

Functional diversification of heat shock factors

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Supplementary Fig. 1. Conserved amino acid residues can be subjected to similar posttranslational modifications

(a) Alignment of human heat shock factors HSFs hHSF1, hHSF2, and hHSF4 shows that S13, K62, K80, and K118 are conserved in human. DNA binding domain of human HSFs were highlighted by gray boxes. Alignment was performed using *Clustal Omega*.

(b) Alignment of murine heat shock factors mHSF1, mHSF2, and mHSF4 shows that S13, K62, K80, and K118 are conserved in mice. DNA binding domain of murine HSFs were highlighted by gray boxes. Alignment was performed using *Clustal Omega*.

In both human and murine HSF1 PTMs were identified at these amino acids but not in HSF2 and HSF4. The highly conserved nature of these sequences suggests that these amino acids might undergo posttranslational modifications in HSF2 and HSF4 as well. These amino acids are highlighted with yellow ellipses.

[illegible]

				S13		
P38532	HSF1_MOUSE	1	--MDLAVGPGAGG	SV	EFETTKTWTIVSDPDDTALICWSPSGNSFHVFDQGGQFAKTVLP	58
P38533	HSF2_MOUSE	1	-----MKQ	SN	EFALSKLWTLVEETHNEFIITWSQNGQSFLVLDEORFAKEILP	50
Q9R0L1	HSF4_MOUSE	1	MQEAPALPTEPG	SPVFA	LGLKLWLVDFGTDHLIRWSPSGTSFLVSDQSRFAKEILP	60
			K62	K80	K118	
P38532	HSF1_MOUSE	59	KYF	HNHMASFVRQINMYGFI	WHIEFGGILVKPERDDTEFQHECFILRGQEOLLENIK	118
P38533	HSF2_MOUSE	51	KYF	HNHMASFVRQINMYGFI	WHIEFGGILVKPERDDTEFQHECFILRGQEOLLENIK	110
Q9R0L1	HSF4_MOUSE	61	QYF	HSNMAISFVRQINMYGFI	WVIEFGGLLRPERDHVEFQHPHFVFRGELWELVRV	120
			*****	*****	*****	
P38532	HSF1_MOUSE	119	VTSVSTLKS	EDIKIRQDSVT	RLTLLTDVQLMKGKQECMDSKLLAMKHENEALWREVASLRQK	178
P38533	HSF2_MOUSE	111	V5	-----SSKPEENKIRQEDLTKI	ISSAQKVQIQKQETIESRLSELKSNESLWKEVSELRAK	167
Q9R0L1	HSF4_MOUSE	121	VP	-----ALRGDSDRWRPEDLSRL	LGVEALRGVQESTEARLQQLQNEILWREVLTRQS	177
			*	:	:	*
P38532	HSF1_MOUSE	179	HAQQQKV	VNKLIFQLISLVQSN	-RILGVKRKIPMLSDSNSAHSVPKYGR---QYSLEHV	234
P38533	HSF2_MOUSE	168	HAQQQKVIRKIVQ	FIQVITLVQNN	-QLVSLKRRKPLLLNTNGAPKKN-LYQHIVKEPTIDNH	224
Q9R0L1	HSF4_MOUSE	178	HAQQHRRVIGKLI	QCLFGLFGLTQGPSSTGAKRKL	SIMLDEGSACASAKFNA---CFV-SGA	233
			*****	*****	*****	
P38532	HSF1_MOUSE	235	HGPGFPYSAPSPAY	SSSSSLYSDDVITSSGPIISDITELAPTSPLASPGRSIDERPLSS---		291
P38533	HSF2_MOUSE	225	HHKVPHSR	T-----EGLKSRERISDDII	IYDVTDDNVDEENIPVETNEDVWDDSN	277
Q9R0L1	HSF4_MOUSE	234	LLQDPYFI	QSPLEP---TTLGLSPHRARGPIISDIPEDSPSP	EGHRLSPSGGCRVK---	287
			*	:	:	*
P38532	HSF1_MOUSE	292	--STILVRVKQ	EPSP---SP-PHS	PRV---LEASPRG---PSSMDTFLSPTAFIDSILRESEPT	341
P38533	HSF2_MOUSE	278	QYPDIVIVEDDNE	DEYAFYVQSGEQSEPA	REPLRVGSAGSSPLMSSA-----	325
Q9R0L1	HSF4_MOUSE	288	---GLALLKEEPA	---SP-GGDGEA-GLALAPNEC	DFCVIAPPFLVAVVQAILLEGKGS-	338
			:	:	:	:
P38532	HSF1_MOUSE	342	PAASNTAP	MDITGAQAPALPTPSTP-EKCLSVACL---	DKNELSDHLDAMDSDNLNLTQM-	397
P38533	HSF2_MOUSE	326	-----VQLNGSS	SLTSEDFTVMTSDI	LNNDINLLGKVELLDYLSIDCSLEDFOAM-	376
Q9R0L1	HSF4_MOUSE	339	-----YSPEGR	SRVQPEPRGP-REV	PDRGTLGLDRGNRSP-----E---SLLPML	381
			*	:	:	*
P38532	HSF1_MOUSE	398	LTSHGFS	VDTSALLDLFSPSVTPMDMSLPDL	DSSLA-SIQELLSPQEPFRPTIEAENSND	456
P38533	HSF2_MOUSE	377	LSGRQFS	IDPDLILDFTSSVQMNFTDN	IKYTKSENKGLEATKSSVVQHVSEEGRKSKSK	436
Q9R0L1	HSF4_MOUSE	382	LRAPETIE	LVFAFVDVLGSPSLHGREWTLMDL	DMELS-LMQFLAPETDEA-ELTVKEL-NS	438
			*	:	:	*
P38532	HSF1_MOUSE	457	SGKQLV	VHYTAQPLFLLDPAV---	DTGSS-----ELP-----VLFEFG---	502
P38533	HSF2_MOUSE	437	PDKQLI	QYTAFLPLAFLDGNSASAIE	QGSTTASSEVWPSVDKPIEVDLLDSSLDE---	493
Q9R0L1	HSF4_MOUSE	439	SGVGK	DHTLGTPLMLDVQADL---	EGAAI-----SVPGALTYLVNTEASNYLDPGASP	489
			*	:	:	*
P38532	HSF1_MOUSE	503	TDDPTI	SILLTGTEPHKAKDPTVS-----		525
P38533	HSF2_MOUSE	494	---PTQSK	LVRLPLTEAEASEATL	FYLCELAPAPLDSMPPLDS	535
Q9R0L1	HSF4_MOUSE	490	SSP	-----		490