

The sequence logo displays the conservation of residues across 1000 structures. The x-axis represents the amino acid position (1-100). The y-axis represents the information content in bits. The logo is color-coded by amino acid type: basic (blue), acidic (red), polar (green), and non-polar (yellow).

The sequence logo shows that the first 100 amino acids are highly conserved, with a peak in conservation around position 50. The sequence is:

MQQLKQKRVGIYVRVSTEYQSTEGYSIDGQINQIREYCDFHHFVVKDYADRGISGKSMNRPELQRLLKDAKEGYIDSVVMVYKTN

The sequence is aligned with the reference sequence (85) and the predicted structure (85). The alignment shows a high degree of conservation between the two sequences.

RLARNTSDLKIVEDLH^RQNV^EFFSLSERMEVNTSSGKLMQLILASFS^EEFERN^IVENVFMGQTRRAQEGYYQGNLPLGYDKIP^N_D
 RLARNTSDLLKIVEDLH^RQNV^EFFSLSERMEVNTSSGKLMQLILASFS^EEFERN^IVENVFMGQTRRAQEGYYQGNLPLGYDKIP^D 170
 RLARNTSDLLKIVEDLH^RQNV^EFFSLSERMEVNTSSGKLMQLILASFS^EEFERN^IVENVFMGQTRRAQEGYYQGNLPLGYDKIP^N 170

PYIAEGKHSPINQDLWDKVKLRKKQVSQKPPQVHGKGTNLLTGIVHCPQCGAPMAASNTTNTLKDGTKKRIRYYSCSNFRNKGSK
 PTIAEGKHSPIIQDLWDKVKLRKKQVSQKPPQVHGKGTNLLTGIVHCPQCGAPMAASNTTNTLKDGTKKRIRYYSCSNFRNKGSK 340
 PVIAEGKHSPINQDLWDKVKLRKKQVSQKPPQVHGKGTNLLTGIVHCPQCGAPMAASNTTNTLKDGTKKRIRYYSCSNFRNKGSK 340
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VCSANSVRADVIEKYVMQILEIVKSDKVINQLERVNQENKVDIGALNHDIAKQQQYDEVSGKLHNLVKTIEDNPDLTSAKRA 425
 VCSANSVRADVIEDYVMKQILEIVKSDKVINQLERVNQENKVDIGALHHDIAKQQQYDEVQIKLNLVKTIEDNPDLTSVIRP 425

 non conserved
 similar
 $\geq 50\%$ conserved