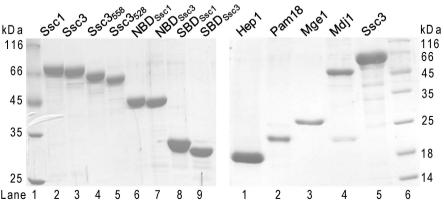
Supplemental Fig. S1



Supplemental Fig. S1:

SDS-PAGE analysis of purified Ssc1, Ssc3 and their variants. *A*, 5 µg of different proteins are separated on 12.5% SDS-PAGE: molecular weight marker (*lane 1*), Ssc1 (*lane 2*), Ssc3 (*lane 3*), Ssc3₅₅₈ (*lane 4*), Ssc3₅₂₈ (*lane 5*), NBD_{Ssc1} (lane 6), NBD_{Ssc3} (*lane 7*), SBD_{Ssc1} (*lane 8*), SBD_{Ssc3} (*lane 9*). *B*, SDS-PAGE analysis of recombinantly expressed and purified Hep1 (*lane 1*), Pam18 (*lane 2*), Mge1 (*lane 3*), Mdj1 (*lane 4*), Ssc3 (*lane 5*) and molecular weight marker (*lane 6*).

MLAAKNILNRSSLSSSFRIATRLOSTKVOGSVIGIDLGTTNSAVATMEGKVPKTIENAEG Ssc1 MLPSWKAFKAHNI---LRILTRFOSTKIPDAVIGIDLGTTNSAVAIMEGKVPRIIENAEG SRTTPSVVAFTKEGERLVGIPAKROAVVNPENTLFATKRLIGRRFEDAEVORDIKOVPYK 120 Ssc1 SRTTPSVVAFTKDGERLVGEPAKROSVINSENTLFATKRLIGRRFEDAEVORDINOVPFK 117 Ssc3 TVKHSNGDAWVEARGOTYSPAOTGGEVLNKMKETAEAYLGKPVKNAVVTVPAYENDSORO 180 Ssc1 TVKHSNGDAWVEARNRTYSPAOTGGETLNKMKETAEAYLAKSVKNAVVTVPAYENDAORO Ssc3 177 Ssc1 ATKDAGOTVGLNVLRVVNEPTAAALAYGLEKSDSKVVAVEDLGGGTEDTSTLDTDNGVEE 240

Supplemental Fig. S2

ATKDAGOIIGLNVLRVVNEPTAAALAYGLDKSEPKVIAVFDLGGGTFDISILDIDNGIFE 237 Ssc3 VKSTNGDTHLGGEDFDIYLLREIVSRFKTETGIDLENDRMAIORIREAAEKAKIELSSTV Ssc1 300 VKSTNGDTHLGGEDFDIYLLOEIISHFKKETGIDLSNDRMAVQRIREAAEKAKIELSSTL Ssc3 Ssc1

STEINLPFITADASGPKHINMKFSRAOFETLTAPLVKRTVDPVKKALKDAGLSTSDISEV STEINLPFITADAAGPKHIRMPFSRVOLENITAPLIDRTVDPVKKALKDARITASDISDV Ssc3 LLVGGMSRMPKVVETVKSLFGKDPSKAVNPDEAVATGAAVOGAVLSGEVTDVLLLDV Ssc1

LLVGGMSRMPKVADTVKKLFGKDASKAVNPDEAVALGAAIOAAVLSGEVTDVLLLDV Ssc3

В β1 ß2 DVLLLDVTPLSLGIETLGGVFTRLIPRNTTIPTKKSOIFSTAAAGOTSVEIRVFOGEREL Ssc1 DVLLLDVTPLSLGIETLGGVFTKLIPRNSTIPNKKSOIFSTAASGOTSVEVKVFOGEREL 60 Ssc3

β5 β6 β7 ß8 VRDNKI, I GNETI, AGI PPA PKGVPO I EVTEDI DA DGI I NVSARDKATNKDSSITVAGSSGI. 120 Ssc1 VKDNKLIGNFTLAGIPPAPKGTPOIEVTFDIDANGIINVSAKDLASHKDSSITVAGASGL 120 Ssc3

 αA αΒ αC

SENEIEQMVNDAEKFKSQDEARKQAIETANKADQLANDTENSLKEFEGKVDKAEAOKVRD

SDTEIDRMVNEAERYKNODRARRNAIETANKADOLANDTENSIKEFEGKLDKTDSORLKD

 αD αE

OITSLKELVARVOGGEEVNAEELKTKTEELOTSSMKLFEOLYKNDSNMNNNNNNNNNAESG 240

QISSIRELVSRSQAGDEVNDDDVGTKIDNLRTSSMKLFEQLYKN-SDNPETKNGR----- 234

Ssc3 ENK- 237

ETKO 244 Ssc1

Supplemental Fig. S2:

Sequence comparison of Ssc1 and Ssc3. A, Sequence alignment of nucleotide-binding domain (NBD); and B, substrate-binding domain (SBD) of Ssc1 and Ssc3 using ClustalW2 tool. Identical amino acids are shaded by gray boxes. Secondary structure elements including β strands (β 1- β 8) and α helices (α A- α E) are indicated by modelling the structure of Ssc1 using Pymol software and structure of DnaK as a template (2KHO1).

10 µg/mICFW 25 µg/mICFW Control

Supplemental Fig. S3



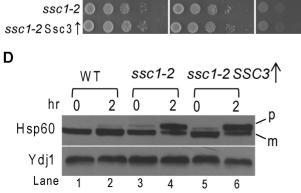


Supplemental Fig. S3:

Calcofluor white (CFW) hypersensitivity test of $ssc3\Delta$ strain. CFW hypersensitivity of $ssc3\Delta$ strain was checked by drop test on YPD plates containing $10\mu g/ml$ ($middle\ panel$) and $25\mu g/ml$ ($right\ panel$) of CFW solution. Parent strain BY4741 MATa ($his3\Delta 1\ leu2\Delta\ met15\Delta\ ura3\Delta$) was used as a control.

Supplemental Fig. S4 Α ssc1 Δ 2μ SSC3 SSC1 . GPD pRS423 2μ SSC3 TEF 5563Intinak SSC3GPD S5C3TEF В Ssc3 Mge1 Lane 2 C 24 °C 30 °C 34 °C

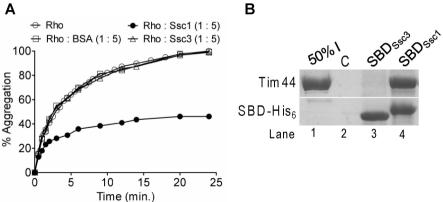
37 °C



Supplemental Fig. S4:

Growth complementation analysis of $ssc1\Delta$ cells upon Ssc3 overexpresion. A, Haploid $ssc1\Delta$ strain expressing wild type copy of SSC1 gene from a URA plasmid was transformed with either SSC1 on a CEN plasmid or SSC3 from a high copy pRS423 plasmid driven by TEF or GPD promoter. The cells were streaked on media containing 5-fluoroorotic acid and grown at 30 °C for 3 days. The empty pRS423 plasmid was used as a vector control. B, Total lysates prepared from cells overexpressing HA-tagged Ssc3 under different promoters as indicated were resolved by SDS-PAGE, electroblotted, and immunodecorated with anti-HA antibodies. Mge1 was used as a loading control. C, 10-fold serial dilutions of an equivalent number of $ssc1\Delta$ cells expressing either wt Ssc1 from its own promoter (WT), or ssc1-2, or ssc1-2 overexpressing wild type Ssc3 from GPD promoter (ssc1-2 Ssc3 \uparrow) were spotted on selective medium and incubated at indicated temperatures for 3 days. D, Wild type (WT), ssc1-2 and ssc1-2 Ssc3 \uparrow yeast strains were grown at permissive temperatures in minimal media to early log phase. The culture was shifted to 37 °C for 2 h to induce the temperature sensitive phenotype. Subsequently, the whole cell lysates were resolved by SDS-PAGE followed by immunoblotting using Hsp60-specific antibodies; (p), precursor form of Hsp60; (m), mature form of Hsp60.

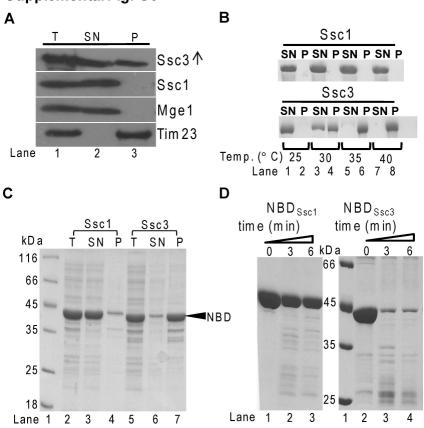
Supplemental Fig. S5



Supplemental Fig. S5:

In vitro analysis of chaperone like activity of Ssc3 by rhodanese aggregation assay and Tim44 interaction. *A*, Bovine rhodanese was first denatured in 6 M guanidine hydrochloride and subsequently diluted into the reaction mixture and absorbance changes at 320 nm were used to monitor aggregation at different time intervals at 25 °C. Aggregation of denatured rhodanese (0.46 μm) in the presence of either 2.3 μM of Ssc1 or Ssc3 was monitored for 25 min by measuring the changes in turbidity. Percent aggregation values were plotted against time. Under similar conditions, 0.46 μm denatured rhodanese alone was used as an internal control (absence of chaperones) and in the presence of 4.6 μm bovine serum albumin (*BSA*) as a negative control. *B*, 4 μM of His-tagged SBDs of Ssc1 and Ssc3 were preincubated with 1 μM of non-tagged Tim44 in buffer F (20 mM HEPES pH 7.5, 100 mM KCl, 0.2 % Triton and 10 mM imidazole) for binding at 20 °C for 15 min. The reactions were then incubated with 10 μl of Ni-NTA resin (bed volume) for 30 minutes. The resin was washed 3 times with buffer F and bound proteins were analysed by SDS-PAGE followed by Coomassie dye staining. 50% of the input was used as loading control and Ni-NTA resin alone (absence of SBDs of Ssc1/Ssc3) used as negative control (C).

Supplemental Fig. S6

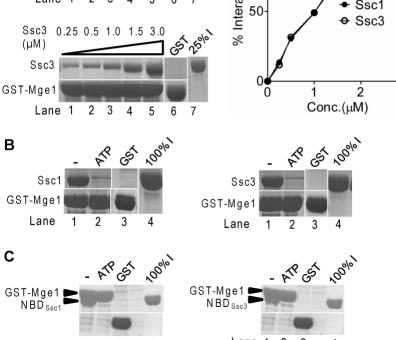


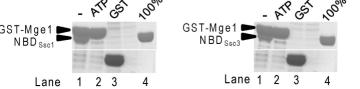
Supplemental Fig. S6:

Analysis of alteration in stability and solubility of Ssc3 upon overexpression. A, Mitochondria from Ssc3 overexpressing yeast strains (under Ssc1 promoter) were isolated and subjected to fractionation using sonication by hypotonic swelling method. The sonicated mitochondrial samples were subjected to ultracentrifugation. The equivalent amounts of supernatant (S) and pellet (P), and unfractionated extract (T) were analyzed by SDS-PAGE and immunoblotted with yeast specific antibodies as indicated. B, Thermal stability of Ssc1 (top panel) and Ssc3 (bottom panel) were analyzed by incubating the proteins at indicated temperatures for 30 min in buffer A containing 5% glycerol. The samples were separated into a supernatant (SN) and pellet (P) fraction by centrifugation and analyzed by SDS-PAGE followed by Coomassie dye staining. C, The NBDs of Ssc1 and Ssc3 along with the linker region were coexpressed with Hep1 in E. coli cells. The cells were lysed as described above and analyzed for its solubility by SDS-PAGE. D, 5 µg of NBDs of Ssc1 (left panel) and Ssc3 (right panel) were subjected to partial tryptic digestion as a function of time as described in Fig. 2. The samples were analyzed on SDS-PAGE and subjected to Coomassie dye staining.

Supplemental Fig. S7 Α 250/01 Ssc1 0.25 0.5 1.0 1.5 3.0 (μM) 100-Ssc1 GST-Mge1 % Interaction 2 3 Lane 1 5 6 Ssc1 50-OSc3 Ssc3 0.25 0.5 1.0 1.5 3.0 G5 25% (μM) Ssc3

ż





Supplemental Fig. S7:

Nucleotide-dependent Mge1 interaction analysis of Ssc1, Ssc3 and their respective NBDs. *A*, Immobilized GST-Mge1 (1.5 μM) was incubated with increasing concentrations of full-length Ssc1 (*left top panel*) and Ssc3 (*left bottom panel*) as indicated in the absence of nucleotides. The bound proteins were analyzed by SDS-PAGE followed by Coomassie dye staining. GST alone was used as a negative control and 25% input (offered to the beads) was used as a loading control. The data was quantified by densitometric analysis using ImageQuant software (*right panel*). *B*, Immobilized GST-Mge1 (1.5 μM) was incubated with 2.5 μM of full-length Ssc1 (*left panel*) and Ssc3 (*right panel*) in the presence or absence of 250 μM of ATP. *C*, 1.5 μM of immobilized GST-Mge1 was incubated with 2.0 μM of NBD_{Ssc1} (*left panel*) and NBD_{Ssc3} (*right panel*) in the presence or absence of 250 μM of ATP. The bound proteins were analyzed by SDS-PAGE followed by Coomassie dye staining. GST alone was used as a negative control and 100% input was used as a loading control.

Supplemental Fig. S8 Α A_1P_{YI} $A_{YI}P_{YI}$ $A_{YI}P_1$ SSC1 P_{YI} P_1 ssc1∆ CEN SSC1 **GPD Empty** vector В $A_{Hs}P_{Hs}$ SSC1 $A_{Hs}P_1$ A_1P_{Hs} P_{Hs} A_1 A_{Hs} $A_{\underline{\mathsf{H}} \underline{\mathsf{s}}}$ P_{Hs} $ssc1\Delta$ CEN SSC1 **GPD Empty** vector

Supplemental Fig. S8:

5-FOA counterselection of $ssc1\Delta$ cells complemented with various mtHsp70 constructs. The $ssc1\Delta$ cells expressing wild type copy of SSC1 gene from a URA plasmid was transformed with either SSC1 on a CEN plasmid or A, $A_{Yl}P_{Yl}$ (left panel), $A_{Yl}P_{I}$ (middle panel), $A_{I}P_{Yl}$ (right panel) from a CEN pRS413 plasmid driven by GPD promoter. B, $A_{Hs}P_{Hs}$ (left panel), $A_{Hs}P_{I}$ (middle panel), $A_{I}P_{Hs}$ (right panel) from a 2μ pRS423 plasmid driven by TEF promoter. The cells were streaked on media containing 5-fluoroorotic acid and grown at 30 °C for 3 days. The empty vector was used as a negative control.

Supplemental TABLE S1:

Plasmids used in this study

Plasmid name	Expressed protein	Leader sequence	Vector	Host Organism used	Restriction sites
pRS314-SSC1	Ssc1	Ssc1	pRS314	S.cerevisiae	PstI/ BamHI
pRS313- <i>SSC3</i>	Ssc3	Ssc3	pRS313	S.cerevisiae	HindIII/BamHI
pRS423- <i>SSC3</i>	Ssc3	Ssc1	TEF/GPD pRS423	S.cerevisiae	BamHI/XhoI
pRS423- A ₁ P ₃	A_1P_3	Ssc1	TEF/GPD pRS423	S.cerevisiae	BamHI/XhoI
pRS423- A ₃ P ₁	A_3P_1	Ssc1	TEF/GPD pRS423	S.cerevisiae	BamHI/XhoI
pRS423- A_{Hs} P_{Hs}	$A_{Hs} P_{Hs}$	Ssc1	TEF pRS423	S.cerevisiae	BamHI/XhoI
pRS423- A_1P_{Hs}	A_1P_{Hs}	Ssc1	TEF pRS423	S.cerevisiae	BamHI/XhoI
pRS423- A _{Hs} P ₁	$A_{Hs}P_1$	Ssc1	TEF pRS423	S.cerevisiae	BamHI/XhoI
pRS413- $A_{Yl}P_{Yl}$	$A_{Yl}P_{Yl}$	Ssc1	GPD pRS413	S.cerevisiae	BamHI/EcoRI
pRS413- $A_I P_{YI}$	A_1P_{Yl}	Ssc1	GPD pRS413	S.cerevisiae	BamHI/EcoRI
pRS413- $A_{Yl}P_1$	$A_{Yl}P_1$	Ssc1	GPD pRS413	S.cerevisiae	BamHI/EcoRI
pRS314- <i>ssc1-2</i>	Ssc1-2	Ssc1	pRS314	S.cerevisiae	PstI/ BamHI
pRSFDuet-1-Ssc1	Ssc1(His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1-Ssc3	Ssc3(His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc3 ₅₅₈	Ssc3(1-558) (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc3 ₅₂₈	Ssc3 (1-528) (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pET-3a-SBD _{Ssc1}	SBD _{Ssc1} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-21d-SBD _{Ssc3}	SBD _{Ssc3} (His ₆)	_	pET-21d	E. coli BL21	NcoI/XhoI
pET-3a-SBD _{Ssc1} - (ABCD) _{Ssc3}	SBD _{Ssc1} - (ABCD) _{Ssc3} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-3a-SBD _{Ssc1} - (A) _{Ssc3}	SBD_{Ssc1} - $(A)_{Ssc3}$ (His_6)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-3a-SBD _{Ssc1} - (B) _{Ssc3}	SBD _{Ssc1} -(B) _{Ssc3} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-3a-SBD _{Ssc1} - (C) _{Ssc3}	SBD _{Ssc1} -(C) _{Ssc3} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-3a-SBD _{Ssc1} - (D) _{Ssc3}	SBD _{Ssc1} -(D) _{Ssc3} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pET-3a-SBD _{Ssc3} - (D) _{Ssc1}	SBD _{Ssc3} -(D) _{Ssc1} (His ₆)	-	pET-3a	E. coli BL21	NdeI/ BamHI
pRSFDuet-1-NBD _{Ssc1}	NBD _{Ssc1} (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1-NBD _{Ssc3}	NBD _{Ssc3} (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- V28IQ29PG30DS31A	Ssc1- V28IQ29PG30DS 31A(His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1-	Ssc1-	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI

I80EA86SV88IP90S	I80EA86SV88I				
pRSFDuet-1- Ssc1- G135NQ136R	P90S (His ₆) Ssc1- G135NQ136R(Hi	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- G160AP162S	s ₆) Ssc1- G160AP162S	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- S214P	(His ₆) Ssc1- S214P (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- V238I	Ssc1-V238I (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- S314A	Ssc1- S314A (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- N320RK322P	Ssc1- N320RK322P (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- A326VF328LT330NL 331I	Ssc1- A326VF328LT33 0NL331I (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- V336IK337D	Ssc1- V336IK337D (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- G351RL352IS353TT3 54A	Ssc1- G351RL352IS353 TT354A (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- S378K	Ssc1- S378K (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- P384A	Ssc1- P384A (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc1- I396LV400IG402A	Ssc1- I396LV400IG402 A (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1- Ssc3- A157GS159P	Ssc3- A157GS159P (His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pRSFDuet-1-Hep1	Hep1	-	pRSFDuet-1	E. coli BL21	BamHI/SalI
pRSFDuet-1-Mge1	Mge1(His ₆)	-	pRSFDuet-1	E. coli BL21	BamHI/SalI
pRSFDuet-1-Mdj1	Mdj1(His ₆)	-	pRSFDuet-1	E. coli BL21	NdeI/XhoI
pET-3a-Pam18	Pam18(His ₆)	-	pET-3a	E. coli C41	NdeI/ BamHI
pET-20b-Tim44	Tim44 (TEV cleavable His ₆₎	-	pET-20b	E. coli BL21	BamHI/XhoI

Supplemental TABLE S2:

S. cerevisiae strains used in this study

Strain	Genotype	Source
PJ53-52C	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	Voisine, C.
	$GAL2+ met2-\Delta 1 lys2-\Delta 2 ssc1\Delta ClaI::LEU2 pRS316-SSC1)$	et al. (41)
PJ53-52C CEN SSC3	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
	pRS313-SSC3)	
PJ53-52C 2μ SSC3	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-∆1 lys2-∆2 ssc1∆ClaI::LEU2 pRS316-SSC1	
	pRS423-SSC3)	
$PJ53-52C A_1P_3$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
	pRS423- A ₁ P ₃)	
$PJ53-52C A_3P_1$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
4.0	pRS423- A ₃ P ₁)	TT1 : 1
A_1P_3	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
DI52 52C 4 D	$GAL2+ met2-\Delta 1 lys2-\Delta 2 ssc1\Delta ClaI::LEU2 pRS423- A1P3)$	This study
$PJ53-52C A_{Hs} P_{Hs}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100 GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	This study
	1	
PJ53-52C A ₁ P _{Hs}	pRS423- A _{Hs} P _{Hs}) (trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta ClaI::LEU2 \ pRS316-SSC1$	Tills study
	pRS423- A_1P_{Hs})	
PJ53-52C A _{Hs} P ₁	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla$ I::LEU2 pRS316-SSC1	
	pRS423- $A_{Hs}P_I$)	
$A_{l}P_{Hs}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla$ I::LEU2 pRS423- A_1P_{Hs})	_
$A_{Hs}P_{I}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta ClaI::LEU2 \ pRS423- A_{Hs}P_1)$	
$PJ53-52C$ A_{Yl} P_{Yl}	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
	$pRS413-A_{YI}P_{YI})$	
$PJ53-52C A_1 P_{Yl}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
D150 50G / D	$pRS413-A_1P_{YI})$	- T
$PJ53-52C A_{Yl}P_{I}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	GAL2+ met2-Δ1 lys2-Δ2 ssc1ΔClaI::LEU2 pRS316-SSC1	
$A_{YI}P_{YI}$	pRS413- A _{Yl} P ₁) (trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$(lrp1-1 \ ura3-1 \ leu2-3, 112 \ ms3-11, 13 \ aae2-1 \ can1-100$ $GAL2+ \ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla1:: LEU2 \ pRS413- A_{\gamma l} P_{\gamma l})$	Tins study
$A_l P_{Yl}$	GAL2+met2-31 tys2-32 ssc13Cta1LEO2 pRS415- Ay1 Fy1) (trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
11 j1 Yl	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla1::LEU2 \ pRS413- A_1P_{Y1})$	Tins study
$A_{Yl}P_{I}$	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
11 - 1	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla1:: LEU2 \ pRS413- A_{7l} P_1)$	2 ms staay
PJ53-52C ssc1-2	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	Voisine, C.
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla1::LEU2 \ pRS314-ssc1-2)$	et al. (41)
ssc1-2 2µ SSC3	(trp1-1 ura3-1 leu2-3, 112 his3-11, 15 ade2-1 can1-100	This study
	$GAL2+ met2-\Delta 1 \ lys2-\Delta 2 \ ssc1\Delta Cla1::LEU2 \ pRS314-ssc1-2$	
		1

	pRS423-Ssc3)	
BY4741	$MATa$ his $3\Delta 1$ leu 2Δ met 15Δ ura 3Δ	Open
		Biosystems
BY4741 <i>ssc3∆</i>	MATa his3∆1 leu2∆ met15∆ ura3∆ ssc3∆::kanMX4	Open
		Biosystems

Supplemental TABLE S3: $\label{eq:SBD} Kinetic \ parameters \ for \ F-P5 \ binding \ with \ SBD_{Ssc1}, \ SBD_{Ssc3} \ and \ chimeric \ proteins.$

Protein	$K_{d}\left(\mu M\right)$	\mathbb{R}^2
$\mathrm{SBD}_{\mathrm{Ssc1}}$	0.264 ± 0.041	0.98
SBD_{Ssc1} -(ABCD) $_{Ssc3}$	22.724 ± 1.008	0.97
SBD_{Ssc1} - $(A)_{Ssc3}$	0.293 ± 0.031	0.99
SBD_{Ssc1} -(B) $_{Ssc3}$	0.351 ± 0.033	0.99
SBD_{Ssc1} -(C) _{Ssc3}	0.285 ± 0.032	0.98
SBD_{Ssc1} -(D) $_{Ssc3}$	20.782 ± 0.983	0.97
SBD_{Ssc3}	26.897 ± 2.639	0.97
SBD_{Ssc3} - $(D)_{Ssc1}$	0.911 ± 0.087	0.99

Supplemental TABLE S4:

Aggregation of various mtHsp70 proteins at 37 °C in bacterial system.

Protein	Aggregation at 37 °C
Ssc1	·
WT	-
V28IQ29PG30DS31A	-
I80EA86SV88IP90S	*
G135NQ136R	-
G160AP162S	**
S214P	-
V238I	*
S314A	-
N320RK322P	-
A326VF328LT330NL331I	-
V336IK337D	-
G351RL352IS353TT354A	*
S378K	-
P384A	-
I396LV400IG402A	-
Ssc3	
WT	*****
A157GS159P	****

Subjective scoring is based on the amount of protein present in pellet (P) fraction upon solubility analysis at 37 °C in *E.coli*. Here (******) has been assigned to Ssc3 owing to its maximum tendency to aggregate, while others are assigned relative to Ssc3 based on their distribution in supernatant and pellet fraction upon solubility analysis. (-) sign indicates no aggregation under similar conditions.

Supplemental TABLE S5:

Growth complementation of $ssc1\Delta$ strain (PJ53-52C) with various Hsp70 constructs at indicated temperatures.

Strain	Growth complementation at			
	24 °C	30 °C	34 °C	37 °C
WT PJ53-52C	+++	+++	+++	+++
A_3P_3	1	-	-	-
A_3P_1	-	-	-	-
A_1P_3	+++	+++	++	-
$A_{Yl} P_{Yl}$	++	++	+	-
$A_{Yl}P_1$	++	++	+	-
$A_{I}P_{YI}$	+++	+++	+++	+++
$A_{Hs}P_{Hs}$	-	-	-	-
$A_{Hs}P_1$	+	+	+	-
A_1P_{Hs}	++	++	++	+

Subjective scoring is based on temperature sensitive phenotype mentioned in Fig.8 from strongest (+++) to weakest (+). Minus (-) indicates lethal phenotype at indicated temperature.