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Protein structure analysis of the Nucleosome Assembly Protein (NAP) from *Arabidopsis thaliana*. The figure displays the protein sequence (1-400 residues) and its predicted secondary structure (alpha-helices and beta-strands). The sequence is color-coded by amino acid type: Cysteine (yellow), Aspartic acid (blue), Asparagine (green), Glutamine (cyan), Lysine (red), Arginine (orange), Serine (purple), Threonine (pink), Valine (brown), Alanine (grey), Glycine (white), Proline (dark blue), Isoleucine (light blue), Leucine (light green), Methionine (light yellow), Phenylalanine (light purple), Tyrosine (light pink), and Tryptophan (light brown). The secondary structure is shown as a green ribbon model. The protein is divided into four domains: the N-terminal domain (residues 1-100), the coiled-coil domain (residues 101-200), the DNA-binding domain (residues 201-300), and the C-terminal domain (residues 301-400). The N-terminal domain contains a coiled-coil structure. The coiled-coil domain is a long, straight alpha-helix. The DNA-binding domain is a long, straight alpha-helix. The C-terminal domain is a long, straight alpha-helix. The protein is predicted to be a monomer. The disorder confidence is high (0.99) for the N-terminal domain and the coiled-coil domain, and lower (0.88) for the DNA-binding domain and the C-terminal domain. The disorder confidence is 0.99 for the N-terminal domain, 0.99 for the coiled-coil domain, 0.88 for the DNA-binding domain, and 0.88 for the C-terminal domain.

Confidence Key
High(9)  Low (0)
? Disordered
 Alpha helix
 Beta strand