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

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Citation

Thomassen, E. A. J. (2005, April 28). *The application of X-ray crystallography and site-directed mutagenesis to the study of protein structures*. Retrieved from <https://hdl.handle.net/1887/834>

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Note: To cite this publication please use the final published version (if applicable).

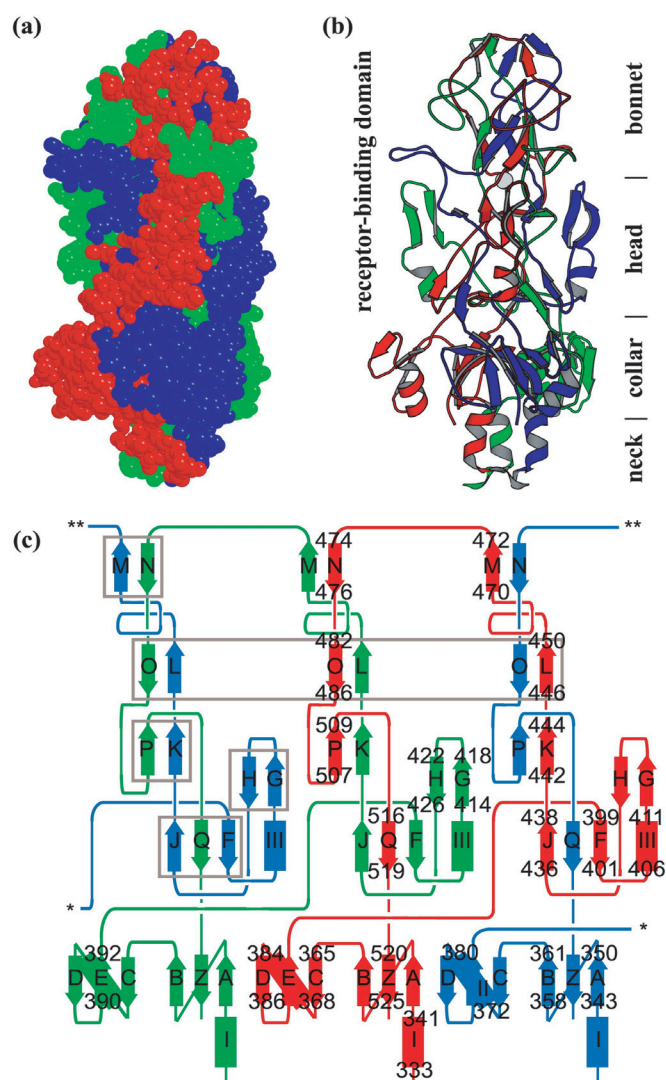


Figure 3.4. Structure of the ordered region of the 45 kDa fragment. a) Space-filling model of the structure illustrating the extensive intertwining in the receptor-binding domain. b) Ribbon diagram in the same orientation as a). At the bottom the neck region (the alpha-helical residues 336-339), in the middle the collar region (397-517), divided into head and bonnet as described in the text. c) Topology diagram. Alpha-helices are marked I, II and III, beta-strands A to Q (excluding I) and Z. Begin and end residues of the secondary structure elements are numbered in one of the monomers (not always the same to avoid overlaps). Grey boxes surround the six-stranded beta-barrel domain and the other, smaller beta-sheets. In the three-dimensional structure, the blue loops marked with * connect, as do those marked **. With a small thought experiment the reader can convince him- or herself that the structure is knitted rather than knotted; move the JKL strands to the left under the red OP-strands, then lift to the right over the red OP-strands. Do this for all three monomers and the "knit" is resolved.