

W0071

Yeast Copper Thionein: Solving A Small But Long-Standing Puzzle. Calderone V.^{*,#}, Dolderer B.[°], Hartmann H.-J.[°], Echner H.[°], Luchinat C.[§], Del Bianco C.[§], Mangani S.[#], Weser U.[°], [#]Depat. of Chemistry, Univ. of Siena, via Aldo Moro, 53100 Siena, Italy, [§]CERM, Univ. of Florence, Italy, [°]Anorganische Biochemie, Univ. of Tübingen, Germany, vito.calderone@unisi.it.

In these postgenomic days the Protein Data Bank is featuring protein structures of increasingly large size, thanks to the progress in the power of the X-ray sources and in the computer programs to solve X-ray structures.

Yet, there are small proteins whose structures remain elusive. One of the most striking examples is a stable and well-folded protein whose existence has been known for nearly thirty years, whose central importance in eukaryotes metabolism is undisputed, whose size is ridiculously small (M_r 5655), but *whose detailed structure is still unknown*. Such protein is yeast copper thionein (Cu-MT) (Figure 1).

Strange enough, solving this particular structure turned out to be a puzzle. Molecular replacement techniques using the protein solution structure as a model failed, probably due to its lack of eight strong anomalous scatterers (the Cu atoms) and direct methods could not be applied for phasing because the resolution, although good, was not at the true atomic level. On the other hand, the enormous anomalous signal present in the data (about 20% of the diffracted intensities) could not be straightforwardly used for the structure solution due to the high number of anomalous scatterers and to the high symmetry of the crystal cell (cubic, $P4_332$).

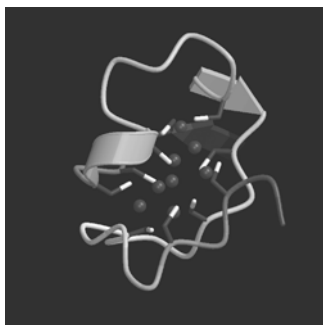


Figure 1