

### Small angle X-ray scattering studies of Sgt1 protein from *Hordeum vulgare*

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Sgt1 is a 41kDa protein conserved in eukaryotes, which is involved in many important cellular processes [1]. First it was found in yeast as a component of centromere assembly and suppressor of *skp1-4* mutation in SCF ubiquitin ligase subunit gene. Sgt1 protein, both in human and plants, is able to interact with Heat shock protein 90kDa (Hsp90) an important molecular chaperone, that take part in activation and proper folding of receptors, kinases and transcription factors. In addition, in plants Sgt1 is involved in disease resistance response and mutation in its gene can cause loss of resistance and plant death in case of pathogen infection. Sgt1 protein interacts with SCF ubiquitin ligase complex and with COP9 signalosome complex, both playing key role in protein degradation through 26S proteasome machinery.

Sgt1 consist of three distinct domains, none of which poses enzymatic activity. N-terminal - tetratricopeptide repeat domain (TPR) is known to interact with other TPR containing protein SRFR1 in *Arabidopsis*, but not with Hsp90, what is unusual because this domain is recognized in Hsp90 co-chaperones. Middle Sgt1 and chord specific domain (CS) interacts with N-terminal domain of Hsp90 and also with Rar1 protein in plants. This domain is structurally related to another Hsp90 co-chaperone p23. C-terminal domain named Sgt1 specific domain (SGS), known to be intrinsically disordered, also interacts with leucine repeat domain protein such as barley Mla1 and yeast *cdc35p*. In addition SGS interacts with EF-hand S100 proteins. Between domains are located two variable regions (VR1 and VR2) with no specific function known [2].

Sgt1 TPR domain in solution of low ionic strength can form a dimers. In this study we tested the dimer/monomer equilibrium using small angle scattering of synchrotron radiation and *ab-initio* low-resolution modeling. Using multivariate curve resolution least square method (MCR-ALS) [3] we were able to separate the scattering curves of monomeric and dimeric species from a complex mixture. Using rigid body modeling with *ab-initio* structure prediction we created a model of the dimer and monomer conformation of barley Sgt1.

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