Supporting Information

Crystal Structure of an Activated Variant of Small Heat Shock Protein Hsp16.5

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Running Title: Structural Basis of Hsp16.5 Oligomer Expansion

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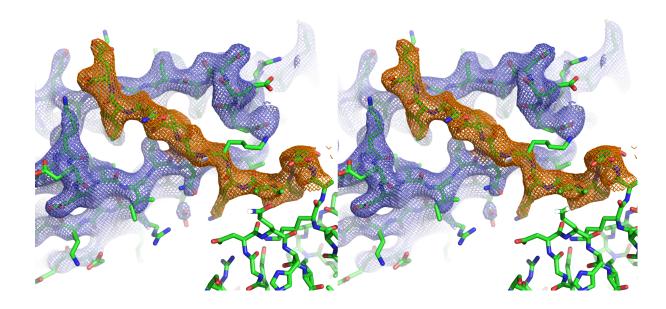


Figure S1: Electron density map. The refined model was used to calculate a 2mFoDfc map using Phenix (1). The map was displayed around all atoms in two neighboring subunits and a region corresponding to the peptide in groove interaction and orientation similar to Figure 4D of the main text is shown. blue, green, orange, and red. This figure was prepared with Pymol (2, 3).

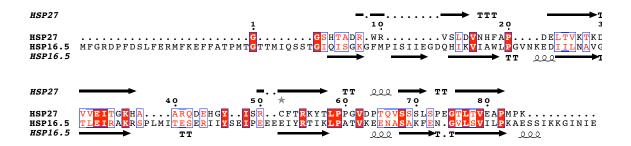


Figure S2: A structure-based alignment between Hsp16.5 and Hsp27. Secondary structure elements are indicated above the alignment: arrows are strands, coils are alpha helices, and T denotes turns. Amino acids are shown in standard one-letter abbreviations. White on red background denotes identity. Red on white background denotes similarity. This figure was prepared with ESPript (4, 5).

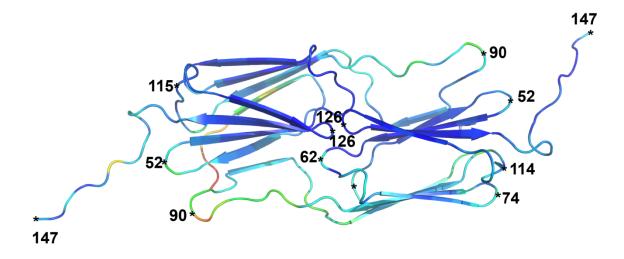


Figure S3: A ribbon diagram colored by B-factor of $C\alpha$ atoms. Lowest B-factors are dark blue, followed by light blue, green, orange, and red. This figure was prepared with Pymol (2, 3).

References:

- 1. Adams, P. D., Grosse-Kunstleve, R. W., Hung, L. W., Ioerger, T. R., McCoy, A. J., Moriarty, N. W., Read, R. J., Sacchettini, J. C., Sauter, N. K., and Terwilliger, T. C. (2002) PHENIX: building new software for automated crystallographic structure determination, *Acta Crystallogr D Biol Crystallogr* 58, 1948-1954.
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- 4. Gouet, P., Courcelle, E., Stuart, D. I., and Metoz, F. (1999) ESPript: analysis of multiple sequence alignments in PostScript, *Bioinformatics* 15, 305-308.
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