Fig. B.1: Maximum likelihood analysis of Hsp70 from *Calanus finmarchicus*, several diapausing insect species, and representative cytosolic, endoplasmic reticulum, mitochondrial, plastid, and bacterial Hsp70 members. Bootstrap percentages of 1000 replicates are indicated above branches when they are greater than 50%. Sequences of bacterial origin were used as the outgroup. Sequences selected for these analyses are principally from Rhee et al. (2009), Boorstein et al. (1994), Daugaard et al. (2007), and MacRae (2010) with some additions (see Table B.1 for full list of sequences and accession numbers). Symbols and colors denote Hsp70 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 length scale, or the number of substitutions per amino acid site.