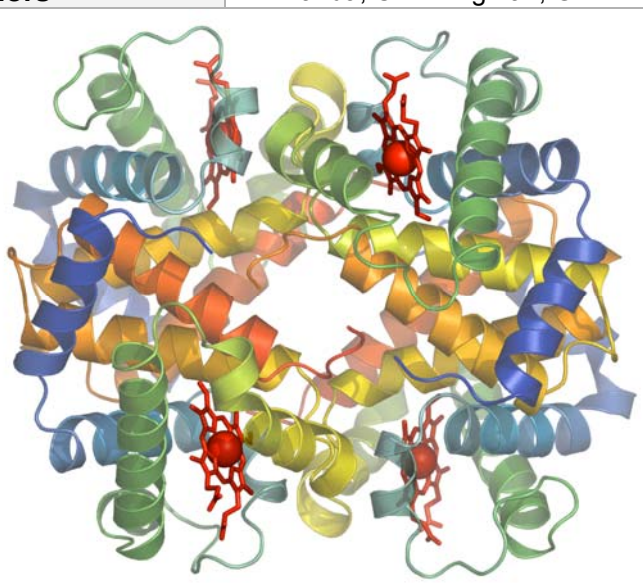
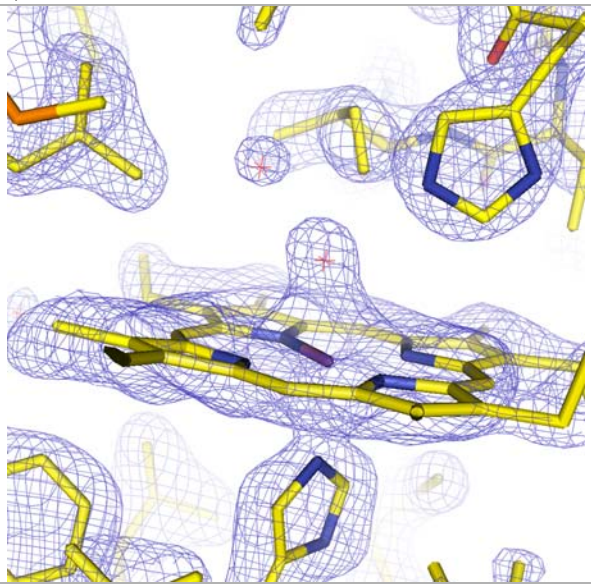
Center for Eukaryotic Structural Genomics

Protein Structure Initiative

Target ID	GO.34368	
Source Organism	*Perca flavescens*	
Target Name	Perch hemoglobin	
PDB Entry	1XQ5	Deposition: 11-Oct-2004
Function	oxygen transport (hemoglobin)	
Produced From	Natural source (blood)	
Structure by X-ray	Resolution: 1.9 Å	R-value (R-free): 24.3% (29.5%)
	No of Residues:	Subunits/ASU: one $\alpha_2\beta_2$ tetramer
Data Collected At	Advanced Photon Source SBC 19-BM 31-Jul-2004	
Authors	R. Aranda, C.A. Bingman, G.N. Phillips, Jr.	





Structural Features

The structure of hemoglobin from the perch, *Perca flavescens*, was determined to a resolution of 1.9 Å using molecular replacement. This target was a request by Professor Mark Richards of the Department of Animal Sciences at the University of Wisconsin-Madison. The rationale for the study of this protein comes from the fact that oxidized lipids contribute to off odors in fish. These appear before the fish is unsafe to eat, but limits shelf life and perceived quality. Thus, this hemoglobin is interesting because, when oxidized, has a high rate of enzymatic oxidation of lipids. Furthermore, studies by Richards and Olson (*unpublished*) show an unusual rate of auto-oxidation. This structure may lead to a better understanding of this enzymatic activity, which could have significant nutritional and economic value. CESG used PCR to sequence the beta chain, and a combination of PCR and inspection of electron density maps to sequence the alpha chain. The tetramer exhibits a high degree of symmetry, which is typical, except that electron density corresponding the sixth ligand of the iron, normally molecular oxygen in the physiological state, shows varying degree of occupancy.

Percent Identity with Nearest PDB Structure at Time Solved	α: 66.6% to 1V4U β: 72.6% to 1S5Y
Pfam Cluster	globin
Protonet Cluster Size : Structures in PDB	941 : 34

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