

## LOW RESOLUTION STRUCTURAL STUDIES SUGGEST AN EXTENDED SHAPE FOR THE HUMAN REGULATORY PROTEIN KI-1/57

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The regulatory protein Ki-1/57 is associated with protein kinase activity and gets phosphorylated on serine and threonine residues upon cellular activation. Recent work from our group has revealed its interaction with other regulatory proteins involved in either transcriptional regulation or RNA metabolism. Arginine methylation of Ki-1/57 at RGG-clusters seems to influence its sub-cellular localization. Moreover, we have recently observed that Ki-1/57 can also bind RNA, suggesting it may have pleiotropic functions. Previous experiments exploring circular dichroism spectroscopy have shown a low content of secondary structure in the protein, suggesting a partially unfolded state. Here, we present small angle X-ray scattering studies on 6xHis(122-413) Ki-1/57, which suggest an expanded conformation of this fragment. An elongated particle was also observed when we performed analytical ultracentrifugation and analytical gel filtration experiments. Limited proteolysis studies of the endogenous full-length Ki-1/57 from human HEK293 cells and with 6xHis(122-413) Ki-1/57 *in vitro* showed a high sensitivity of the protein to proteolytical degradation, which is characteristic for intrinsically disordered proteins. Taken together, our results tempt us to speculate that Ki-1/57 may belong to the so-called natively unfolded proteins. Experiments involving the changes of the overall shape of Ki-1/57 upon RNA or protein interaction are currently ongoing.

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