

Figure S1

a)

		α1	β1	β2	α2		α3	β3	
HvHsfA1a	MEGGVALASS---VTTAVAPP-----GQGAG-----APP-----PFLMKTYDMVDDPATDAVSWG-PASNSFIVWNTPEFARDLLPKYFKH-----SNFSS---FVRQLNTYGFRRKVD								92
OsHsfA1a	MEAAVAAAAAAGAVTTAVAPP-----PGAAVSNG-----VATAPP-----PFLMKTYEMVDDPATDAVSWG-PGNNSFVWVNTPEFARDLLPKYFKH-----SNFSS---FVRQLNTYGFRRKVD								102
HvHsfA2a	-----MDPFH---GIVKEEEDFAGAAAADGYSPPSSWGSSPSSWGSSVWVGGA-----LAE LPRPMDGLGEAGTPFLNKTIEVVDHSDTIVSWG-VAGNSFVWVDAHAFSMVLLPRYFKH-----SNFSS---FVRQLNTYGFRRKVD								130
OsHsfA2a	-----MNPLR---VIVKEEELDFAAAAA-----GE-G-SPSSWAVG-----VMDLPRPMEGLGEAGPPFLCKTYEVVDDPGTDTIVSWG-FAGNSFVWVDAHAFSAVLLPRYFKH-----SNFSS---FVRQLNTYGFRRKVD								118
HvHsfA2b	-----MEDPVP---SLVKEEEE-----EG-----AHGR-----GGSPGVGA-----APRPMGLHDAAGPPFLTKTYDMVDDPNTDSVSWG-AGNSFVWVDPHFADATVLLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								108
OsHsfA2b	-----MDDPML---NAVKEEES-----HGDGGGLEV-VAGE-----DGAATAVAA-----GVAPRPMGLHDAAGPPFLTKTYDMVDDAGTDAVSWG-ATNSFVWVDPHFADATVLLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								117
HvHsfA2c	-----MDAAVP---DGIVKEEGLLLLHEERPPAAG-PPQR-----QRQEDGA-----LPRPMEGLHEAGPPFLTKTYDLVEDPATDGVSWG-RAGNSFVWVDPHFADALLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								120
OsHsfA2c	-----MDPAA---AGIVKEE---MLESQ-----QQ-----QRQEDGGA-----APRPMGLHEVGPFLTKTYDLVEDPATDGVSWG-RAGNSFVWVDPHFADALLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								107
HvHsfA2d	-----MEKMM---PGMVKEE-----WP-----PSSPEEGE-----APRPMGLHEVGPFLTKTFDLVADPATDGVSWG-RAGNSFVWVDPHFVAAVFLPRFFKHNNFSSFVRQLNTYFLVRTNLYLNKRSHFYSLRFQGFRRKID								17
OsHsfA2d	-----MEKMM---PGMVKEE-----WP-----PSSPEEGE-----APRPMGLHEVGPFLTKTFDLVADPATDGVSWG-RAGNSFVWVDPHFVAAVFLPRFFKHNNFSSFVRQLNTYFLVRTNLYLNKRSHFYSLRFQGFRRKID								122
HvHsfA2e	MGSAAAMSHRMM---NPVKVEGR-----PSP-----SPSP-----TAAAGGGG-----G-APRPMGLADAGTPFLAKTYDMVDDPTTDAVSWG-ATNSFVWVDPHFLGTVLLPRYFKH-----SNFSS---FVRQLNTYGFRRKVD								116
OsHsfA2e	-----MNYRVV---NPVKVESG---PS-----TGVANQG-----PPRPMGLADGGPPFLTKTYDMVDDPTTDAVSWG-ATNSFVWVDPHFLGNVLLPRYFKH-----SNFSS---FVRQLNTYGFRRKVD								103
HvHsfA2f	-----MDSAAMTMDIKQEPEMMVLD-----DD-----DDAGCCL-----APTPLDAAAANVAPFLAKTFDMVEDPATDAVSWG-AARNFVWVDPHFADATVLLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								112
OsHsfA2f	-----MDYS---TVKQEEVEVVLDG-----EE-----EAAAAAAP-----VPLPAAMGVAAVAPFLVKTIFEMVEDPATDAVSWGGAARNFVWVDPHFADATVLLPRHFKH-----SNFSS---FVRQLNTYGFRRKVD								109
HvHsfA4b	-----ME-----GGSSSLPFLTKTYEMVDEPATDAVVAWTPS-GTSEFVVSQADFCRDLPLKYFKH-----SNFSS---FVRQLNTYGFRRKVD								77
OsHsfA4b	-----ME-----GGSSSLPFLSKTYEMVDDPSTDAVVGWTPA-GTSEFVVAQPEFCRDLPLKYFKH-----SNFSS---FVRQLNTYGFRRKVD								77
HvHsfA4d	-----MEME-----GSSQGAAPFLTKTYEMVEDPATSRVSWGPG-GASEFVWVNPDPFSRDLPLKYFKH-----SNFSS---FVRQLNTYGFRRKVD								79
OsHsfA4d	-----MESS-----NL-----G-GGG-----GGGGGGPPFLTKTYEMVEDAATNHVSWGPG-GASEFVWVNPDPFSRDLPLKYFKH-----SNFSS---FVRQLNTYGFRRKVD								85
HvHsfA5	-----MEAS-----GA-----A-GA-----RGGGGGPPFLTKTYEMVDDPATDAVSWSDASDAFVWVNSPEFAARLLPAYFKH-----SNFSS---FVRQLNTYGFRRKVD								85
OsHsfA5	-----MEVA-----AG-----ARGGG-----AGGGGGPPAPFLTKTYEMVDDPSTDAVSWSDASDAFVWVNSPEFAARLLPAYFKH-----SNFSS---FVRQLNTYGFRRKVD								87
HvHsfA9	-----SARGAP-----VG-----AVPKPPVAPFLTKVYDMVSDAATDRVSWG-DAGNSFVWVDAHAFERDILLRHHFKH-----SNFSS---FVRQLNTYGFRRKVD								83
OsHsfA9	MGSKRS PQH-----PAAAAAPP-----PAVGGGGGVEVSGDGGASTANGPVVPKPSEVAPFLTKVYDMVSDPATDNIWSA-EGGGSFVWVDSHAFERDILLRHHFKH-----SNFTS---FVRQLNTYGFRRKVD								114

DBD

	β4	HR-A-Core	Insert	HR B	NLS		
HvHsfA1a	PDKWEFANEGFLRGQKHLKTIKRRKFLH-----ANNQVQVQQQHQQQHQQQPQLQNAIPSCVEVGK-FG-MEEIEIMLKRDKNVLMQELVRLRQQQQTTHDQLQTLGKRLHGMEQRQQMMMSFLAKAMQSPGFLAQFVQQNENS				K--RR----	IVAANKK	242
OsHsfA1a	PDRWEFANEGFLRGQKHLKTIKRRKFLH-----GNNQVQ-----QPQLPAAPVPACVEVGK-FG-MEEIEIMLKRDKNVLMQELVRLRQQQQTTHDQLQTLGKRLQGMEQRQQMMMSFLAKAMHSPGFLAQFVQQNENS				R--RR----	IVASNKK	240
HvHsfA2a	PDRWEFAAEGFLRGQKELLKTIKRRRFLH-----QSSGTFG-----QQQQQGGG---VCLEVGH-FG-HDGEVQQLKRDKGTLIAEVVKLRQQEQATRVQMQAMEARLAATEQKQQQMTVFLARAMKSPSFLQMLVERQD				Q--SR	RKELADALLS-KKR	269
OsHsfA2a	PDRWEFANEGFLRGKELKTIKRRRFPSSPSSSSSSSSSS-----HQQQQFAA---ACLEVGQ-FG-RDGVNRLQRDKSVLIAEVVKLRQQEQATRAQMAMEERISAAEQKQQQMTVFLARAMKSPGFLQMLVDRQAGHGA					RNRVLEDALS-KKR	267
HvHsfA2b	PDRWEFANEGFLRGQRHLLKTIKRRKFLH-----PAHTA-----SNQQ-SLG---SYLEVGH-FG-NDAEIDRLKRDQQLLMAEVVKLRQQEQNTKAHLKAMEDRLRGTEQKQQQMTSFMARVLRNPEFLKQLISRNG					MRKELHEAIS-KKR	241
OsHsfA2b	PDRWEFANENFLRGQRHLLKTIKRRKFLH-----PSHTA-----SNQQ-SLG---PYLEVGH-FG-YDAEIDRLKRDQQLLMAEVVKLRQQEQNTKANLKAMEDRLRGTEQKQQQMMMAFLARVMKNPEFLKQLMSQNE					MRKELQDAIS-KKR	250
HvHsfA2c	PDRWEFANEGFLRGQRHLLKTIKRRKFLH-----PSNAP-----PSQQQALT---SCLEVGE-FG-FEEEIDRLKRDKNLLITEVVKLRQQEQATKDNVQAMENRQAEEKQQAQMMGFLARAMRNPFLFQQLVQR				QD----	KRKELEDAIS-KKR	254
OsHsfA2c	PDRWEFANEGFLRGQRHLLKTIKRRKFLH-----PSNAP-----PSQQQSLT---SCLEVGE-FG-FEEEIDRLKRDKNLLITEVVKLRQQEQATKDHVKMAEDRLRAAEQKQVQMMGFLARAMRNPFEFQQLAQ				KE----	KRKELEDAIS-KKR	241
HvHsfA2d	PDRWEFANEGFIRGQRLLKTIKRRRFLH-----LSYLP-----SSQQQALG---SCLEVGQ-FG-FDDEIEVLKRDKNALLSEVVKLRQQEQSTRADMRAMEERLHRAEQKQLQMMGFLARAIQNPDFFLQLVQQD					KLKLEDLPPY-TRK	151
OsHsfA2d	PDRWEFANDGFLRGQRHLLKTIKRRRFLH-----LSYLP-----GSQQ-ALG---TCLEVGQ-FG-LDEEIDRLKRDKNLLIAEVVKLRHQQQSTRKANRAMEERLQHAEQKQVQMMGFLARAMQNPDFFHQLIHQQD					KMKGLEDTFS-KKR	255
HvHsfA2e	PDRWEFANEGFLRGQRHLLKTIKRRKFLH-----T-HGS-----QNQQ-SLG---SYLEVGN-FG-HDVEIDQLKRDQQLLMAEVVKLRQQEQNTRSDLQAMEKRLQGTQKQQQMMMSFLARVMQNPFLIRQLISQSE					MRKELEDAIS-NKR	248
OsHsfA2e	PDKWEFANEGFLRGQKHLKSIKRRKFLH-----P-NSS-----PSQQ-SLG---SFLEVGH-FG-YEGEIDQLKRDKHLMAEVVKLRQQEQNTRSDLQAMEKRLQGTQKQQQHMMAFLSRVMNPEFIRQLFSQSE					MRKELEEFVS-KKR	235
HvHsfA2f	PDRWEFANAGFLGGQRHLLKTIKRRRFLH-----GADTG-----RRPAAALSPPSCAEGAGGFGSVEGELERLRQREALKRELQAGLRQQVEARATLLDMERRVDTERRQEQCKAFLARAVRNPAFLANLARRND					LAAPAPAVDGGKK	251
OsHsfA2f	ADRWEFANEDFLGGQRHLLKTIKRRRFLH-----GAGTG-----STTPRNVN---CGGGG-----EGEVERLRDKKALRELARLRRQQEQEARQLDMERRVDTERRQEQCTEFLARALRSPDVLNRIARRH					AAA--VE--RK	232
HvHsfA4b	PERWEFANEDEFIRGQRHLLKTIKRRKFLH-----IFSHS-----SHT-QGAGPLADSERRD---YEEIEIERLKCNASLNQLER---KKTDMDSMKKALEDKLLAIEDQQRNLSISYVEIVKAPG					FLSS-----FIEQSDHHGKK	199
OsHsfA4b	PERWEFANEDEFIRGQRHLLKTIKRRKFLH-----IFSHS-----SHS-QGAGPLADNERKD---YEEIEIERLKSNAALSSELQNNITLKKLNMEKRMQALEEKLQVVEDQQRSLISYVREIVKAPG					FLSS-----FVQQDHHHKK	202
HvHsfA4d	PERWEFANDDFIRGHMHLKTIKRRKFLH-----VHSHS-----LQN-QVNGPLAESERRE---YEDEISRLKHENSLVAELQKQAHQCCGIGWLMQSLDRLMVMQRQT					DVSSVRDILQRRRGAHHPGQTM-----LELEPTDRFSKK	211
OsHsfA4d	PERWEFANEDEFIRGHTHLLKTIKRRKFLH-----VHSHS-----LQN-QINGPLAESERRE---LEEEINRLKYEKSLVADLQRNQQQQVINWQMQAMEGRVLAEMEQRQKNIVASLCEMLQRRGGAVSS					-----LLESDFHSKK	211
HvHsfA5	PERWEFEGNEYFVIRGQRHLLKTIKRRKFLH-----IHSHS-----HQ-----PAAQSDNERSF---FEDEIDRLAREKANLQAEWKPKQEQEPGTMQIEALEARRAVDMEQRQKMI AFLQQAASKNPHFVSKLVKMAE					-----ASSMFADALHKK	214
OsHsfA5	PERWEFANEYFIRGQRHLLKTIKRRKFLH-----IHSHS-----HP-----PGALPDNERAI---FEDEIERLSREKSNLQADLWKSQQQSGTMNIQIEDLERRVLGMEQRQT					KMIAFLQQAASKNPHFVSKLVKMAE-----ASSIFDPAFNKK	216
HvHsfA9	PERWEFANEFLRGQRHLLKTIKRRKFLH-----QEASRE-----LEKAPVKASPGTENIEIGR-YGGLVKEVETLRDKKALLMQQLVDLRHYQQSNDMSKLIQRLQLMEQNKQMMALLAIVVQNPSSLNQLVQQQQQ					QD---RRNSWR-YEDGNKK	227
OsHsfA9	PDRWEFANEFGIMQKHLKTIKRRKFLH-----QESPSE-----IQKAPVKTAPGTENIEIGK-YGGLKEVETLRDKKALLMQQLVDLRHYQQTNSLEVQNIERLQVMEQNKQMMALLAIVVQNPSPFLNQLVQQQQQ					QD---RRSNW-SPDGSKK	258

HvHsfA1a	<b>RRLPK</b> QDDG--LN-----PESALLDGGIKYQPMINEAAKAMLRKILQDDTSPHRFESMGNSDNLLLENMPSAQTFDSSSSTRNSA-----VTLAEVPGNS-----GMPYMTSSGL-----SAICSSSSPPEMQCPVLD-----	362
OsHsfA1a	<b>RRLPK</b> QDGS--LD-----SESASLDGQIVKYQPMINEAAKAMLRKILKLDSS-HRFESMGNSDNFLENYMPNGQLDSSSSTRNSG-----VTLAEVPANS-----GLPYVATSSGL-----SAICSTSTP-QIQCPVLD-----	358
HvHsfA2a	<b>GRPIEYLLPR</b> -NG-----ETCYS-AAAQYGHGL-----VD-----GGEGRRADGED <b>ESFWK</b> -----	315
OsHsfA2a	<b>RRPIEYLLPR</b> -NG-----ETCAAGESAAMLAADGV-----AEPDG-----DT-----TPRGDGGGGGGDT <b>ESFWM</b> -----	322
HvHsfA2b	<b>RRRIDGQPE</b> --AY-----DVGAS-SSSLEQESPVV-----FDSHGSVELLADVSPVELLADGIPPLEGVS-----ELLADGIPPLEGVSALLADGIPPLEGVS-----ELLVDG-IPSDLGGSGIDA-----	348
OsHsfA2b	<b>RRRIDQGPE</b> --VD-----DVGTS-SS-IEQESPAL-----FDPQ-----E-----SV-----EFLIDG-IPSDLENSAMDA-----	301
HvHsfA2c	<b>RRPIDNVFFY</b> -GS-----GVVTS-QS-EQLDSQFL-----FDSG-----VL-----SDPCTRLENLAQNI-----	302
OsHsfA2c	<b>RRPIDNVFFY</b> -DP-----GE-TS-QT-EQLESPYL-----FDSG-----VL-----NEL-SEPGIPELENLAVNI-----	291
HvHsfA2d	<b>RRSINVMPFL</b> -GP-----EG-TS-QS-EQLESTFI-----FEDR-----EF-----SELENLAMNI-----	193
OsHsfA2d	<b>TRSIDIVPFL</b> -NP-----GE-VS-QG-DQLESTLL-----FDPR-----AELNDEPAKSELENLALNI-----	306
HvHsfA2e	<b>RRRIDQGPEA</b> -VD-----SMGTG-ST-LEQGSVHM-----FEQQ-----E-----PV-----DSFVNG-VISDLESSSVDT-----	300
OsHsfA2e	<b>RRRIDQGPE</b> --LD-----SMGTG-SS-PEQVSQVM-----FEPH-----D-----PV-----DSLFGV-VPSDLESSSVEA-----	286
HvHsfA2f	<b>RRRLDAIPSLPA</b> -----EDGFTFEE-LALAAGVV-----EEA-----AAPTQGSAGGVTT <b>DMIWY</b> -----	302
OsHsfA2f	<b>RRRMLAAAAD</b> -----DDGLTFEA-LALAA-----AADTSHSTGGAVTT <b>DMIWY</b> -----	274
HvHsfA4b	<b>RRLPKISIFHEGAS</b> -----TQGNQIMHCDLANSPAHKLYR-----ESFDKMESLNSLENFFKEAT-EALGNDISYDGDVPR---HSSAVVLTLELHSSGESDPHAQSPSPMMHTCSAGVGDSSHS-----SRDIAESASC-PESPPLPEAHSRADSRAK	337
OsHsfA4b	<b>RRLPISIFHEDAN</b> -----TQENQIMPCDLTNSPAQTFYR-----ESFDKMESLNSLENFLREAS-EFEGNDISYDDGVFG---PSSTVVLTLELHSPGESDPRVSSPPTMRTSSAGAGDSSHS-----SRDVAESTSC-AESPPIQMHRSRVDTRAK	340
HvHsfA4d	<b>RRVVK</b> IDLDFVE-----EQRVYYPRAIGDETPGMIQVN-----AEPFKMEMALVSLKLVQRA---AAATPTPSTDDPALG-----DLQAAPMEAGVNLEL-----SPPNIRHVHSPP---ELAVAESPGYAVQSPMLLFPDIQQDKHKT	335
OsHsfA4d	<b>RRVVK</b> MDLFDVDDCAAG--EEQKVQFQIGTDPAMPFVLP-----VTNGEAFDRVELSLVLEKLFQRAN-DACTAAEEMYSHGHHGTEPSTAICPEEMNTAPMETGIDLQLPASLHPSSPNTGNAHLHL---STELTESPGF-VQSPPELMAEIREDIHVT	362
HvHsfA5	<b>RRLSGLDYAVEATETASFCDDHSATSROEMGNLLNQHFSDK</b> -----LKLGLCPAETESNLITLSTQSSHEDNCSLHGRHPHGHGDMGTGCLPLVPQMMELSDTGTISICPSKSSFFRPVAVNDEGLSPCHLSLTLASCMSMDVDRGQASNADGSTTVN--KGSNDNPLE	372
OsHsfA5	<b>RRLPGLDYSIENTETTSFYDDHSSTSKQETGNLLNQHFSDK</b> -----LRLGLCPAMTESNIITLSTQSSNEDNRSFHGKHP-ECDDMMGRECLPLVPQMMELSDTGTISICPSKSSCFAPPISDEGLLTLCHLSLTLASCMSMDVDRGQASNADGSTTVN--KGSNDNPLE	375
HvHsfA9	<b>RRFPALQGPVTD</b> -----QETSGAGAEIIQYRPPV-----P-----ETS-----S-----Q-----VIADE-----AYLSATAE-PISSPPLN-----	284
OsHsfA9	<b>RRFHALEQGPVTD</b> -----QETSGRGAHIVEYLPPV-----P-----ETS-----G-----Q-----VNFVEG-----AICSANSQ-PVPSPAVA-----	316

AHA-motif

HvHsfA1a	-----SNSSTQLPNMSAVPSVPKA---MTPGLSD---ISIPGFPDLHDLITEDAINIPVENYAMPGPCIFPLPEGSDSVPMDDIDTDEIDDTQKLPGII <b>DSFWEQFLCAS</b> PLSVNDNEVDSGLLDTREAEQENGWTRTENLAN <b>LTEQMGLL</b> SSNHRG	510
OsHsfA1a	-----NGIPKEVPNMSAVPSVPKA---VAPGPTD---INILEFPDLQDVAEENVDIPGGGFEMPGEVFSLPPEEGDSDVPIETDEILYNDTQKLPAAII <b>DSFWEQFLVA</b> SPLSVNDNEVDSGLVDQKETQQNGWTKAENMAN <b>LTEQMGLL</b> SSHHTG	506
HvHsfA2a	----- <b>ELLSL</b> GLEER---QREA---GGGGGGE---AS---GAEVD---DDVD---DEMDE <b>LVQSLYHL</b> SPNRPHGHHHQ	371
OsHsfA2a	----- <b>QLLSL</b> GLEEK---QRED---GVAGGVQ---ESNSGGADVND---E---EDDD---DDVDV <b>LVQSIYHL</b> SPK	376
HvHsfA2b	-----NGV-TEPQDFGLGTCEPQQ---NRVP-GL---FR <b>DSFWEELLNK</b> GLS---DESD---EPVNVDDMDV <b>LSEKMGYL</b> IPNSPTQTT	418
OsHsfA2b	-----GGL-VEPQDFDVGASEQQQ---IGPQ-GE---LN <b>DNFWEELLNE</b> GLVG---EEND---NPVVEDDMNV <b>LSEKMGYL</b> NSNGPTAGE	372
HvHsfA2c	-----QDLGQKGTDE---GKKD---EANGQVE---LN <b>NEFWAELFSD</b> DFGD---GDGSLSE---LEGRRPEDIDE <b>LAQQLGYL</b> SSSTSPL	372
OsHsfA2c	-----QDLGKGVDE---ERQN---QTNGQAE---LG <b>DDFWAELLVE</b> FTG---KEEQ---SE---LDG-KIDGIDE <b>LAQQLGYL</b> SSTSPK	358
HvHsfA2d	-----QGIRKGMEDD---KGGRS---QCGEAE---LT <b>DDFWAELLSE</b> GMRD---EAEM---LE---LERRRSRYVDA	248
OsHsfA2d	-----QGLGKQDVNRTRNQPRN---QASNETE---LT <b>DDFWAELLNE</b> GARD---DAGI---PG---MERRRPRYVDA <b>LAQKLGYL</b> SNSSQK	379
HvHsfA2e	-----KGA-EVQQSVASSRSEQLR---GRPS-GE---LN <b>DDFWEDLLHE</b> GGLG---EEAS---PG---NLVVPDDMN <b>LLAQEMH</b>	360
OsHsfA2e	-----NGG-KAQQDVASSSSEHGK---IKPSNGE---LN <b>EDFWEDLLHE</b> GGLD---EDTR---NPAI---DDMN <b>LLSKMGYL</b> NSSSTKSPQ	357
HvHsfA2f	----- <b>ELLEGG</b> QAEID---VEVED---LVAAAG---DMAP---WE---FGEE---EDPDDGVCRDARRGRE	350
OsHsfA2f	----- <b>ELIGEE</b> QAEID---IEVDQ---LVASASA---AADT-ASEAEP---WE---EMGE---EEVQE <b>LVQQIDCL</b> ASPSS	331
HvHsfA4b	-----VSDIDVNLEPAVTEGSPSRDQQTQDPPAD---AN <b>DGFWQFLTE</b> QPGS---SDTHQEAQERRD---REANQTVTRDRGSFWWG-KSVEQMT <b>EKLGLI</b> TSAEKT	432
OsHsfA4b	-----VSEIDVNSEPAVTEGSPSRDQ-PAEPPAVTPG---AN <b>DGFWQFLTE</b> QPGS---SDAHQEAQERRDG---GNKVDEMRSGRQHLWWGKRNVQIT <b>EKLGLI</b> TSAEKT	440
HvHsfA4d	-----MSEADLSSEAS---TTDTSQDETTAETGVPREPAVAAN <b>DLFWERFLV</b> TPKP---CCGYAFQESHESK---DDVKIGIDCNWYGHDRNDVQIT <b>QMGHL</b> ASAQKT	431
OsHsfA4d	RY---PTQADVNSEIAS-STDTSQD-GTSETEASHGP---TN <b>DFWVERFLTE</b> TPR---SCLDESEQRQESPK---DDVKAEKGCNGFHHREKVDQIT <b>QMGHL</b> ASAEQTLHT	459
HvHsfA5	AD---AAAMGNSQKASVDAG-TDATTTPREDTRVATEPAAP---VKAN <b>DNFWQFLTE</b> RPG---DASSGPRDP---S---MDKQTEGREKDDREA <b>TEQLKL</b>	457
OsHsfA5	KDDTIDRSFDDNQKKSADSRADATTPRADARVASEAPAAPAAVVD <b>DKFWQFLTE</b> RPGC---SETEEASSGLRTPD---TSREQMENRQAYDHSRNDRED <b>VEQLKL</b>	475
HvHsfA9	-----MPMDIDTETTSNDL-----NTQSSG---DIFADMPALPDFD---M---Q---LWFG---DGEL---TLTIQD-----Y <b>DESPQEQD</b> CQMEAQHNHNPNQYASR	363
OsHsfA9	-----TPMDMQTSNVAD-----TLGSSE---EPFADNSTLHEWDDND---M---Q---LLFDDN---LDPILPPFENDG <b>QMGF</b> ---PLSVQD-----Y <b>D-FPQLBQD</b> CLMEAQYNSNPNQYADVITEA	410

b)

		α1	β1	β2	α2	α3	β3	
HvHs fB1	--VIIK RAGMAGAAAAAQQQKGGGGV-----V-----MKGG--GGG	PAPFLTKTQMV	EERGTDEVISWGEH	GRS	FVWVWRP	VELARDLLPLHF	KCNFSS	SFVRLNTYGF
OsHs fB1	-----MAAAEAAAAVGKQQKGGGG-----RGGG--GGG	PAPFLTKTNQMV	EESATDEVISWGEH	GRS	FVWVWRP	VELARDLLPLHF	KCNFSS	SFVRLNTYGF
HvHs fB2a	-----MASPAL---GAG-----	TPPFLTKTYAM	VDDPETDDTISWNES	GTAFV	VWRRAE	FERDILLPKNF	KHSNFS	ASFVRLNTYGF
OsHs fB2a	-----MASPA---AG-----	TPPFLTKTYAM	VDDPETDDTISWNDS	GTAFV	VWRRAE	FERDILLPKNF	KHSNFS	SFVRLNTYGF
HvHs fB2b	-----MVSSGQICTVV---GGGG--VMGEQAAPVSCGETPAQAEVGTGVGQ---RSI	PTPFLNKTYQLV	DDPAVDDVISWSED	GS	AFVWVWRP	AEFARDLLPKY	FKHNNF	SFVRLNTYGF
OsHs fB2b	-----MADQTAATAVVV---GGGAAATMGEPSPPPPA-PAAEAAGVGVGQQQ---RT	PTPFLTKTYQLV	DDPAVDDVISWNDD	GS	TFVWVWRP	AEFARDLLPKY	FKHNNF	SFVRLNTYGF
HvHs fB2c	-----MAAEHGAAAAAV---DGAG-----AEP PPPAPMPGLAATAADAAGQ---RSI	PTPFLTKTYQLV	DDPAVDDVISWGED	GS	TFVWVWRP	AEFARDLLPKY	FKHNNF	SFVRLNTYGF
OsHs fB2c	-----MAEQGAGEADA---GGG-----EPPPAAVMT--AAAEALAGQ---RSI	PTPFLTKTYQLV	DDPAVDDVISWNED	GS	TFVWVWRP	AEFARDLLPKY	FKHNNF	SFVRLNTYGF
HvHs fB4b	MAFLVERCGEMVVSMEGSGAHGGGG-----GGGGGVGKVP	PAPFLTKTYQLV	DDPCTDHVSWGED	DATFV	VWRPE	EFARDLLPNY	FKHNNF	SFVRLNTYGF
OsHs fB4b	MAFLVERCGEMVVSMEGMP--HGGGG-----AAAG--KVP	PAPFLTKTYQLV	DDPCTDHVSWGED	DTFV	VWRPE	EFARDLLPNY	FKHNNF	SFVRLNTYGF
HvHs fB4c	---MERC GSWSES DAAAQ-----AAAQ---KAV	PAPFLTKTYQLV	DDPATDHVSWGDDRV	STFV	VWRPE	EFARDLLPNY	FKHNNF	SFVRLNTYGF
OsHs fB4c	---MERC GSWSDCEAAA-----AAAQ---KAV	PAPFLTKTYQLV	DDPATDHVSWGDDRV	STFV	VWRPE	EFARDLLPNY	FKHNNF	SFVRLNTYGF

	β4							
HvHs fB1	WEFANENFRRGEQSLLSGTRRRRATT-----TTTTQSSKTCGTAVN-----VAFP-----PP---LPALPP-----ASASTSGTNDLSSS-----							173
OsHs fB1	WEFANGNFRRGEQLLSGIRRRRATT-----PQSSKSCGSGVN-----VAFP-----PP---LPPLPP-----EPSATTSSGNDRSSS-----							163
HvHs fB2a	WEFANECFRKGEKQLLGAIQRRRSGS-----AGAPAPAMMATPIA-----TAIPISP---TP--TSSGGDP-----AVSSSPPLGLALVAT-----							151
OsHs fB2a	WEFANDCFRRGEKHLGGIQRRRGSG-----TGG-AGAAPAGGIP-----TAPISS---PP--TSSGGEF-----AVSSSPPRGAAGIAAGV-----							150
HvHs fB2b	WEFANDCFRRGEKRLLCDIHRRRVTPV-----AATAAVTVAAAAAIP-----VALPVTK-RQGSF--VLSGDEQ-----VLSSSSSPEPFLNQYAPSY----							197
OsHs fB2b	WEFANDCFRRGERLLCEIHRRRVTP-----PAPAATTAAVAAAIIP-----MALPVTTRDGSF--VLSGEEQ-----VISSSSSPEPPLVLPQAPSG----							197
HvHs fB2c	WEFANDCFRRGEKRLLCDIHRRRVQSA-----GLAAAAAAAAGAVTVAAAAAIP-----MALPVTTR--SGSELPQLSSEEQ-----VLSSNSGSAAELPLAPSGSGGSAP							205
OsHs fB2c	WEFANDCFRRGEKRLLCDIHRRRVAAAAAAPPSPGMATAAAAVASGAVTVAAAIIP-----MALPVTTR--AGSF--AHSSEEQ-----VLSSNSGSAGEHRQA-SGSG-SAP							205
HvHs fB4b	WEFANEFFRKGAKHLLAEIHRRRSS-----QPPPPSMVPHQAAAYH-----HHYHLG--NTFSQPQ---PPAAAAHHQHHP-----VYQQHFVQEEPAAAAA-----							192
OsHs fB4b	WEFANEFFRKGAKHLLAEIHRRRSS-----QPPPP-PMHPQ--Y-----HHHHHL--NPSLPP---PPP---AYHHHH-----LIQEEPATTAHCTVAGD-----							178
HvHs fB4c	WEFANEFFRKGKQLLCEIHRRRVTSGST-----T-SS-SPPFFAPPHFPLFH-PGVSVAHHHQQFVGEDGAMAAHAG-MGVPFMQPHWREQ---GAPRLLALGGPAAPSPGVE-----							196
OsHs fB4c	WEFANEFFRKGKQLLCEIHRRRVTSAS-----T-ASPSPPFFAPPHFPLFHHFVGVAAQHHHAFVGDGVAAGH--IGMFPFPQPHWREPNLVAATRLALGGPAAPSPSSAEAG-----							201

	HR-A-Core	Insert	HR-B											
HvHs fB1	---SASSPTRPDLSSENEQLRKDNHALAAELAMARRHCEE	LLGFLSRFL	DVRQL	---DLR-----				LLMDEDMQG-----AAGGARG	244					
OsHs fB1	---SASSPPRADITSENEQLRKDNQTLTLMELARARRHCEE	LLGFLSRFL	DVRQL	---DLR-----				LLMQEDMRA-----AAGGVGGE	234					
HvHs fB2a	---GAMA---LLEENARLRRENARLARELARARRVCDGVRHLVWRYD	QGGEE	---VGVED-----	ER-----				HGAAGGKP-----MLFGVAIGS	222					
OsHs fB2a	---SGAVA---ELEENARLRRENARLARELARARRVCDGVRRLVSRDYH	---D---	HGGGE	---EE-----				AGEGDVKP-----MLFGVAIGG	219					
HvHs fB2b	---SGSGGVASG-DLGEENLRRENSRLTRELGMKKLNNIFVLMISKY	TDGQV	---DAANATSAATDADAGHCSGESAE	T-MPLP--	PPVLELLP	SCPSAPT	---AADLGADEEEKMSA	RLFGVICIGR	317					
OsHs fB2b	---SGSGGVASG-DVGDENERLRRENAQLARELSMRKLCNNILLMSKYA	STQQL	---DAANASSAAGNNNNNCSGESAE	AATPLP--	LPVLDLMP	SCPGAAS	---AAPVSDNEEGMMSA	KLFGVSIGR	318					
HvHs fB2c	GGAAAGSSSG-DMGEENRLRRDNARLTRELGMKKLNNIFVLSMFKF	ASSQQ	---DGGPGS---	LSSVNC	SGES--	ALAPPPLPAAILDLMP	SCSALAT	---AAGFAVDGGPDADA	RLFGVSIGL	322				
OsHs fB2c	GGGGGSASGGDMGEENERLRRENARLTRELGHMKKLNNILLMSKYA	ATQHV	---EGSAG---	ISSIANCS	GESSEAVPPPPPLP	PAILDMP	SCPALATAAAAAGLAIDGEP	DPISA	RLFGVSIGL	327				
HvHs fB4b	---ASHGGDFLAALSEDNRQLRRRNSVLLSELAHMKKLYNDI	IYFQNHV	VPVTS	---PSSAASQR-----	QHPLPGA	-----GASNSCR	LLELDMDVDRGSP	-----AAEDDD	286					
OsHs fB4b	---GGEGGDFLAALSEDNRQLRRRNSLLSELAHMKKLYNDI	IYFQNHV	VPVTTTTTTPS	STAMAA	-----AQHHL	PLP-----	AAASCR	LMELSDPDHS	PPPPP	PKTPATDGG	278			
HvHs fB4c	---GNGRATSAAVLMDENERLRRNSNTALLQELSHMRKLYNDI	IYFQNHV	RPVAP	---SPAAATFLQG-----	LGNMQP	RKMP	PATTGAGN	LNTSGS	TSSSS	LTIADELS	PPPN	HLSAEKSSG	312	
OsHs fB4c	---GAGRAATAAVLMEENERLRRNSNTALLQELAHMRKLYNDI	IYFQNHV	RPVAP	---SPAAAAFLQG-----	LG--MQA	RKKF	---AAANV	LNSG	STSS	SLTIAE	EPSP	PPQQL	LAGEKSSG	313

	NLS	NES	
HvHsfB1	SADQEQCCEKK-----VKLFGVILKD---ASARKRGR-----CDEAAAGERSVKMTR---IGEP-----WVGVPSW-----PAR-----CGGN		308
OsHsfB1	QRVQEHAREEK-----VKLFGVLLDDTHGAATKKRAR-----CEEAASERPIKMIR---IGEP-----WVSVPSG-----PAR-----CGGN		302
HvHsfB2a	KRSREDG--HEG-----GDEENGAEDGEDDEEEQE-----HNDDDERHAARRE---QGKSMR-TERSDLNVLSSLVRAAAAAAR-----PDGGSRLA		299
OsHsfB2a	KRSRENGEDEE-----EEEEEGAEDGEDDEVEE-----DDEERERHAARRVPRREGKVRRTTELSDDLVLALSVRAAAAAAR-----PGGASRDRKSSVS		305
HvHsfB2b	KRMRHDGEDQSSR-----GAAEVKP-EPMDAQPSLDG-----HTTEVQTPWIYRPRP--AYHPLR--ASNGSNCSYSGS----DDH-----NGSSSR		390
OsHsfB2b	KRMRHDGGGDDD-----HAATVKA-EPMDGRPHGKDE-----QSAETQAWPIYRPRP--VYQPIR--ACNGEYDRAG-----SDQ-----DGSNST		390
HvHsfB2c	KRARDEEDEDVREE--RPNGDGDADVKEEAADRRPDGG-----SEERQSWPIYRPKP--VYR-----ACNGQDGAGAG-AGSGSDQ-----DRNSR		402
OsHsfB2c	KRTRDDAAAAAEDDGGGEDQAEHGGADVKE-EEADPHPAGGGGSSTEASPEHPWPYRPTP--MYHAVR-PTCNGPDRAGSDQDGSSSSQTMGPGFEFDDLQKMMVVQQSNFVMHWGRSECGSGVRGFGW		454
HvHsfB4b	DT-----VKLFGVALHH---GKKKRAHG-----DD-----AVADHLGSEV		316
OsHsfB4b	DT-----VKLFGVSLH---GRKKRAHR-----DD-----DGVHDQGSEV		310
HvHsfB4c	EAGSSAALS-AP-----TKLFGVHLSAAPVGAGSKRPPSP-----EELPSTPPATKAR---L--V---LESDDLSSLVAPP-----AQFCAASSPARS		388
OsHsfB4c	EAGNSAARSAP-----TKLFGVHLSAAPCGAGSKRASSP-----EE-HPPTSPATKPR---L--V---LECDLSSLTVAPSSSQ-----QQLSAASSPTSTS		394

c)

	α1	β1	β2	α2	α3	β3	β4	
HvHsfC1a	-MDSLHTEALGLIGCGHGD--FC	TAPFVAKTYQMVCDPRTDALVRW	GKGNNSFLVPD	VAGFSQLLLPCFFKHG	NFSSFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQTHLLPRIVRKKRGEAG	121
OsHsfC1a	-MDGLHTEALGLIGCCGGDQQQ	TAPFVAKTYQMVCDPRTDALVRW	GRDNNSFVVVDP	AASFQQLLLPCFFKHG	NFSSFVRQLNTYVSI	IQSPAPGFRKVPDRWEFAHES	FRLRGQTHLLPRIVRKKRGEAG	132
HvHsfC1b	-MGSECKGHQHQ--DDGG-----	VAPFVAKTFHMSDPATDAVVCW	GGASNTFLVLDPA	AASFDYLLPSYFKHRNF	ASFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQAKLLPLIVRKKRAGAG	115
OsHsfC1b	MMGGECKVHQLQAAGDGGPG--	VAPFVAKTFHMSDPSTNAVVRW	GGAGNTFLVLDPA	AASFDYLLPSYFKHRNF	ASFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQAQLLPRIVRKKKGGAA	121
HvHsfC2a	----MSSAGG-----GM-----	VAPFVAKTYDMVDDPATDSVVAW	GPASNSFVVADP	FAFSEMLLPAHFKHANF	SFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQTHLLPRIVR--RQSGG	106
OsHsfC2a	----MTTTAEG-----GGG-----	VAPFVAKTYRMVDDPATDGVIAW	GRDSNSFVVADP	FAFSQTLPAHFKHSNF	SFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQTHLLRRIVRR--SSGG	108
HvHsfC2b	----MAAAASV-----GGG-----	AAPFVWKTYRMVDDPGTDGVI	GWKGNNSFVVADP	FSQTLPAHFKHNNF	SFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQTHLLRNIIVRR--AVAGG	111
OsHsfC2b	----MAAAG-----GG-----	AAPFVWKTYRMVDDPGTDGVI	GWKGNNSFVVADP	FSQTLPAHFKHNNF	SFVRQLNTY-----	GFRKVPDRWEFAHES	FRLRGQTHLLRNIIVRR--AAAGG	108

	HR-A-Core	Insert	HR-B	
HvHsfC1a	VG---ASCSSAVG-GAEQHQHVVANMGDEVEEEEEEE-----ESEALLEEVQRLRKEQTAIGEQLARMSRRLQATERRPDLMSFLARLAE		DPSATSLHLFEQAAEKQRMQFPSRDFTSPLIALPL	240
OsHsfC1a	GGGGGASCSFGGGAGEHQVAAAAASVMSGEEEDAED-----VLAKEAALFEVQRLRHEQTAIGEELARMSRRLQATERRPDLMSFLAKLAD		DPNAVTHGLLEQAAERKRRQHLS--HE--PTVCPL	255
HvHsfC1b	AA-----REVCEEEEE-----G-----VRGTIEAVQRLRDERRGMEEELQAMDRRLRAAENRPGQMMAFGLKLADDPGVVLRAMVAKKEE		-----LAAAG	196
OsHsfC1b	PG-----RELCEEGEE-----C-----RELCEEGEE-----VRGTIEAVQRLRREEQGMEEELQAMDQRLRAAERSRPGQMMAFGLKLADDPGVVLRAMVAKKEE		-----LAAAG	201
HvHsfC2a	AR-----RPSKDDHAEDS-----SSAMLAMEVMRLKQEQRATEERVAAMWRRVQDAERRPKMLAFLKVVGD		P-DVLRRLMGSSS-----DAGLF	189
OsHsfC2a	GG-----AKRKEEAGCGGGGEEAAGDVDEESAVVALEVARLRREQREIEGRVAMWRRVQETERRPKMLAFLKVVGD		P-QVLRRLVDRDNT-----NAAAS	201
HvHsfC2b	GG-----KRKDAAADLTG-----DMTMTVATEVVRVLRKEQSTIDDRVAMWRRVQETERRPKMLAFLKVVGD		P-DTLQRLVANSN-----AASGD	194
OsHsfC2b	GGGG-----GGGKRRDASADGGGG-----GDEDMTMTVATEVVRVLRKEQRTIDDRVAMWRRVQETERRPKMLAFLKVVGD		P-DKLHRLVGGGGNGNAA-----TAAAD	205

HvHsfC1a	Q---PAPSP---PPP-PLLALG-----DAAMGGVVRW-QWAEP-----IPLK-----LTTFEQPSASS---GVQQVPEFE		294
OsHsfC1a	P---PAPP---QPPQPLLALG-----AAAMDGTYYW-TTEHHHHHHQMKPMT-VLPSLEPPTASC---GVHQVPELGGGGVGLT		348
HvHsfC1b	A---GGMDP---RPD-KRRRIGA-----EAEEA---AQR-----AVPFPFS---NAGHVY		235
OsHsfC1b	N---NGSD---PC-KRRRIGA-----DTGRGGVATG-GDAEM---AQR-----TVPFPFS---VLGVVY		250
HvHsfC2a	P---GDGAEF---KRPRLLDG-----EVHVGMKMRVDG-----DGLMYGDRDQDVVREPGADFAGFYTGDDGFS--DVPVDDPP		266
OsHsfC2a	N---ADDSAVHHQVPRPRLLDSSSTTTTHGDRHLVTAADGFYAGGCGPEAAAAAFAVPPDAVDFTGLYTGDDGFG--NAVVDAGVDY		298
HvHsfC2b	Q---EPVEG---GEKRARLLDG-----DFGNVSAFGP-DAVDFAGFYADGDAFANVVPVVEAAGSGGGGAGCSFAFGVDSGY		266
OsHsfC2b	NGFADAARAGCGEKRARLLDG-----D---NTGAFGP-DAVDFAGFYTGADMF--DVAVDAAAAAGGSAGCSFAFGVDSGY		278