

# Helicity of $\alpha$ (404-451) and $\beta$ (394-445) tubulin C-terminal recombinant peptides

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We have investigated the solution conformation of the functionally relevant C-terminal extremes of  $\alpha$ - and  $\beta$ -tubulin, employing the model recombinant peptides RL52 $\alpha$ 3 and RL33 $\beta$ 6, which correspond to the amino acid sequences 404-451(end) and 394-445(end) of the main vertebrate isotypes of  $\alpha$ - and  $\beta$ -tubulin, respectively, and synthetic peptides with the  $\alpha$ -tubulin (430-443) and  $\beta$ -tubulin (412- 431) internal sequences,  $\alpha$ (404-451) and  $\beta$ (394-445) are monomeric in neutral aqueous solution (as indicated by sedimentation equilibrium), and have circular dichroism (CD) spectra characteristic of nearly disordered conformation, consistent with low scores in peptide helicity prediction. Limited proteolysis of  $\beta$ (394-445) with subtilisin, instead of giving extensive degradation, resulted in main cleavages at positions Thr409-GLu410 and Tyr422-GLn423-Gln424, defining the proteolysis resistant segment 410-422, which corresponds to the central part of the predicted  $\beta$ -tubulin C-terminal helix. Both recombinant