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EcDnaK      1  -----MGKIIIGIDLGTNTSCVIGMDGTTPTPVLENAGDRTTPSIIAITDGE
TbHsp70.c   1  -----MTYEGAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-NNE
TbHsp70.4   1  -----MPAPAIIGDLGTTTSCVGVGNKNDQVEIANDQGNRTTPSYVSTFTE
TcHsp70B    1  -----MTYEGAIIGDLGTTTSCVGVGNONEVEIIANDQGSRTTPSYVAFT-DTE
TbHsp70      1  -----MTYEGAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-DTE
PfHsp70-1   1  MASAKGSKPNLPESNIAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-DTE
HsHSPA6     1  -----MQAPREIAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-DTE
HsHSPA1A    1  -----MAKAAAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-DTE
BtHsc70     1  -----MSKGPAAIIGDLGTTTSCVGVGNONEVEIIANDQGNRTTPSYVAFT-DTE

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[illegible]

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EcDnaK      107  ---GQKMAFPQISAEVLKMKMKTAEDYLGEFVTEAVITVPAYFNDSQRQATKDAGTIAGL
TbHsp70.c   109  IEGEMLLQFPEEISARVLAYLKSCAEISYLGKQAKAVITVPAYFNDSQRQATKDAGTIAGL
TbHsp70.4   107  QGERITFFPPEEISARVLMVKMKKEAESYLGEKVKSAVITVPAYFNDSQRQATKDAGTIAGL
TbHsp70B    109  FGETIKFNPPEEISSMVLTKMKEAESYLGEKQKAVITVPAYFNDSQRQATKDAGTIAGL
TbHsp70      109  FGETIKFNPPEEISSMVLTKMKEAESYLGEKQAKAVITVPAYFNDSQRQATKDAGTIAGL
PfhHsp70-1  120  QGEKKLFHPPEEISSMVLTKMKENAEALGKSKNAVITVPAYFNDSQRQATKDAGTIAGL
HsHSPA6     110  GEDKILFFPPEEISSMVLTKMKETAAYLGLQPKFAVITVPAYFNDSQRQATKDAGTIAGL
HsHSPA1A    108  LGITKAFYFPEEISSMVLTKMKEIABAYLGYPVTNAVITVPAYFNDSQRQATKDAGTIAGL
BtHsc70     108  FGETKSFYFPEEISSMVLTKMKEIABAYLGKTVITNAVITVPAYFNDSQRQATKDAGTIAGL

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EcDnaK      164 EVKRRIINEPTAAAIAYGLDKRGT--ERNRTAVADLGGGTFDSLTIEIDVDGKEITFEVLAT
TbHsp70.c   169 EVIRIINEPTAAAIAYGLDKADEGKERNVLIHFDLGGGTFDVSVISVS-----GIFEVKAT
TbHsp70.4   167 EVIRIINEPTAAAIAYGWDSSGEKMVTILIEDLGGGTFDVLTLNIDE-----GIFEVKAT
TcHsp70B    169 EVLRINEPTAAAIAYGLDKVEDGKERNVLIHFDLGGGTFDVTILTIDG-----GIFEVKAT
ThHsp70      169 EVIRIINEPTAAAIAYGLDKADEGKERNVLIHFDLGGGTFDVTILTIDG-----GIFEVKAT
PfHsp70-1   180 NVIRIINEPTAAAIAYGLHKKGKGEINLVLIHFDLGGGTFDVSULTIID-----GIFEVKAT
HsHSPA6     170 NVIRIINEPTAAAIAYGLDRGA-GERNVLIHFDLGGGTFDVSULSIDA-----GIFEVKAT
HsHSPA1A    168 NVIRIINEPTAAAIAYGLDTGK-GERNVLIHFDLGGGTFDVSULTIID-----GIFEVKAT
BtHsc70     168 NVIRIINEPTAAAITAYGLDKVVG-GERNVLIHFDLGGGTFDVSULTIID-----GIFEVKST
          ***.*****.***                *****.*****
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EcDnaK	222	NGDTHLGGEDFD SRLINYL EEFKNDQ GIDLRNDPLA QRL EAAEAKIELSSAQTD
TbHsp70.c	225	NGDTHLGGEDFDAAL EHA AIN IYGLIEQGLSRLMLSLRLRRCBEVKRVLSISTVE
TbHsp70.4	223	AGDTHLGGEDFDRLVDYFATEFTIT TCKDILRGNARLRRLTACERAKRTLSSASTN
TcHsp70B	225	NGDTHLGGEDFDNRLVSHFT EFKRKNRGKDLITSORALRRLRTACERAKRTLSSAAQ
TbHsp70	225	NGDTHLGGEDFDNRLVHFT EEFKRNKRGKDLSSNLRALRRLTACERAKRTLSSAAQ
PfHsp70-1	235	AGDTHLGGEDFDNRLVNFCE EFKRKNRGKDLSSNLRALRRLTACERAKRTLSSSTQ
HsHSPA6	225	AGDTHLGGEDFDNRLVNHF EEF EFKRH GKDLSSNLRALRRLTACERAKRTLSSSTQ
HsHSPA1A	223	AGDTHLGGEDFDNRLVNHF EEF EFKRH KKDISENKRRLRLTACERAKRTLSSSTQ
BtHsc70	223	AGDTHLGGEDFDNRVNHF EEF EFKRH KKDISENKRRLRLTACERAKRTLSSSTQ

EcDnaK 281 V N P Y T A T A T G P K H M N I K V T R A L E S V E D I V N R S E P F K V A L Q D A G S V S D I D V L V L V
TbHsp70.c 285 T A D G L P L P --- G E F V L K I T R A R F E E L C T K F A R C L S V V Q F A L K D A S M K V E D I D V V L V L V
TbHsp70.4 282 I E I D A L F - E --- G D F S K I T R A R F E E L C R D F R E R C L P V R K V L D A E D A S A D I D V L V L V
TcHsp70B 284 I E I D A L F - E --- N D F Q A T I T R A R F E E L C G D L F R G T L Q P V E V L Q D A K M D R R A H D V L V L V
TbHsp70 285 I E I D A L F - E --- N D F Q A T I T R A R F E E L C G D L F R G T L Q P V E V L Q D A K M D R R A H D V L V L V
PfHsp70-1 295 I E I D S L F - E --- G I D F S V T V R A R F E E L C I D F R D T L P I V E K V L K D A M D R K S H E V V L V L V
HsHSPA6 284 I E I D S L F - E --- G I D F Y T S I T R A R F E E L C S D L F R S T L P E V E K A L R D A K L D R A Q I H D V L V L V
HsHSPA1A 282 I E I D S L F - E --- G I D F Y T S I T R A R F E E L C S D L F R S T L P E V E K A L R D A K L D R A Q I H D V L V L V
BtHsc70 282 I E I D S L F - E --- G I D F Y T S I T R A R F E E L N A D L F R G T L P E V E K A L R D A K L D R S Q I H D V L V L V

Protein sequences for TbHsp70.c and its homologues and orthologues were retrieved from TriTrypDB and NCBI and their accession numbers are given in brackets: HsHSPA1A (AQY76873.1); HsHSPA6 (NP_002146.2); BtHsc70 (NP_776770.2); PfHsp70-1 (PF3D7_0818900); *EcDnaK* - *E. coli* DnaK (NP_414555.1); TbHsp70 (Tb927.11.11330); TcHsp70B (Tc00.1047053511211.170); TbHsp70.4 (Tb927.7.710); TbHsp70.c (Tb927.11.11290). ClustalW and Boxshade (http://www.ch.embnet.org/software/BOX_form.html) software was used to generate this alignment. Identical residues are white against a black background, and similar residues are against a grey background.