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

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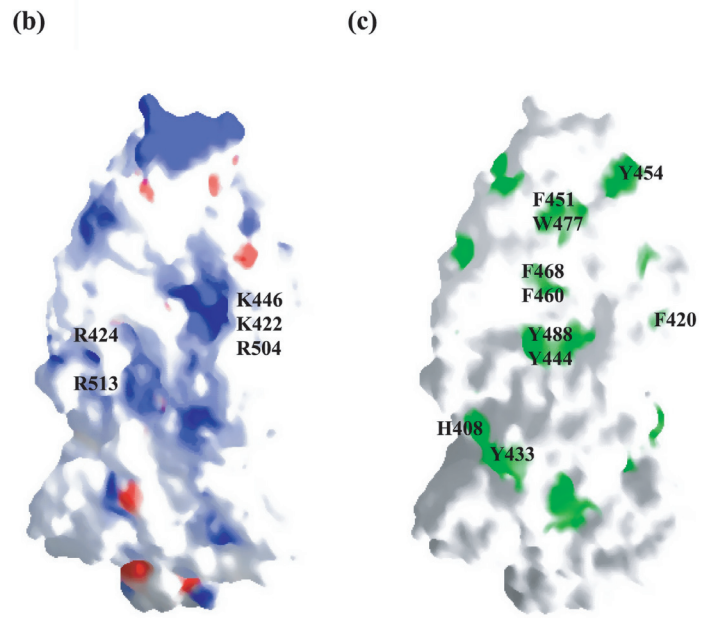

Figure 3.5. Possible LPS binding residues. b) Electron surface potential of the trimer. Positive charges are marked in blue, negative in red. Putative receptor-binding amino acids (see text) are labelled. Please note that although the five labelled residues appear to cluster in two groups, they are in fact all very close to each other due to the 3-fold symmetry. c) Surface diagram showing in green aromatic amino side-chains that may be involved in LPS binding. Labels identify the amino acids. The protein is tilted forwards to afford a better view of the top of the trimer. Residues are labelled by their one-letter amino acid code.

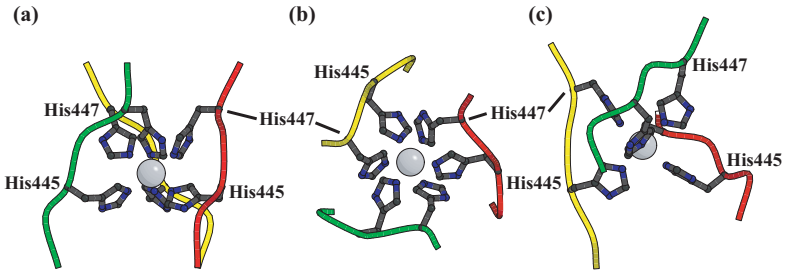

Figure 3.6. The zinc ion in the centre of the receptor-binding domain. Shown here are the main chains of the three monomers (residues 443-448 in each case) in yellow, red and green and the side-chains of the ligating histidine residues. The coordination is octahedral with a Zn-His445 NE2 distance of 2.2 Angstrom and a Zn-His447 NE2 distance of 2.25 Angstrom. For angles zee the text. b) View from the top down the three-fold axis. c) View down one of the four-fold axes of the octahedron formed by the NE2 atoms of the six ligating histidine residues.