



Figure S3. Maximum likelihood phylogenetic analysis of the *Pinctada maxima* ETS4/PDEF protein. Percent bootstrap values greater than 70 are displayed on the relevant branches. Analysis is based upon that in Yagi *et al* 2003, and Pfam accession numbers are provided for each sequence. The scale bar indicates the branch length for 0.5 amino acid substitutions. HUMAN; *Homo sapiens*, DROME; *Drosophila melanogaster*.