



Fig. B.2: Maximum likelihood analysis of *Hsp90* from *Calanus finmarchicus*, several diapausing insect species, and representative cytosolic (*Hsp90A*), endoplasmic reticulum (*Hsp90B*), chloroplast (*Hsp90C*), and mitochondrial (TRAP) *Hsp90* members. Bootstrap percentages of 1000 replicates are indicated above branches when they are greater than 50%. Bacterial *Hsp90* homologs (i.e., high-temperature protein G, HTPG) were used to root the *Hsp90* tree. Sequences selected for these analyses are primarily from Chen et al. (2005; 2006) with some additions (see Table B.2 for full list of sequences and accession numbers). Symbols and colors denote *Hsp90* forms that are non-inducible [●], inducible [(+)], down-regulated [(-)], or show variable expression in response to diapause [~] according to findings in our study and those reviewed by MacRae (2010). Distance bar at the bottom of the tree indicates branch lengths or the number of substitutions per amino acid site.