Gene	GenBank No.	ORF Length	Protein Length	Molecular Weight	pI
LbHsp70-1	MN599717	2070 bp	690 aa	167.4 kDa	4.97
LbHsp70-2	MN599718	1515 bp	505 aa	125.2 kDa	5.06
LbHsp70-3	MN599719	1971 bp	657 aa	161.2 kDa	4.95
LbHsp70-4	KR349165	1971 bp	657 aa	159.3 kDa	4.95
LbHsp110-1	KR349166	2487 bp	829 aa	201.3 kDa	4.91

Table S1. Molecular properties of five *Liposcelis bostrychophila* heat shock protein genes.

LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	MLYVARNVGRKALNHTNFTTEKMVLKNVSTLVKKALSPSPYLKYNQIRLKSDTVKGAVIGIDLGTTNSCVAVMEG.KQAKVIENAEGARTTPSVVAFTKD MALFGEHVGNSASLAIYKDEDRVDIVANDAGERVTPTVVQWT.P MAKAPAVGIDLGTTYSCVGVFQH.GKVEIIANDQGNRTTPSYVAFT.D MIRYRILGLIGCLLAVAWAAKDDKNPDVGTVIGIDLGTTYSCVGVYKN.GRVEIIANDQCNRTTPSYVAFTPD gi g n grtp v t	99 45 46 72
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	GERLVGMPAKRQAVTNSANTFYATKRLIGRKFEDPEVKKDMKTLSYKVVKASNGDAWIQGQDGKMYSPSQVGAFVLIKMKET <mark>ABAYLN.TS</mark> VKNAVVT TNCIVGRAAQIEQFRYTTCTVIRNQLINENISQSEFEGLKSQIAYKVNKTESNVKYELLFEGKQHHVSPREIVSLIFKKIYGIAEAAVGGNKEMNAVLC TERLIGDAAKNQVAMNPNNTIFDAKRLIGRREDATVQSDMKHWPFTVISDGGKPKIQVEYKGETKTFFPEEISSMVLTKMKETABAYLG.KTVTNAVIT GERLIGDAAKNQLTNPENTIFDAKRLIGREWTDSTVQHDIKYFPFKVKEKNSKPHIEVQTSQGAKIFAPEEISAMVLGKMKETABAYLG.KKVTHAVVT g a t k l v p k aea av	196 145 145 171
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	VPAYFNDSQRQATKDAGQIAGLNVLRVINEPTAAALAYGMDKSEDKIIAVYDLGGGTFDISILEIQKGVFEVKSTNGDTFLGGEDFDNLLVNFLVN VPLYFSNKSIELIKDIATKVGFKILQVVDEPCAAALGYNLAVE.PEESLSYCLIYVKGGFSIDATILLIQDCMFSVLGYVHKHNLGGSLFTEKLSEFLAA VPAYFNDSQRQATKDAGAIAGLNVLRIINEPTAAAIAYGLDKKTASTGERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRWNHFVQ VPAYFNDAQRQATKDAGTISGLVVMRIINEPTAAAIAYGLDKKEGEKNVLVFDLGGGFFDVSLLTIENGVFEVVSTNGDTHLGGEDFDQRVMDHFIK vp yf kd g ep aaa y gg d l i g f v lgg f	292 244 245 268
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	EFKKEQCIDITKDPMAVQRLKEAAEKAKIELSSSLQTDINLPYLTVDSSGPKHMNLKLS <mark>RSKFESI</mark> VDSLIKKTVAPCQKALQDADVKKSDIGEVLLVGG EFKRQY.TTDITERGKFKLLAAAENVKQILSIQNVAQCSVESIGGGYDLSCSVS <mark>RAREENI</mark> MLPFIPEMLSPITEVLNQTGLSVNQINKVIGGG EFKRXYKKOLTSNKFALFRLRIACEKAKKILSSSTQASIEIDSLFEGVDFYTSITRAFEELNADLFRSTMEPVEKSLRDAKMDKSQIHDIVLVGG LYKKKK <mark>KDIRKONRAVQKLRFEVEKAKKA</mark> LSSSLQVRIEIESFFEGDDFSELT <mark>RAFEEI</mark> NADLFRSTMEPVEKSLRDAKMDKKDVDEIVLVGG k l e k ls r fe p l gq	392 339 341 364
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	MTRMPKVQQTVQEIFG.RQPSKSVNPDEAVAVGAAVQGGVLAGDVTDVLLLDVTPLSLGIETLGGVFTRLISRNTTIPTKKSQVFSTAADGQ SLKIPKLQESICSLFPSAEALINIAPDELIALGAAKQAGYCIKYENLPESLSIDTPALSNSLSITVRQGNSNEEESYLLLKNSSVPLRR.RYNVLSAENS STRIPKVQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILHGDKSEEVQDLLLDVTPLSLGIETAGGVMTTLIKRNTTIPTKQTQTFTTYSDNQ STRIPKIQQUVKEFFGGKEPSRGINPDEAVAYGAAVQAGVLTGEQDTGIVLLDVNPLTMGIETVGGVMTKLIPRNTVIPTKKSQIFSTASDNQ pk q f pde a gaa q 1 1 1 1 n p	483 438 437 458
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	TQVDIKVHQGEREMASDNKLLGQFTLVGIPPAPRGVPQIEVTFDIDANGIVHVSARDKGTGKEQQIVIQSS.GGLSKDEIENMVKNAEQYAQADKVKKDR LSVDVDIPEKNNLNLGSVSLNDLEPDSTVIIELDINKDGKLLLNLVNESSSRKNCLKFDLNEMSIS PGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQVEVTFDIDANGILNVTACEKSTGKENKITITNDKGRLSKEEIERMVNEAEKYKAEDEKQKAT HTVTIQVYEGERPMTKDNHLLGKFDLTGIPPAPRGVPQUEVTFEIDANGILNVTACEKSTGKENKITITNDKGRLSKEEIERMVNEAEKYKAEDEKQKAT v n lg l p i g	582 504 537 558
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	VEARNSAEGIIHQTESKMDEFKSQLPQEECDKLRTQITELRSLLDKGEDADPEEIRKSSTSLQQASLKLFEMAYRKMASENQGSPGS ISAKNALESYCFNMKSTIED.EKLKDKISETEKQTIMDKCNDIIKWLDANQLAEAEEYEHKQKELEAICNPIITKLYQGAGGMPGGMPGGMPGGPPGAFG VESRNDLESYAYSLKNQLGDKEKLGAKVSDEDKAKMEEAIDEKIKWLDQNPDADVEEYKKQKKELEDVTQPIIAKLYSSTGGAP	669 504 636 642
LbHSP70-1 LbHSP70-2 LbHSP70-3 LbHSP70-4 Consensus	SSSEQTEQQEPKEEKKEEKN AAPGGAPGAGGTGPTIEEVD PPSAGDDDLKDEL.	689 504 656 656

Figure S1. Multiple amino acid sequence alignments of four *Hsp70s* from *Liposcelis bostrychophila*. Three signature sequences of the Hsp70 family are indicated by grey shading. The putative ATP-GTP binding site is colored with yellow shading. The potential non-organelle eukaryotic consensus motif and putative bipartite nuclear location signal are in green and purple shading, respectively.

CsHSP110 LbHSP110-1 PhHSP105 Consensus	MAAMS <mark>VIGIDFGN</mark> ESCYVAVARAGGIETIANDYSLRATPSCVALSGKNRILGVAAKNQMVTNMKNTIHGFKRFLGRKYNDPHVQQELKYLPFRVVQQPNG MS <mark>VIGIDFGN</mark> ESCYIAVARAGGIETIANDYSLRATPSCVAFSDRNRIMGVAAANQTVTNMKNTIVGFKRLLGRKFNDPYVQQEMQFLPYAVVPNQDG MS <mark>VIGIDFGN</mark> ESCYIAVARAGGIETIANDYSLRATPSCVAFSDRNRIMGVAAANKRVTNMKNTIVEFKRLLGRKYNDPYVQHELQYLPFSVVPNQDG msvigidfgnescy avaraggietiandyslratpscva s nri gvaa n vtnmknti fkr lgrk ndp vq e lp vv g	100 97 97
CsHSP110 LbHSP110-1 PhHSP105 Consensus	SIGVKVNYLDEEHTFSPEQITAMLFTKLKEVSENALKTKVNDCVISVPSFFTNAERKALLDAASIAGLNVLRLMNETTATALAYGIYKQDLPAPEEKPRN SLGIKVHYMNEEHVFTPEQITAMLFTKLKEIAESALKTKVNDCVISVPSFYTQAERKALLDAAHIAGLNVLRLFNETTSTALAYGIYKQDLPNAEEKPRN SLGIKVNYLNEEHIFTPEQITAMLFTKLKEIAENALRTKVNDCVISVPSFYTQAERKSLLDAAHIAGLNVLRLFNETTSTALAYGIYKQDLPNAEEKPRN s g kv y eeh f peqitamlftklke e al tkvndcvisvpsf t aerk lldaa iaglnvlrl nett talaygiykqdlp eekprn	200 197 197
CsHSP110 LbHSP110-1 PhHSP105 Consensus	VVFVDCGHASLQVFACAFHKGKLKMLASASDPNLGGRDIDLILAEHFCTDFQSRYHIDPHSNHRAFLRLTSEV <mark>FKLK</mark> KQMSANSTKLPMNIECFMDDKDV VVFVDCGHSSLQVFAAAFNKGKLKMLASASDASLGGRDFDRILAEHFSKEFVSKYKIDPRKNARAYLRLTTEVENLKQMSANSTKLPLNIECFMEDKDV VVFVDCGHSSLQVFAAAFNKGKLKMLASAS.SSIGGRDIDRILAEHFSKEFVSKYKIDPRKNARAYLRLMTEVGKLKKQMSANSTKLPLNIECFMDDKDV vvfvdcgh slqvfa af kgklkmlasas ggrd d ilaehf f s y idp n ra lrl ev klkkqmsanstklp niecfm dkdv	300 297 296
CsHSP110 LbHSP110-1 PhHSP105 Consensus	HGDMKRADMEQLCGHLFKRVEKTLRKCLEDSKLHLEEIHA <mark>VEIVGGSSRIPAIKH</mark> VIEVVFGKQPSTTLNQDEAVSRGCALQCAMLSPAIRVREFSITDI HSGLQRSDMEGLCSGLIARVERTLRKCLADSKLSLDDIYAVEIVGGSTRIPSIKHLIEDIFKKHPSTTLNQDEAVARGCALQCAALSPAIRVREFSVTDI HSDMQRSDMEELCAGLFQKVEKTLTKCLKDSNLSLEEIYA <mark>VEIVGGSTRIPAIKH</mark> LIEEVFKKQPSTTLNQDEAVARGCALQCAALSPAIRVREFSVADI h r dme lc l ve tl kcl ds l l i aveivggs rip ik ie f k pstlnqdeav rgcalqca lspairvrefs di	400 397 396
CsHSP110 LbHSP110-1 PhHSP105 Consensus	QNYPIKLVWDASMGEDG.EMEVFSQNHAVPFSKMLTFFRKEPFSMKAFYAGNIPYPDPYIGQFVVKDVKPSPEGESVKVKVKVRVNLHGILTISSASLVL QNFPVVLKWDAAPGEEGGEMEIFSANHAVPFSKLLTFYRREPFSVQAFYSGQTPYPDPYIGRFTIKDVHPTPENESAKVKVKVRINLHGILTVAGATLTE QNYPVTLKWDAYPGEEEGEMEIFTANHAVPFSKLLTFYRKEPFSVHAFYSHPTSYPDSYIGKFTIKDVRPTVDNEPATVKVKVRINLHGILTVAGATLTE qn p l wda ge emef nhavpfsk ltfrepfs afy ypd yig f kdv p e vkvkvrnlhgilt a l	499 497 496
CsHSP110 LbHSP110-1 PhHSP105 Consensus	$\label{eq:construction} \begin{split} & \mbox{KQDASEQDTNEQDNAGPEAMDTEAQKNEVNGSANQ.QQQQGTENSQANHIGNEDDTENQTASEKKDG.TRKKKQLVKTVELPIEAYTHGYSQAELN \\ & \mbox{KLTQAEIDAEANKEAMETDTNTEQPVNNVENGEEK.EQTNEEEMDQQPAQEQSNQQNQQQQNQQGSDKKEKKKKQLVKNVDLSIESETHGLSQLQLN \\ & \mbox{KLTQAEIEAESKESMELDSNSQEQQDQNNWMENGEEQGKDKDQGNEDENDQSKDQQQSQSQQQQQSADKKEKKKKSHVKKIDLNIDTETHGLTKLQLD \\ & \mbox{k} e & \mbox{e} & \mbox{q} & \mbox{d} & \mbox{kk} & \mbox{vk} & \mbox{l} & \mbox{i} & \mbox{th} \\ & \mbox{e} & \mbox{e} & \mbox{q} & \mbox{d} & \mbox{kk} & $	593 594 596
CsHSP110 LbHSP110-1 PhHSP105 Consensus	NYIELECKMVASDRQEKERIDARNALEEYVYEVRGKLSSEEELATFVSENDRNSLCRQLDNMENWLYEEGEECNRQIYVDKLNVLKNLGEPIKTRRLEFE SYYEFECKMMANDKQEKERVDARNALEEYVYDLRCKLTDDSQLANYVTDQDREGLSSQLNDMENWLYEEGEDCQRQVYNDKLDQLKKLGEPIKNRKIEAD SFYEFECKMIANDRQEKERADARNAMEEYVYDLRGKLGDEAQLASFVNDADRDSLMSQLNDMESWLYEEGEDCNRQIYIDKLDQLKKLGEPIKNRKIEAD e e km a d qeker darna eeyvy rgkl la v dr l ql me wlyeege c rq y dkl lk lgepik r e	693 694 696
CsHSP110 LbHSP110-1 PhHSP105 Consensus	LRPNALEELACVLQLTRKAVDQYRAGDERYSHLEESDIQKVQQTAEQTHRWLEEKRAALAGTPRTQNPPVTVAQIRQEKQNFENVVNPILTKPKPKADPP IRPTVFEDLARSIQQSYKIIDQYRNKDERYNHIPEEDILKAQQETERVGKWLDEKRAKAQSTPKYENPVVTVAQIRQEKQNFENIVAPIFNKPKPKPKNE IRPTVIEDLARSIQQSYKIIDQYNNNDERYNHIPEGDINKALQETQKVEKWLDEKRMKIQSTPKYENPVVTVAQIRQEKQAFENLVAPIFNKPKPKPKTE rp e la q k dqy deryh e di k q wl ekr tp np vtvaqirqekq fen v pi kpkpk	793 794 796
CsHSP110 LbHSP110-1 PhHSP105 Consensus	PPVNKENGNTAEKKDAQEDDSPKQEQQSDENMDVE TPPAPAP.EENQKATGDSNQPQGETNNAEEKMETE APPPTAAPPSSEDANNKATGDSVEPNNFFEEPMETDSFI D e m	828 828 834

Figure S2. Multiple alignments of the deduced amino acid sequences of *Hsp110s* from *Liposcelis bostrychophila* and other insect species. The amino acid sequences constituting a single ATP-binding motif are in green color. The amino acid letters with red color indicate HSPA4 like nucleotide-binding domain, and the letters in blue color indicate periplasmic substrate-binding domain. Cs: *Cryptotermes secundus*, Ph: *Pediculus humanus corporis*.