



STRUCTURAL BIOLOGY
COMMUNICATIONS

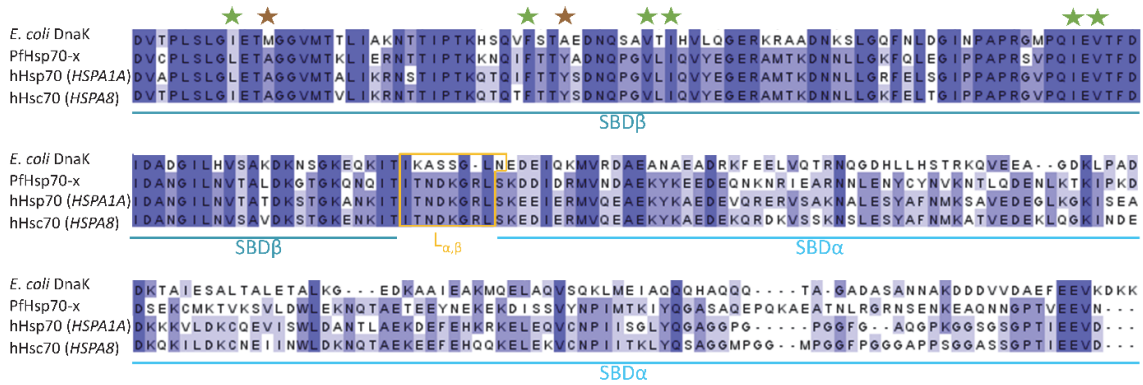
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Supporting information for article:

**Structure of the *Plasmodium falciparum* heat-shock protein 70-x
substrate-binding domain**

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Figure S1



Sequence alignment of PfHsp70-x SBD with homologous domains. Shown here is a sequence alignment of PfHsp70-x SBD (UniProt K7NTP5, residues 426-679) against the equivalent domains of *E. coli* DnaK (UniProt P0A6Y8, residues 393-638) and of human erythrocytic Hsp70-class chaperones (Hsp70, also known as HSPA1A, UniProt PODMV8, residues 395-641; Hsc70, also known as HSPA8, UniProt P11142, residues 395-646). The sequences of SDB β and SDB α sub-domains are underlined, the L $_{\alpha,\beta}$ loop connecting the two sub-domains is boxed in yellow. Green stars above the sequence denote SDB β residues forming the hydrophobic pocket that binds the substrate L₅ amino acid. Brown stars denote SDB β residues forming an arch above the substrate-binding groove.