

High Resolution Structure of Cytoglobin Reveals the Extra Helix in N-terminus

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Cytoglobin (Cgb), a recently discovered member of vertebrate globin family, binds O₂ reversibly *via* the Fe²⁺ ion of a heme group. Sequence comparison shows that some key residues close to the active site related to ligand binding have been highly conserved among globin family. Cgb was found to be expressed in a broad range of mammalian tissues.

In the present study, we determined the structure of the ferric state of human Cgb in two different space groups at 2.4 Å and 1.68 Å resolution. The overall backbone structure of Cgb exhibits a traditional globin fold with an additional helix in the pre A-helix region and ordered loop structure in the C-terminal region. Cgb forms a homo dimer by the interaction between the E-helices and AB corners in these crystals. A similar dimeric arrangement is found in Lamprey Hemoglobin, whose ligand affinity is regulated by dimerization coupled with a movement of the distal residues. Therefore it might be possible that the structure on the dimerization interface of Cgb is affected by the ligand binding.

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