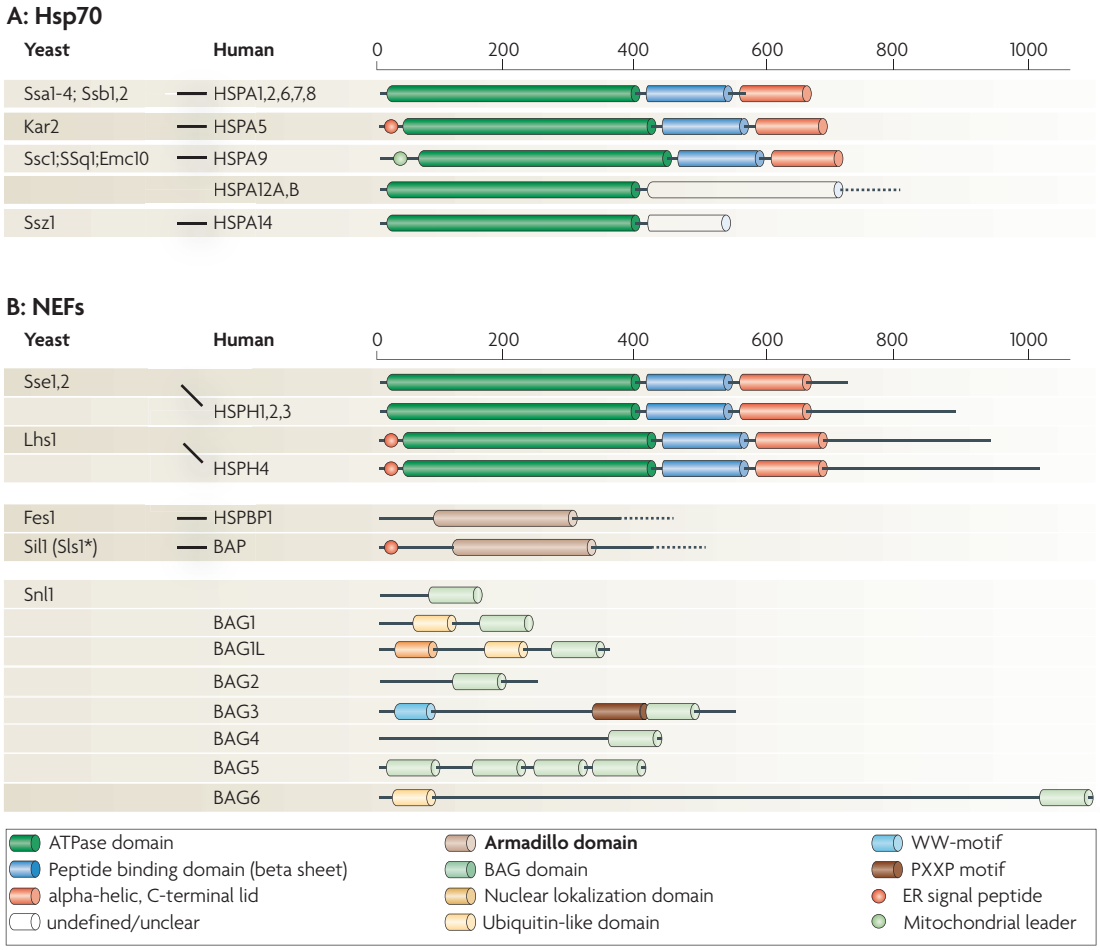
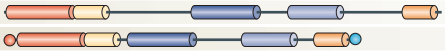
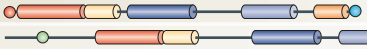
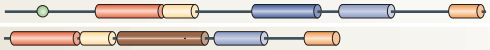
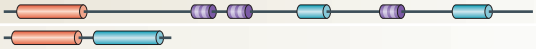
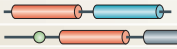
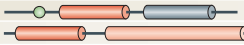
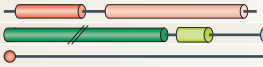
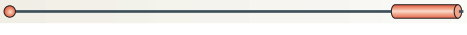
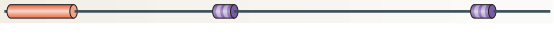
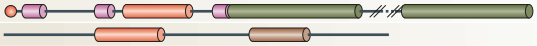
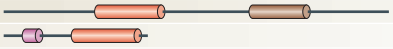
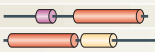
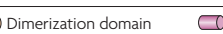
In format provided by Kampinga and Craig (AUGUST 2010)



Supplementary information S1 (Figure) | **Diversity in domain architecture of Hsp70-proteins (panel A) and Nucleotide Exchange Factors (panel B) from yeast (*Saccharomyces cerevisiae*) and *Homo sapiens*.** True functional orthologs are connected by lines. For Hsp70s and HspH/Sse's, the distinctions between the indicated peptide-binding domain and C-terminal lids are imprecise: also, the size-variable, acidic loop (between the beta-sheet of the peptide binding domain and the alpha-helical C-terminal lid) in HspH/Sse's is not indicated.

Supplementary information S2 (figure) | **Domain structure of yeast (A) and human (B) J-proteins:** Extension of figure 3 with all individual J-proteins from *Saccharomyces cerevisiae* (A) and *Homo Sapiens* (B) and their most prominent domain features. Proteins are categorized in terms of type (I: bleu, II: green, or III: red) and (assumed) client binding ability and mechanistic mode of functioning. Established functional human-yeast orthologs are indicated. Abbreviation for intracellular localization: C = cytosol; N = nucleus; M = membrane association; Mit = mitochondrial; ER = Endoplasmatic Reticulum; i = inside; a = associated. ERAD = ER associated protein degradation; CBD = Client Binding Domain; HDAC = Histone Deacetylase. Numbers under Refs (references) refer to a list with the most pertinent references that is provided below.

Panel A| Domain structure of yeast J-proteins

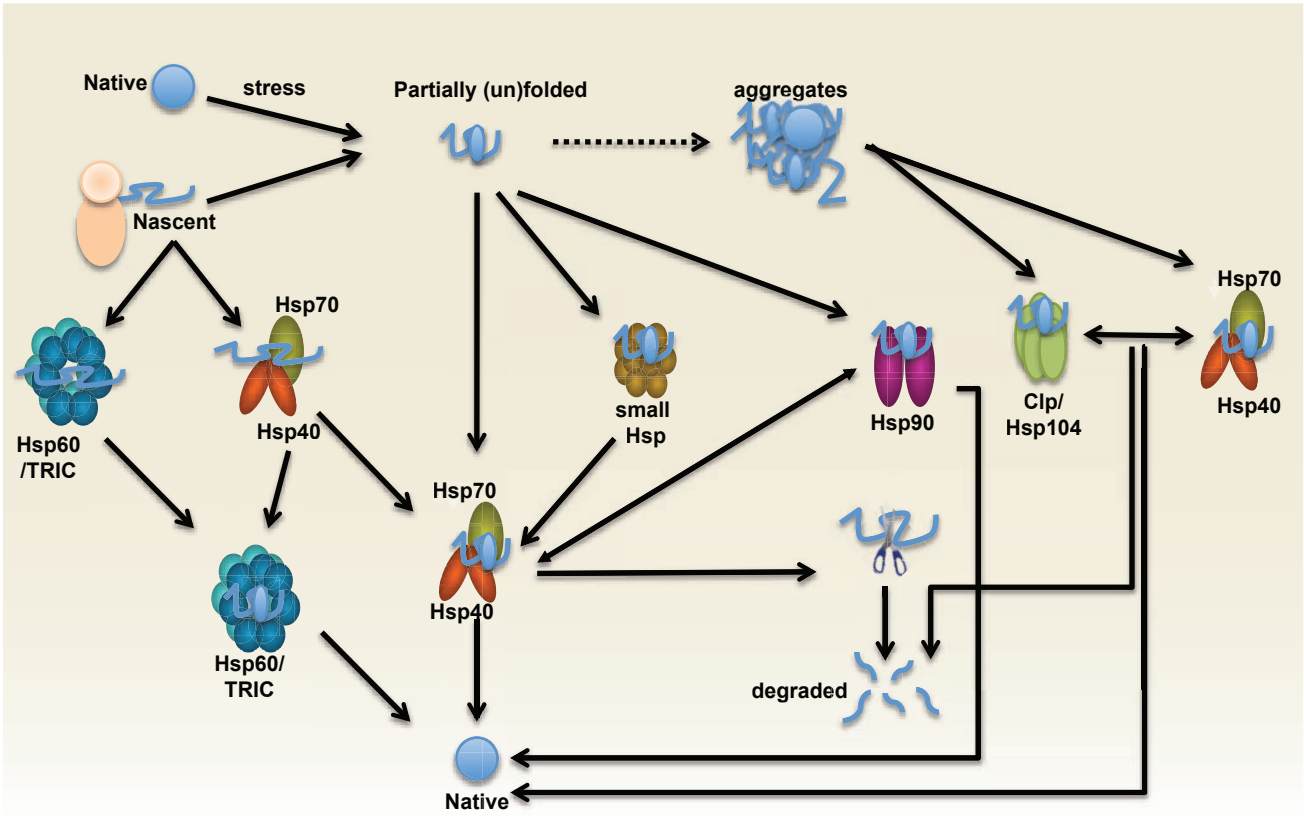
Name	Human Ortholog	Schematic Domain structure	Localization	Function/remarks	*Refs*
DnaJ-like promiscuous client binding domain					
Ydj1	DNAJA1		C/N/Mit	folding	*1-16*
Xdj1			C/N	folding (?)	*17*
Apj1			C/N	folding (?)	*18*
Scj1			ER-i	folding/ERAD	*19-21*
Mdj1	DNAJA3		Mit-i	folding	*22-25*
Sis1	DNAJB1		C/N	(re)folding	*4,5,8,10,12 26-32*
Client binding domain for wide selection of specific clients					
Djp1			C	peroxisomal import	*33,34*
Caj1			N	unknown	*35*
Erj5			ER-i	folding (CBD uncleear)	*36*
Client binding domain with large degree of specificity					
Jjj1	DNAJC21		C	ribosome biogenesis	*5,37-39*
Jjj3	DNAJC24		C	dipthamide synthesis	*5*
Jac1	DNAJC20		Mit-i	Fe-S cluster biogenesis	*40-45*
Cwc23	DNAJC17		C/N	mRNA splicing	*5,46*
Swa2	DNAJC6		C	clathrin uncoating	*47-50*
Jem1			ER-i	nuclear membrane fusion	*19,20,51-53*
Existence of client binding domain unclear					
Jid1			Mit-i	unknown	*54*
Jjj2			C	unknown	*18*
No client binding domain					
Sec63	DNAJC23		ER-i	protein import	*55-61*
Zuo1	DNAJC2		C	folding/translation (?)	*5,62-64*
Mdj2			Mit-i	protein import	*65,66*
Pam18	DNAJC19		Mit-i	protein import	*67-73*
Hlj1			ER-a	ERAD	*74,75*

Panel B| Domain structure of human J-proteins

Name	Alternative names	Yeast Ortholog	Schematic Domain structure	Localization	Function/remarks	Refs
DnaJ-like promiscuous client binding domain						
DNAJA1	HSJ2;Dj-2;DJA1	Ydj1		C/N/M?	horm. receptor maturation	***76-80***
DNAJA2	DNAJ;DNAJ3			C/N/M	G-protein signalling	***81,82***
DNAJA4	DJ4;Hsj4			C/N/M	folding	***83-85***
DNAJA3	TID1;hTid-1	Mdj1		Mit-i/C?	signalling	***86-90***
DNAJB1	Hsp40;Hdj-1	Sis1		C/N	(re)folding	***82,91-95***
DNAJB4	HLJ1;Hsc40			C/N	unknown	***77,96***
DNAJB5	Hsc40;HSP40-3			C/N	HDAC shuttling	***96,97***
DNAJB11	ERdj-3;HEDJ			ER-i	folding	***98-102***
Client binding domain for wide selection of specific clients						
DNAJB9	ERdj-4;Mdg1			ER-i	ERAD; folding	***91,99,103,104***
DNAJB2a,b	Hsj1a,b			C/ER-a	proteasomal degradation	***105-110***
DNAJB6a,b	HSJ2;MRJ;MSJ1			C/N	anti-aggregation	***111-118***
DNAJB8	mDj6			C/N	anti-aggregation	***111,119***
DNAJB7	Dj-5;mDj5;HSC3			C/N	unknown	***111,119***
DNAJB12a,b	DJ10;mDJ10			ER-a	ERAD	***120***
DNAJB14a,b	FLJ14281			?	unknown	
DNAJC18	MGC29463			?	unknown	
Client binding domain with large degree of specificity						
DNAJC21	DNAJA5;JJJ1	Jjj1		?	unknown	
DNAJC24	DPH4;JJJ3	Jjj3		C	dipthamide synthesis	***121***
DNAJC5,5b,g	CSP			exosomes?	exocytosis	***122-128***
DNAJC20	HSCB;Hsc20	Jac1		Mit-i	FeS cluster biogenesis	***41,129,130***
DNAJC17	FLJ10634	Cwc23		?	unknown	
DNAJC10	ERdj-5;JDI		793	ER-i	ERAD	***97,131,132***
DNAJC16	KIAA0962		782	?	unknown	
DNAJC6	auxilin	Swa2	366 409 760 913	C	clathrin uncoating	***133-141***
DNAJC26	GAK		314 399 710 870 1157 1311	C/N	clathrin uncoating	***136,142-145***
DNAJC27	RBJ;RabJS			?	unknown	
DNAJC3	PRKRI;P58IPK			ER-i	translation under stress	***146-150***
DNAJC7	TTC2;TPR2;mDJ11			C	hormone maturation	***151-153***
DNAJC29	ARSACS;sacsin		4306 4579	C/Mit?	protein degradation?	***154,155***
DNAJC14	DRIP78;HDJ3;LIP6		702	C/ER-a/M	cell surface export	***156-158***
DNAJC22	wus;FLJ13236			C	endocytosis?	***159,160***
Existence of client binding domain unclear						
DNAJB13	TSARG6;RSPH16A			C?	no HPD!	***161,162***
DNAJB3	HCG3;Hsj3;Msj1			C	folding in sperm	***163-165***
DNAJC13	RME-8;KIAA0678		1301 2243	C/M	endosome trafficking	***166-170***
DNAJC28	Orf28;C21orf55			?	unknown	
DNAJC9	JDD1;HDJC9			N	nuclear exit upon stress	***171,172***
DNAJC8	SPF31			C	protein phosphorylation?	***173***
DNAJC25	bA16L21.2.1			?	unknown	
DNAJC11	FLJ10737			Mit-i?	unknown	***174***
No client binding domain						
DNAJC23	Sec63L;ERdj2	Sec63	760	ER-M	protein import	***175,176***
DNAJC1	ERdj1;Mtj1			ER-i	translation	***177-181***
DNAJC2	MPP11;zuotin	Zuo1		C	translation	***182-184***
DNAJC15	DNAJD1;MCJ			Golgi	degradation oncoproteins	***185***
DNAJC12	JPD1			?	unknown	***186***
DNAJC19	TIMM14;Tim14	Pam18		Mit-i	protein import	***187-189***
DNAJC30	WBSCR18			?	unknown	
DNAJC4	HSPF2;MCG18			?	unknown	***190***

J-domain
G/F rich domain
CTD I with ZFLR
CTD II
Dimerization domain
Putative CTD II
CTD I lacking ZFLR
Transmembrane domain
Putative CTD I
Ubiquitin-interacting motif
CTD I with HDAC BD
Unidentified protein motif
Coiled coil
Zinc finger domain
Cystein Rich Stretch
Isu1 binding domain
Putative spliceosome interaction domain
RNA recognition motif
Thioredoxin box
Extracellular fragment
Tensin binding motif
Clathrin binding region
Protein kinase domain
GTP binding site
Tetratricopeptide repeat
HEPN domain
Sec63 domain
SANT domain
Putative ribosome binding region
ER signal peptide
ER retention peptide
Mitochondrial leader
Acetylatable lysine

In format provided by Kampinga and Craig (AUGUST 2010)



Supplementary information S3 (figure) | **Chaperone networks:** Hsp70 core-machines can form partnerships with at least three other Hsp-families. These include partnerships with the ATP dependent chaperonins (Hsp60/TRIC family), the Hsp90 family and the ATP-independent chaperones of the small Hsp protein (small Hsp) families. In addition, a number of AAA-protease (Clp/Hsp104) protein families, which have also been grouped within the Hsp family, can form partnerships with the Hsp70 core machines. Each of these families is comprised of several members and the size of these families (especially the small Hsps) has increased substantially during evolution. In various processes, the Hsp70 core machine can act simultaneously or sequentially with these other Hsp families in protein (re)folding, -assembly, -degradation, or even –disaggregation (arrows indicate client transfer to and from the various chaperone complexes).