**Table S1.** Sequence alignment of human and *E. coli* Hsp70s from BLASTp program. Residues of *E. coli* Hsp70 relevant for interdomain communication and extracted from the FEL analysis are underlined (91 residues) and positive residues (59 residues) are shown in bold.

|  |  |  |  |
| --- | --- | --- | --- |
| h.E.C. | 75 | IGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFT-DTERLIGDAAKNQVALNPQNIGIDLG**TT** **S**CV + ++ N +G+RTTPS +A+T D E L+G AK Q NPQ**N**IGIDLG**TTNS**CVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQ**N** | 6564 |
| h.E.C. | 6665 | TVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLT**T+F** KRLIGR**+F** **D** VQ D+ PF++I **D** **V** KG+ A P +IS+ VL**TLF**AIKRLIGR**RFQD**EEVQRDVSIMPFKIIA-A**DNGDAWVE**VKGQKMA--PPQISAEVLK | 125121 |
| h.E.C. | 126122 | KMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLKMK+ AE YLG PVT AVITVPAYFND+QRQATKDAG IAGL V RIINEPTAAA+AYGLKMKKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGL | 185181 |
| h.E.C. | 186182 | DRTGKGERNVLIFDLGGGTFDVSILTID--DG--IFEVKATAGDTHLGGEDFDNRLVNHF D+ G G R + **++DL**GGGTFD+SI+ ID D**G** FEV AT GDTHLGGEDFD+RL+N+DK-GTGNRTIA**VYDL**GGGTFDISIIEIDEVD**GEKT**FEVLATNGDTHLGGEDFDSRLINYL | 241240 |
| h.E.C. | 242241 | VEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGI----DFYTSI VEEFK+ **D+** **+** A++RL+ A E+AK LSS+ Q + + + +VEEFKKD**QGIDLRND**PLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKV | 297300 |
| h.E.C. | 298301 | TRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGR TRA+ E L DL ++EP++ AL+DA L + I D+**+LVG**G TR+P VQK + +FF G+TRAKLESLVEDLVNRSIEPLKVALQDAGLSVSDIDDV**ILVG**GQTRMPMVQKKVAEFF-GK | 357359 |
| h.E.C. | 358360 | DLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLSLGLETAGGVMTALIKRN + K +NPDEAVA GAAVQ +L GD **V+D+**LLLDV PLSLG+ET G**GVMT** LI +NEPRKDVNPDEAVAIGAAVQGGVLTGD----**VKDV**LLLDVTPLSLGIETMG**GVMTT**LIAKN | 417415 |
| h.E.C. | 418416 | STIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNNLLGRFELSGIPPAPRGVPQIEVT +TIPTK +Q+F+T **DNQ** V I V +**GER** **D**N LG+F L G**I** **PAPR**G+PQIEVTTTIPTKHSQVFSTAE**DNQS**AVTIHVLQ**GERKRAAD**NKSLGQFNLDG**INPAPR**GMPQIEVT | 477475 |
| h.E.C. | 478476 | FDIDANGILNVTATDKSTGKANKITITNDKGRLSKEEIERMVQEAEKYKAEDEVQRERVS FDIDA+GIL+V+A **DK++GK** KITI **G** **L+++**EI++MV+**+AE** **D** E VFDIDADGILHVSA**KDKNSGKE**QKITIK**ASSG**-**LNED**EIQKMVR**DAEA**N**AEAD**RKFEELVQ | 537534 |
| h.E.C. | 538535 | AKNALESYAFNMKSAVEDEGLKGKISEADKKKVLDKCQEVISWLDANTLAE-KDEFEHKR +N + + + VE+ G K+ DK + + ++ L+ E K E KTRNQGDHLLHSTRKQVEEAG--DKLPADDKTAI----ESALTALETALKGEDKAAIEAKM | 596588 |
| h.E.C. | 597589 | KELEQVCNPII+EL QV ++QELAQVSQKLM | 607599 |