

The Hsp70 chaperone system: distinct roles in erythrocyte formation and maintenance

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Supplementary material

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Figure S1: Expression profiles of selected chaperone systems in red cell progenitors, erythroblasts and mature erythrocytes^{1,2} versus unstressed and heat-shocked Jurkat cells,³ obtained from quantitative proteomics data. The black dotted line represents the median relative abundance of non-hemoglobin proteins in each cell type. Inset: zoom on the HSP70/110, HSP90 and HSP60 categories in unstressed versus heat-shocked Jurkat cells. CT indicates control/unstressed; HS stands for heat-shocked (41°C for 4 hours).

References

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Table S1: mass fractions of individual chaperone proteins from Jurkat cells and erythrocytes

class	proteins	Mass fractions (% of total protein)		
		Jurkat (control)	Jurkat (Heat-Shocked)	RBC (total)
HSP70	HSC70	1,62E+00	1,87E+00	7,17E-02
	HSPA1A/B	1,46E-03	3,84E-03	1,89E-02
	BIP	2,80E-01	3,25E-01	6,58E-04
	HSPA9	2,19E-01	2,41E-01	0,00E+00
	HSPA2	0,00E+00	0,00E+00	0,00E+00
	HSPA6/7	4,09E-02	5,13E-02	0,00E+00
	HSPA1L	0,00E+00	0,00E+00	0,00E+00
	HSPA14	5,50E-03	4,06E-03	0,00E+00
	HSPA13	3,34E-04	1,13E-04	0,00E+00
HSP110	APG2	2,40E-01	2,40E-01	7,54E-03
	APG1	4,77E-02	4,40E-02	3,09E-06
	HSP105	1,68E-03	5,24E-03	1,80E-04
	HYOU1	8,16E-02	8,02E-02	0,00E+00
DNAJ A	DNAJA4	8,01E-05	0,00E+00	1,20E-03
	DNAJA2	7,10E-03	6,65E-03	1,68E-04
	DNAJA1	4,55E-02	4,53E-02	0,00E+00
	DNAJA3	6,34E-03	5,47E-03	0,00E+00
DNAJ B	DNAJB2	0,00E+00	0,00E+00	3,25E-03
	DNAJB1	1,22E-02	1,88E-02	1,35E-03
	DNAJB4	0,00E+00	0,00E+00	1,77E-04
	DNAJB11	1,23E-02	1,14E-02	0,00E+00
	DNAJB6	1,17E-03	8,28E-04	0,00E+00
	DNAJB14	4,43E-03	5,76E-03	0,00E+00
	DNAJB12	6,48E-04	6,38E-04	0,00E+00
	DNAJB9	8,62E-06	0,00E+00	0,00E+00
HSP70 NEFs	BAG6	3,64E-02	2,90E-02	1,70E-04
	BAG1	0,00E+00	0,00E+00	8,15E-05
	BAG2	2,60E-02	2,81E-02	5,97E-05
	HSPBP1	2,88E-03	2,16E-03	0,00E+00
	BAG5	1,79E-03	1,26E-03	0,00E+00
	BAG3	2,44E-04	2,54E-04	0,00E+00
HSP90	HSP90AA1	2,39E+00	2,91E+00	3,29E-02
	HSP90B1	2,14E-01	2,04E-01	2,67E-05
	HSP90AB1	9,92E-01	1,07E+00	3,61E-03
	HSP90AB4P	1,03E-03	3,94E-04	0,00E+00
	HSP90AB2P	1,97E-02	1,95E-02	0,00E+00
HSP60 / CCT	CCT2	3,03E-01	3,04E-01	2,77E-02
	CCT3	2,59E-01	2,49E-01	1,11E-02
	CCT5	2,26E-01	2,24E-01	1,53E-02
	CCT8	2,61E-01	2,64E-01	2,42E-02
	TCP1	2,64E-01	2,76E-01	1,18E-02
	CCT7	2,31E-01	2,19E-01	1,32E-02
	CCT6A	2,58E-01	2,50E-01	1,35E-02
	CCT4	1,67E-01	1,58E-01	1,40E-02
	CCT6B	0,00E+00	0,00E+00	0,00E+00
	HSPD1	8,91E-01	9,76E-01	0,00E+00
	HSPE1	1,39E-01	1,82E-01	0,00E+00
sHSP	HSPB1	0,00E+00	0,00E+00	2,11E-03
	HSPB11	4,64E-03	4,63E-03	0,00E+00
	sum:	9,31E+00	1,03E+01	2,75E-01

Table S2: Mass fractions of chaperone groups in Jurkat cells and erythrocytes

class	Mass fractions (% of total protein)		
	Jurkat (control)	Jurkat (Heat-Shocked)	RBC (total)
HSP70s	2,163	2,492	0,091
HSP110s	0,371	0,369	0,008
DNAJAs	0,059	0,057	0,001
DNAJBs	0,031	0,037	0,005
NEFs	0,067	0,061	0,000
HSP90s	3,613	4,203	0,037
HSP60s / CCTs	2,999	3,103	0,131
sHSPs	0,005	0,005	0,002

Table S3: mass fractions of individual UPS proteins from Jurkat cells and erythrocytes

class	GeneNames	Mass fractions (% of total protein)		
		Jurkat (control)	Jurkat (Heat-Shocked)	RBC (total)
E1	UBA3;UBE1C	8,3E-03	7,1E-03	3,9E-04
	UBA6	2,3E-03	1,6E-03	0,0E+00
	UBA2	1,1E-02	1,0E-02	0,0E+00
	SAE1	9,5E-03	7,0E-03	0,0E+00
E2	UBE2N;UBE2NL	2,6E-02	2,4E-02	8,4E-03
	UBE2L3;hCG_1789329	2,6E-02	2,6E-02	5,2E-03
	UBE2O	1,1E-02	6,7E-03	6,9E-03
	UBE2I	3,0E-02	2,6E-02	0,0E+00
	UBE2K;HIP2	6,9E-03	5,8E-03	5,2E-03
	UBE2M	5,4E-03	4,0E-03	1,2E-03
	USE1	5,2E-04	4,1E-04	0,0E+00
	UBE2D4	0,0E+00	0,0E+00	0,0E+00
	UBE2H;Ube2h	5,7E-04	2,5E-04	0,0E+00
	UBE2L6	2,3E-03	4,9E-04	0,0E+00
	UBE2F	9,6E-04	5,3E-04	0,0E+00
	UBE2G1	9,2E-04	7,3E-04	0,0E+00
	UBE2Z	5,1E-04	7,4E-04	0,0E+00
	UBE2C	2,5E-04	0,0E+00	0,0E+00
	UBE2S	1,5E-02	1,4E-02	0,0E+00
	UBE2A	3,0E-03	2,3E-03	0,0E+00
	UBE2G2	2,7E-03	1,9E-03	0,0E+00
	UBE2R2	1,8E-03	1,1E-03	0,0E+00
	BIRC6	1,8E-03	1,2E-03	0,0E+00
	UBE2E2;UBE2E3;UBE2E1	8,7E-04	4,0E-04	0,0E+00
E3	SKP1	3,3E-02	2,7E-02	7,8E-03
	CUL1	1,9E-03	1,6E-03	2,3E-03
	DDB1	1,0E-01	8,3E-02	5,0E-03
	HUWE1	3,2E-02	2,4E-02	1,2E-03
	CUL3;Cul3	6,1E-03	4,7E-03	1,7E-03
	CUL2	5,7E-03	4,3E-03	1,3E-03
	CUL5	1,3E-03	8,7E-04	5,4E-04
	TCEB2	1,1E-02	1,2E-02	6,3E-04
	TCEB1	2,1E-02	1,9E-02	6,9E-04
	RBX1	1,0E-02	9,0E-03	4,7E-04
	STUB1	3,1E-03	2,8E-03	0,0E+00
	ANAPC4	6,4E-05	6,1E-05	0,0E+00
	UBE4B	6,5E-04	6,3E-04	0,0E+00
	UBE3C	0,0E+00	0,0E+00	0,0E+00
	SMURF1	0,0E+00	0,0E+00	0,0E+00
	UBE4A	3,2E-03	2,6E-03	0,0E+00
	CDC23	1,6E-03	1,5E-03	0,0E+00
	NEDD4L	0,0E+00	0,0E+00	0,0E+00
	UBE3A	7,5E-03	5,8E-03	0,0E+00
	ANAPC5	2,2E-04	1,8E-04	0,0E+00
	CUL4B	1,9E-03	1,1E-03	0,0E+00
	CDC27	1,9E-03	1,1E-03	1,1E-02
	RNF7	1,4E-03	7,6E-04	0,0E+00
CDC16	1,8E-04	3,0E-05	0,0E+00	

	PRPF19;LILRB4	1,3E-01	1,4E-01	0,0E+00
	PPIL2	1,6E-03	9,3E-04	0,0E+00
	PML	9,5E-03	8,8E-03	0,0E+00
	CDC20	7,2E-03	1,7E-03	0,0E+00
	TRIP12	6,4E-03	4,1E-03	0,0E+00
	ANAPC2	3,8E-03	4,1E-03	0,0E+00
	ANAPC7	3,5E-03	1,9E-03	0,0E+00
	UBR5	1,5E-03	9,1E-04	0,0E+00
	ITCH	9,7E-04	5,3E-04	0,0E+00
	FBXW11;BTRC;DKFZp781N011	6,0E-04	3,9E-04	0,0E+00
	ANAPC11	4,4E-04	5,8E-04	0,0E+00
	TRAF6	3,4E-04	3,1E-04	0,0E+00
	TRIM32	2,7E-04	2,0E-04	0,0E+00
	HERC4	1,7E-04	7,8E-05	0,0E+00
	RCHY1	1,2E-04	7,1E-05	0,0E+00
	SYVN1	1,1E-04	7,1E-05	0,0E+00
	VHL	9,1E-05	1,1E-05	0,0E+00
	FBXW8	0,0E+00	0,0E+00	0,0E+00
	PSMB5	3,0E-02	2,8E-02	7,3E-03
	PSMA5	1,0E-01	9,8E-02	1,0E-02
	PSMA7	8,7E-02	7,8E-02	1,2E-02
	PSMA1	7,8E-02	7,0E-02	1,7E-02
	PSMB4	3,1E-02	3,2E-02	3,8E-03
	PSMA3	4,9E-02	6,0E-02	7,0E-03
	PSMA6	6,0E-02	5,6E-02	7,5E-03
	PSMA4	7,8E-02	7,2E-02	8,8E-03
20S CP	PSMB1	4,4E-02	4,4E-02	7,7E-03
	PSMA2	6,1E-02	5,3E-02	3,7E-03
	PSMB2	3,8E-02	4,2E-02	3,9E-03
	PSMB6	4,2E-02	3,2E-02	5,4E-03
	PSMB3	2,8E-02	2,6E-02	2,2E-03
	PSMB7	3,8E-02	3,2E-02	7,6E-03
	PSMB8;PSM8	9,6E-03	7,1E-03	0,0E+00
	PSMB11	0,0E+00	0,0E+00	0,0E+00
	PSMB10	0,0E+00	0,0E+00	3,6E-06
	PSMB9	0,0E+00	0,0E+00	0,0E+00
	PSMD2;Psmd2	8,5E-02	7,6E-02	6,2E-03
	PSME1	3,3E-02	4,8E-02	1,4E-02
	PSMF1	1,2E-02	1,1E-02	4,0E-03
	PSMC4	2,8E-02	2,5E-02	2,5E-03
	PSME2	1,7E-02	1,9E-02	8,4E-03
	PSMD9	5,8E-03	6,4E-03	8,2E-03
	PSMD5	1,5E-02	9,6E-03	2,8E-03
	PSMC2	3,9E-02	3,4E-02	9,3E-03
	PSMC5	3,7E-02	6,9E-02	5,3E-03
	PSMC3	2,8E-02	2,5E-02	4,0E-03
	PSMD13	3,0E-02	2,8E-02	2,6E-03
	PSMD6	3,1E-02	3,3E-02	2,1E-03
	PSMC1	4,4E-02	4,8E-02	4,1E-03
19S RP	PSMD1	5,8E-02	5,2E-02	3,5E-03
	PSMD11	4,4E-02	4,2E-02	3,6E-03
	PSMC6	2,8E-02	2,5E-02	3,9E-03

PSMD3		4,4E-02	3,9E-02	3,4E-03
PSMD12		2,5E-02	2,5E-02	1,6E-03
PSMD8;Psm8		1,2E-02	1,1E-02	7,0E-04
PSMD14		3,1E-02	2,3E-02	9,5E-04
PSMD10		1,3E-02	1,6E-02	1,2E-03
PSMD4		2,7E-02	2,7E-02	1,2E-03
PSMD7		2,8E-02	2,5E-02	1,3E-03
PSME4		1,1E-03	9,4E-04	0,0E+00
PSME3		2,8E-02	3,1E-02	0,0E+00
PSMC3IP		4,8E-04	3,3E-04	0,0E+00
SHFM1		0,0E+00	0,0E+00	0,0E+00
ubiquitin	RPS27A;UBC;UBB;UBA52;UBBP	4,8E-01	6,9E-01	7,4E-02

Table S4: mass fractions of UPS protein groups from Jurkat cells and erythrocytes

Mass fractions (% of total protein)			
class	Jurkat (control)	Jurkat (Heat-Shocked)	RBC (total)
E1	3,1E-02	2,6E-02	3,9E-04
E2	1,4E-01	1,2E-01	2,7E-02
E3	4,1E-01	3,7E-01	3,2E-02
20S CP	7,8E-01	7,3E-01	1,0E-01
19S RP	7,4E-01	7,5E-01	9,5E-02
ubiquitin	4,8E-01	6,9E-01	7,4E-02

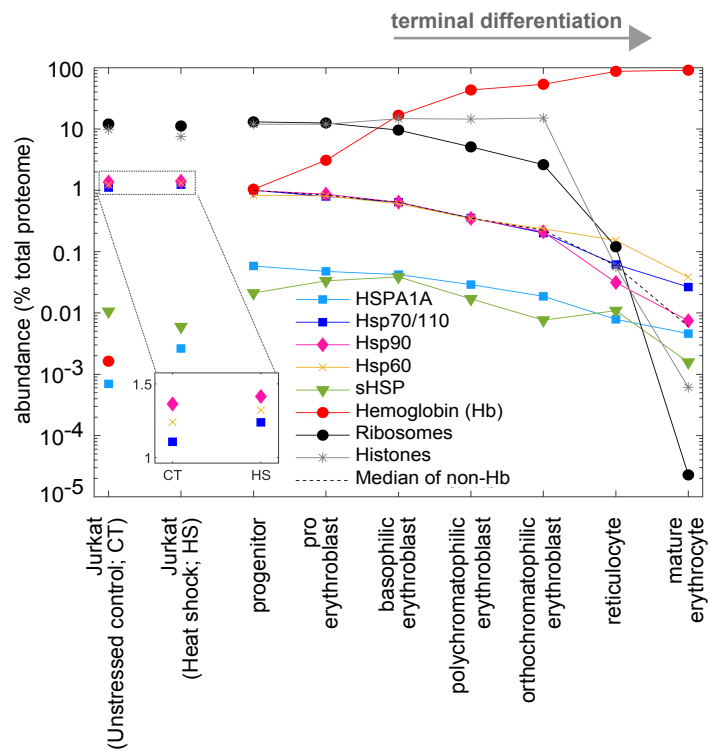


Figure S1