The integrin alpha M I domain (Figure 1) is a protein found in humans (McCleverty, Liddington). This protein has been implicated as a protein involved with the disease Lupus.

![Figure 1](image)

This protein is a ligand binding protein. The surface of the protein is very hydrophilic while a few hydrophobic zone exist as shown in Figure 2.
The protein itself is made of mostly polar residues as seen in Figure 3 and Figure 4.

All blue residues are non-polar residues, green are uncharged polar residues, red are positively charged residues and black represents the negatively charged residues of the protein.
Figure 4
The protein L-chain apoferritin (Figure 5) is a metal binding protein found in horses that binds with Cadmium Ions (Yoshizawa et al.). The binding site exists in the central barrel of the whole protein.

Figure 5
The protein is made up of a single asymmetric unit made up of 5 alpha helices (Figure 6).

The subunit is a very polar molecule with about half the residues being polar (Figure 7). This provides ample force to create multimers, as well as a metal binding site.
The metal binding site is concentrated with a large portion of polar residues. There are slightly more positively charged residues, in red, than negatively charged residues, in blue, however the like charges align themselves on the same sides of the helix (Figure 8). The purple and cyan both specify aromatic residues, with tyrosine in purple and phenylalanine in cyan, which will both have a steric effect on the binding site.
Molecular graphics images were produced using the UCSF Chimera package from the Resource for Biocomputing, Visualization, and Informatics at the University of California, San Francisco (supported by NIH P41 RR-01081).

