As the major copper-activated metallothionine in yeast, Cup1p binds and sequesters cuprous copper, Cu+, providing the principal method of removing this metal ion from the cell. Careful control of copper ion homeostasis is important because trace concentrations are essential for yeast survival, while high concentrations are toxic. CUP1 transcription is specifically induced by the copper-dependent transcription activator Cup2pin response to high levels of copper ions46688>and by Hsf1p in response to heat shock, glucose starvation and oxidation stress. In the presence of copper, Cup1p is also capable of antioxidant activity and thus contributes a significant, albeit minor, role to oxygen radical detoxification, especially in the absence of Cu,Zn-superoxide dismutase Sod1p. Although Cup1p is capable of binding other metal ions in vitro, it is responsible only for copper and cadmium ion tolerance in vivo, and the resistance to Cd++ ions is only observed at high copy number or when CUP1 is overexpressed. This is in contrast to the metallothioneins found higher eukaryotes, which are typically capable of detoxifying an array of metal ions.Naturally occurring tandem duplications of the CUP1 gene are common, and it is typically found in arrays of 2-20 copies per CUP1 locus. In general, the higher the copy number, the greater the copper ion tolerance, and strains containing only one copy are considered to be copper ion sensitive. Most lab strains contain two copies, and these are designated as CUP1-1 and CUP1-2 in the reference strain. CUP1 is notable not just for its role in the biology of yeast, but also for its extensive use as a tool in molecular biology. Most importantly, the copper inducible CUP1 promoter is widely used in expression systems. The CUP1 gene has also been put to use in a wide array of other applications, including as a selectable marker, as a construct to study intron splicing, and as the reporter in a two hybrid assay.