

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

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

LbHSP70-1	MLYVARNVGRKALNHTNFTTEKMLKNVSTLVKKALSPSPYLKYNQIRLKSDEVKGAVIDLGTNNSCVAVMEG.KQAKVIENAEGARTTPSVVAFTKD	99
LbHSP70-2	MAALFGIHVGNSSASLAIYKDEDRVDIVANDAGERVTPTVVQWT.P	45
LbHSP70-3	MAKAPAVGIDLGTTYSVGVFQH.GKVEI IANDQGNRTTPSYVAFT.D	46
LbHSP70-4	MIRYRILGLIGCLLAVAWAAKDDKNPDVGTIVIGIDLGTTYSVGVYKN.GRVEI IANDQGNRTTPSYVAFTPD	72
Consensus	gi g n g r t p v t	
LbHSP70-1	GERLVGMPAKRQAVTNSANTFYATKRLIGRKFEDEPVKKDMKTLISKVVKASNGD..AWIQQDQGMYSQVGAFLIKMKETAEAYLN.TSVKNNAVVT	196
LbHSP70-2	TNCIVGRAAQIEQFRYTTCTVIRNKQLNENISQSEFEGFLKSQIAYKVNKTESNVKYELLFEGKQHVS PREIVSLIFKKIYGAEEAVGGNKEMNAVLC	145
LbHSP70-3	TERLIGDAAKNQVAMNPNTIFDAKRLIGRFEDATVQSDMKHWPFTVISDGGKPKIQVEYKGETKTFPPEIISMVLTMMKETAEAYLG.KTVTNAVIT	145
LbHSP70-4	GERLIGDAAKNQLTTPNTIFDAKRLIGREWTDSTVQHDIKYFPFKVKEKNSKPHIEVQTSQGAIFAPEEISAMVLGKMKETAEAYLG.KTVTHAVVT	171
Consensus	g a t k l v p k aea av	
LbHSP70-1	VPAYFNDSQRQATKDAGQIAGLNVLRINEPTAAALAYGMDKS...EDKIIAVYDLGGGTFDISILEIQKGVFEVKTNGDTFLGGEDFDNLLVNFVFN	292
LbHSP70-2	VPLYFSNKSIELIKDIATKVGFKILQVVDEPCAALGYNLAVE.PEESLSYCLIRYRVGGFSIDATILLIQDGMFSLGVVHKHNLGGSLFTEKLSFLAA	244
LbHSP70-3	VPAYFNDSQRQATKDAGAIAGLNVLRINEPTAAAIAYGLDKKTASTGERNVLIIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNFVQ	245
LbHSP70-4	VPAYFNDAQRQATKDAGTISGLVVMRIINEPTAAAIAYGLDKR...EGEKNVLVFDLGGGTFDVSLLTIENGVFVSTNGDTHLGGEDFDQRVMDHFIK	268
Consensus	vp yf kd g ep aaa y gg d l i g f v lgg f	
LbHSP70-1	EFKKEQGITDITKDFMAVQRLFEAAERAKITLSSSLQTDINLPYLTVDSSGPKHMLKLSRSKFESIVDSLIIKKTVAPCQKALQDADVKKSDIGEVLLVGG	392
LbHSP70-2	EFKRQYR.TTDITERGKFKLLAAENVKQILSIQNVACQSVESIGGGYD...LSCSVSRARFENMLPFIPEMLSPITEVLNQTGLSVNQINKVIGCGG	339
LbHSP70-3	EFKRKYKEDLTSHKRALERLRTACERAKRTLSSSTQASIEIDSLFEGVD...FYTSITRARFEELNADLFRSTMEPVKESLRDAKMDKRSQIHIVLVGG	341
LbHSP70-4	LYKKKKQKDIRKDNRAVQKLRFEVKKAKRALASHQVRIEIESFFEGDD...FSETLTAKKEELNMDLFRSTMKPVQKVEDADMNNKDVDEIVLVGG	364
Consensus	k l e k ls r fe p l gg	
LbHSP70-1	MTRMPKVQQTQVEIFG.RQPSKSVNPDEAVAVGAAGVGGVLGD.....VTDVLLLDVTPLSLGIETLGGVFTRILISRNTPITPKKSQVFSTAADGQ	483
LbHSP70-2	SLKIPKQESICSLFPSAEALINIAPELIALGAAGAGYCIKYENLPESLIDTPALNSLSLTVRQGSNEEESYLILKNSSVPLRR.RYNVLSAENS	438
LbHSP70-3	STRIPKVKQLQDFNKGKLNKSNPDEAVAYGAAGVAAAILHGDK...SEEVQDLLLDVTPLSLGIETAGGVMTTLIKRNTIPTKQTQTFHTYSDNQ	437
LbHSP70-4	STRIPKIQQLVKEFFGGKEPSRGINPDEAVAYGAAGVAGVLTE.....QTDGIVLLDVNPLTMGIETVGGVMTKLIPRNTVIPTPKKSQIFSTASDNQ	458
Consensus	pk q f pde a gaa q l l li n p	
LbHSP70-1	TQVDIKVHQGEREMASDNKLLGQFTLVGIPAPRGVQIEVTFDIDANGIVHVSARDKGTGKEQQIIVIQSS.GGLSKDEIENMVKNAEQYQADKVKKDR	582
LbHSP70-2	LSVDVDIPE.....KNNLNLGSVSLNDLEPDS...TVIIELDINKDGKLLNLVNESSRKNCLKFDLNEMSSIS.....	504
LbHSP70-3	PGVLQIYVEGERAMTKDNNLLGKFELTGIPAPRGVQIEVTFDIDANGILNVTACEKSTGKENKITITNDKGRLSKEEIERMVNEAEKYKADEKQKAT	537
LbHSP70-4	HTVTIYVEGERPMTKDNHLLGKFDLTGIPAPRGVQIEVTFEIDANGILQVSAEDKGTGNKEKIVITNDQNRLTPDDIERMIKDAEKFADEKRLKEK	558
Consensus	v n lg l p i g	
LbHSP70-1	VEARNASAGIIHQTESKMDL...FKSQLPQECCDKLRTQITELRSLLDKGEDADPEEIRKSSTSLQQASLKLFEAMAYRKMASENQGGSP.....GS	669
LbHSP70-2		504
LbHSP70-3	ISAKNALESYCFNMKSTIED.EKLDKISITEKQTIMDKCNDIIKWLDANQLAAEYEHKQKELEAICNPITKLYQAGGMPGMPGMPGPGFPAGG	636
LbHSP70-4	VESRNDLESYAYSLKNQLGDKKELGAKVSDKAKMEEAIDEKIKWLDQNPADVEEYKQKKELEDVTQPIIAKLYSSTGGAP.....	642
Consensus		
LbHSP70-1	SSSETEQEQEPKKEEKKEKN	689
LbHSP70-2		504
LbHSP70-3	AAPGGAPGAGGTGPTIEEVD	656
LbHSP70-4	PPSAGDDDDLLKDEL.	656
Consensus		

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.

