Supplemental Figure 1. Sequence alignment of ACDs from nine human sHSPs performed with Clustal Omega (Sievers et al, 2011 "Fast scalable generation of high-quality protein multiple sequence alignments using Clustal Omega". Mol. Systems Biol. 539). Residues analogous to Cys137 in HSPB1 are highlighted in red. CRYAA and CRYAB are alternate names for HSPB4 and HSPB5, respectively.

Supplemental Figure 2. Sedimentation velocity analysis of reduced HSPB1-ACD. Protein was dialyzed against 50 mM sodium phosphate buffer, pH 7.5, 100 mM NaCl, 5 mM DTT. Sedimentation velocity was measured on a sample of 100 µM HSPB1-ACD at 20 °C at a rotor speed of 50,000 rpm. Under these conditions, the ACD sediments predominantly as a dimer ($S_{20,w} \sim 1.9$), and < 10% of the protein sediments as a monomer ($S_{20,w} \sim 1.2$). Sedimentation velocity experiments were conducted on a Beckman Coulter XL-A/XL-I analytical centrifuge and data were analyzed using the program SEDFIT to obtain a c(s) distribution.