
Supplementary information

HSP40 proteins use class-specific regulation to drive HSP70 functional diversity

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Supplementary Table 1 | NMR and refinement statistics for DNAJB1^{JD-GF}

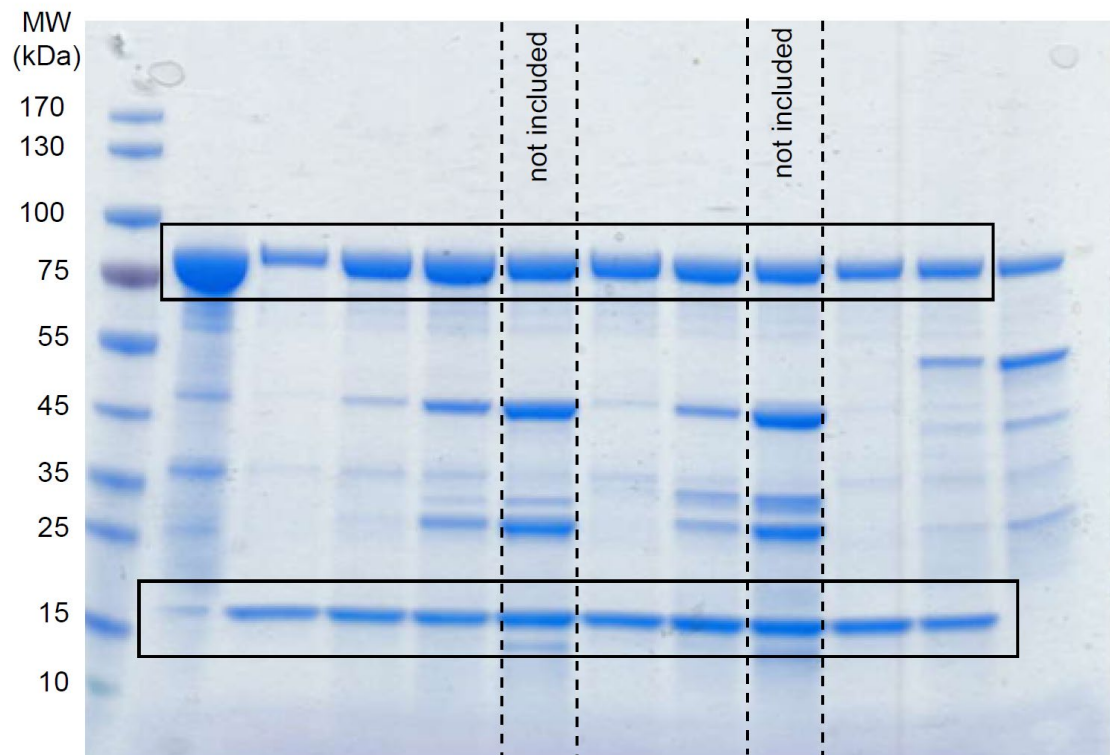
	DNAJB1 chaperone residues 1-111 (PDB 6Z5N)
NMR distance and dihedral constraints	
Distance constraints	
Total NOE	1271
Short range ($ i - j < 2$)	469
Medium-range ($ i - j \leq 4$)	298
Long-range ($ i - j > 4$)	504
¹ HN-Γ ₂ PRE restraints	88
Total dihedral angle restraints	
φ	80
ψ	80
¹ D _{NH} RDC restraints	
PEG/hexanol alignment medium	95
pfl alignment medium ^a	95
Structure statistics^b	
Violations (mean and s.d.)	
Distance constraints (Å)	0.15±0.02
Max. distance constraint violation (Å)	0.9
Deviations from idealized geometry	
Bond lengths (Å)	0.01
Bond angles (°)	0.4
Q-factor (%)	10.9±0.6
Average pairwise r.m.s. deviation ^c (Å)	
Heavy	1.0
Backbone	0.5
Ramachandran plot	
Most favored regions	95.2
Additionally allowed regions	4.7
Generally allowed regions	0.1
Disallowed regions	0.0

^aRDCs from the second alignment medium were used for structure validation.

^bStatistics apply to the 10 lowest-energy structures.

^cPairwise r.m.s. deviation was calculated among 10 refined structures.

Extended Data Fig. 10g



Supplementary Fig. 1 | Gel source data for Extended Data Fig. 10g. The content of Extended Data Fig. 10g is highlighted in a box. The experiment was repeated two times with similar results.