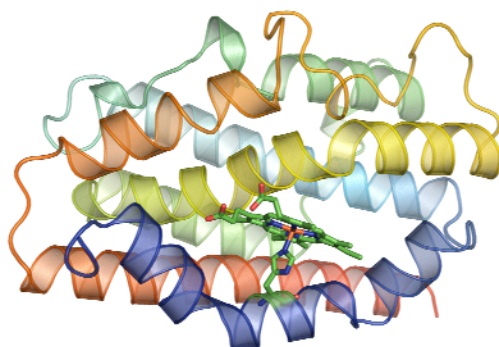


CESG ORF No.	91265	
Organism	<i>Homo sapiens</i>	
Gene Designator	Heme Oxygenase 2	
PDB Entry	2Q32	Deposition: 24-July-2007
Function	Heme degradation, carbon monoxide generation.	
Produced From	<i>E. coli</i> BL21(DE3) PGEX 4T-2	
Structure by X-ray	Resolution: 2.40 Å	R-value (R-free): 20.1% (25.3 %)
	No. of Residues/ASU: 431	Subunits/ASU: 2
Data Collected At	APS GM/CA-CAT 23-ID-B, 06-July-2007	
Authors	Bianchetti, C.M., Bingman, C.A., Bitto, E., Wesenberg, G.E., Phillips Jr., G.N.	



Structure Summary

The crystal structure of heme oxygenase-2 (HO-2) was solved by CESG at the request of Dr. Stephen Ragsdale at the University of Michigan. Heme oxygenase (HO) catalyzes the degradation of heme to free iron, carbon monoxide and biliverdin in the presence of NADPH-dependent cytochrome P450 reductase. Seven electrons are transferred and three molecules of oxygen are consumed in the degradation of one molecule of heme to biliverdin. Subsequently, biliverdin reductase reduces biliverdin to bilirubin. Present in both bacteria and eukaryotes, HO is the only known enzyme that can degrade heme. HO not only plays a critical role in heme and iron homeostasis, but the products of heme degradation have important physiological functions. Two HO isoforms have been reported in mammalian cells, heme oxygenase-1 (HO-1) and HO-2. The mammalian HO-1 and HO-2 exhibit similar catalytic activities. Plants contain several HOs but these lack the C-terminal membrane spanning region seen in mammalian HOs and are more closely related to the bacterial and insect HO-1 than to the mammalian HO-2. The crystal structures of apo (PDB ID 2Q32) and heme-bound truncated HO-2 (PDB ID 2QPP) reveal a primarily α -helical architecture similar to that of HO-1, and other known HOs.

References: Bianchetti, C.M., Yi, L., Ragsdale, S.W., Phillips, G.N., Jr. (2007) Comparison of apo- and heme-bound crystal structures of a truncated human heme oxygenase-2. *J Biol Chem* 282(52):37624-31.

Percent Identity with Nearest PDB Structure at Time Solved	50% (1N3U)
Pfam Cluster	Heme_oxygenase
Sequence Family Size	245

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