Thioredoxins are ubiquitous proteins which catalyse the reduction of disulphide bridge on target proteins. The catalytic mechanism proceeds via a mixed disulphide intermediate whose breakdown should be enhanced by the involvement of residue Asp30 as a base catalyst towards residue Cys39. We report here the crystal structure of wild-type and D30A mutant thioredoxin \( h \) from \textit{Chlamydomonas reinhardtii}, which constitutes the first crystal structure of a thioredoxin isolated from an eukaryotic plant organism. The role of residue Asp30 in catalysis has been revisited since the distance between Asp30-OD1 and Cys39-SG is too long to support the hypothesis of a direct proton transfer: a careful analysis of all available crystal structures reveals that the relative positioning of residue Asp30 and Cys39 as well as hydrophobic contacts in the vicinity of residue Asp30 does not allow a conformational change that would bring the two residues close enough for a direct proton transfer. This suggests that deprotonation of Cys39 should be mediated by a water molecule. Molecular dynamics simulations, carried out either \textit{in vacuo} or in water, support this hypothesis. The results are discussed with respect to biochemical and structural data.

**References**
