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Supporting information for article:

Biochemical and structural study of Arabidopsis hexokinase 1

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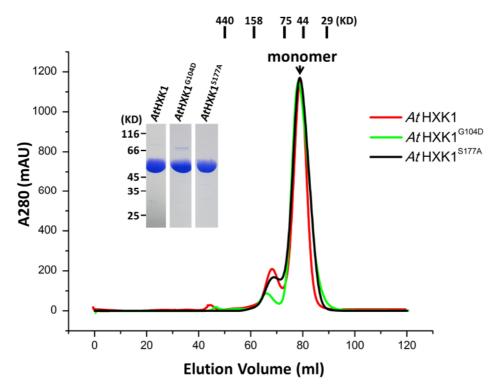


Figure S1. Purification of AtHXK1, AtHXK1^{G104D} and AtHXK1^{S177A}. Elution profiles are shown for AtHXK1, AtHXK1^{G104D} and AtHXK1^{S177A}, and arrow indicates the monomeric fraction. *Inset* shows the SDS-PAGE gel of each monomeric fraction.

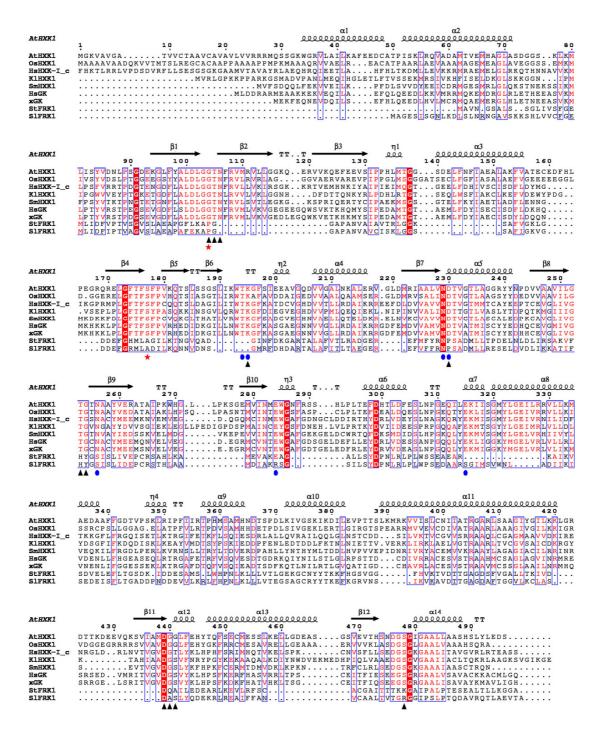


Figure S2. Sequence alignment. The sequences are, from top to bottom, *At*HXK1, *Oryza sativa* HXK1, the C-terminal half of human HXK-I, *Kluyveromyces lactis* HXK1, *Schistosoma mansoni* HXK1, human GK, *Xenopus laevis* GK, *Solanum tuberosum* FRK1, and *Solanum lycopersicum* FRK1. The strictly conserved residues are boxed in red, and the highly conserved residues are highlighted in red. At the top of the sequences, a schematic representation of the secondary structure elements of *At*HXK1 is shown. At the bottom of the

sequences, Gly104 and Ser177 of *At*HXK1 are indicated by red stars, residues for ATP binding are indicated by black triangles, residues for glucose binding are indicated by blue dots.