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Figure 1 displays the protein structure and disorder analysis of the human protein p115RBD. The figure is divided into three panels (a, b, c) showing different regions of the protein. Each panel displays the amino acid sequence, secondary structure (alpha-helices in green, beta-strands in blue), solvent accessibility (SS) as a colored bar, and disorder predictions (Disorder and Disorder confidence) as lines with question marks.

Panel (a): Shows residues 1-60. The sequence is MARTKLKFRLLHRAVIVLFCALLVALMQGASWFSQNHQRQRNPQLEELARTLARQVTLNV. The secondary structure consists of several alpha-helices. The SS bar shows high accessibility in the N-terminal region. Disorder is predicted in the N-terminal region and around residue 30.


Panel (b): Shows residues 70-120. The sequence is APLMRTDSPDEKRIQAILLDQLTDESRI LDAGVYDEQGDLI ARSGESVEVRDRLALDGKKA. The secondary structure includes alpha-helices and beta-strands. The SS bar shows high accessibility in the C-terminal region. Disorder is predicted in the N-terminal region and around residue 100.


Panel (c): Shows residues 130-180. The sequence is GGYFNNQQIVAPIAGKNGPLGYLRLTLDTHTLATEAQQVDNTTNI LRLMLLLSLAIGVVL T. The secondary structure includes alpha-helices and beta-strands. The SS bar shows high accessibility in the C-terminal region. Disorder is predicted in the N-terminal region and around residue 150.

Confidence Key

High(9)  Low (0)

? Disordered

 Alpha helix

 Beta strand