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The application of X-ray crystallography and site-directed mutagenesis to the study of protein structures

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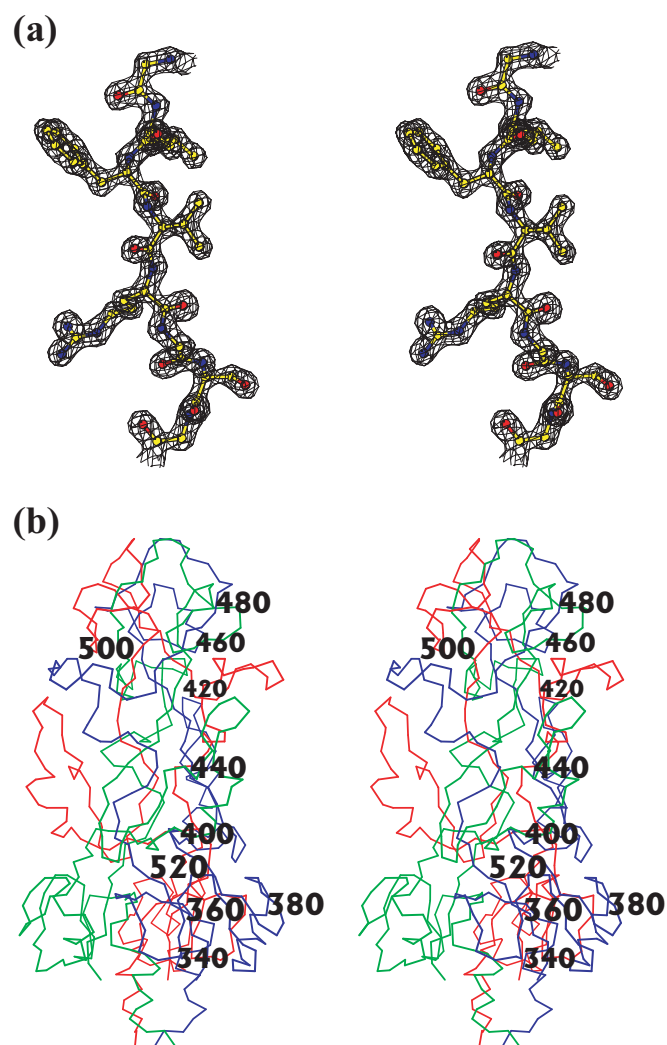


Figure 3.1. Structure of the ordered region of the proteolytic fragment of gp12 generated in the presence of zinc ions. a) Stereo-view of part of the crystallographic electron density. Amino acids Gly397 (top), Leu398, Phe399, Val400, Arg401, Gly402, Ser403 and Gly404 (bottom) are shown in ball-and-stick representation surrounded the final 2Fo-Fc electron density map contoured at 1.5 sigma. b) Stereo-view of the structure. In the blue monomer, every 20th residue is labelled. The other monomers are colored red and green. The N-terminal "neck" is at the bottom, the "collar" domain in the middle and the C-terminal receptor-binding domain at the top.