARLPQQP GSAQEVQPAAWSALGI DAVVVGQVTPNP DGSYNVAYQLVD TGGAPGTVLAQNSYKVNKQWLR YAGHTASDEVFEKLTGI KGAFRTRI AYVVQTNGGQFPY ELRVSDYDGYNQFVVHRSPQPLMSPA WSPD GSKLAYVT FESGRSALVI QTLANGAVRQVA S FPRHNGAPAFSPD GSKLAFALSKTGSLNLVMDLASGQIRQVTDGRSNNTEPTWFPDSQ NLAF TSDQAGRPQVYKVNI NGGAPQRI TWE GSNQDADVSSD GKFMMVMVSSNGGQQHI AK QDLATGGVQVLSSTFLDET PSLAPNGT MVIYSSSQGMGSV LNLVST DGRFKARLPATDGQ.

