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Crystal Structure of a *Clonorchis sinensis* 26 kDa Glutathione S-transferase, *Cs*GST: Implication for the Use of *Cs*GST-fusion Protein as a Useful Tool to Determine Crystal Structures of Small Peptides

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Glutathione S-transferases (GSTs) are a group of enzymes that catalyze the conjugation of glutathione (GSH) to a wide variety of electrophilic substrates, resulting in elimination of the GSH-adducts from the cell. Such detoxification properties of the enzymes are believed to be responsible to the development of resistance of cells towards drugs, herbicides, and pesticides. In case of helminths, the enzymes are known as potential chemo- and immuno-therapeutic targets. So far, crystal structures have been determined for isozymes from *Schistosoma japonicum* (*Sj*GST) and *Fasciola hepatica*.

The three dimensional structure of a helminth GST, a 26kDa isozyme from *Clonorchis sinensis* (*Cs*GST), has been determined using X-ray diffraction technique. The *Cs*GST structure closely resembles those of other helminth 26kDa isozymes. Subunit-subunit interactions are mainly mediated by characteristic "lock-and-key" contact formed among hydrophobic residues. During the course of this study we have observed that two *Cs*GST-fusion proteins containing a 14- and a 48-amino acid peptides at N-terminus, 14NP*Cs*GST and 48NP*Cs*GST, are crystallized under the conditions similar to those used for *Cs*GST. In addition, *Cs*GST-fusion proteins containing varying extents of N-terminal-extended peptides are incorporated into a crystal. The crystal structure clearly revealed that *Cs*GST crystals have large spaces enough to accommodate the fused peptides without significant changes in crystal lattice. These results suggest that the crystallization system of *Cs*GST/peptide fusion protein may be generally applicable to obtain crystals of small peptides.