Conformation variability of the binding site of thioredoxins: calculation based on distance restraints.

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Thioredoxins are small proteins (12kDa) involved biological processes such regeneration of oxidative damage. They act as disulfide oxidoreductase enzymes by a catalytic mechanism which involves a conserved sequence of five amino acids (-TRP-CYS-GLY-PRO-CYS-) located in a loop region which structure is poorly solved. Our group has determined the structure of yeast Trx1 and Trx2 using high resolution NMR and this loop presents conformational variability that results in a low convergence in the structure calculation. To asses the conformation variability of this loop we use cross-validation NOE distances restraints and probability map refinement to generate better representations of these structures ensemble. The calculus was made for an ensemble of 1, 2, 3, 4, 5 and 6 conformations and by analyzing the rms deviations, structure violations and NOE restraints deviations we can estimate the number of conformers contained in the experimental data. Our data enabled the calculation of the probability map for two conformation. We will show the comparison of the two conformers with the structure in the protein data bank. We also expect a more convergent and representative structure helping us to understand the Trx2 function and activity.

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