

Figures

Figure 1. Scheme of the presence and distribution of the domain conserved ThiF (CL0063) in the E1 sequences identified in the transcriptome of *B. glabrata*.

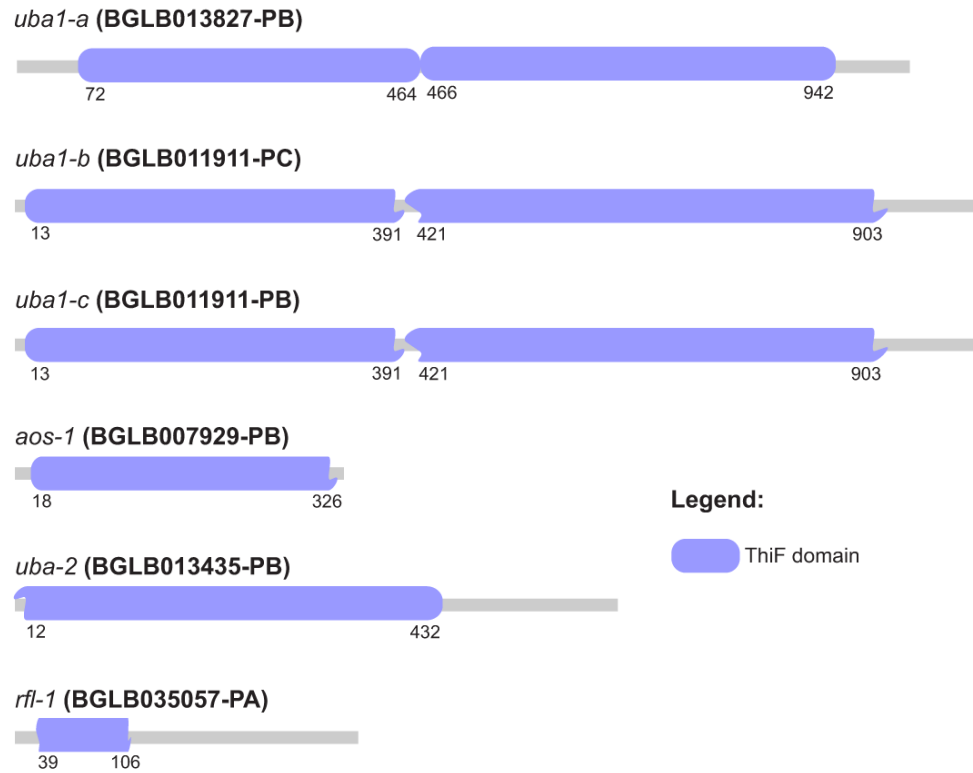


Figure 2. Amino acid residues involved in the formation of the active site of the ubiquitin activating enzymes (E1) identified in *B. glabrata*. The cysteine residue (C) evidenced as an active site in a red arrow and the other amino acid residues probably involved with the catalytic activity indicated by the blue arrows.

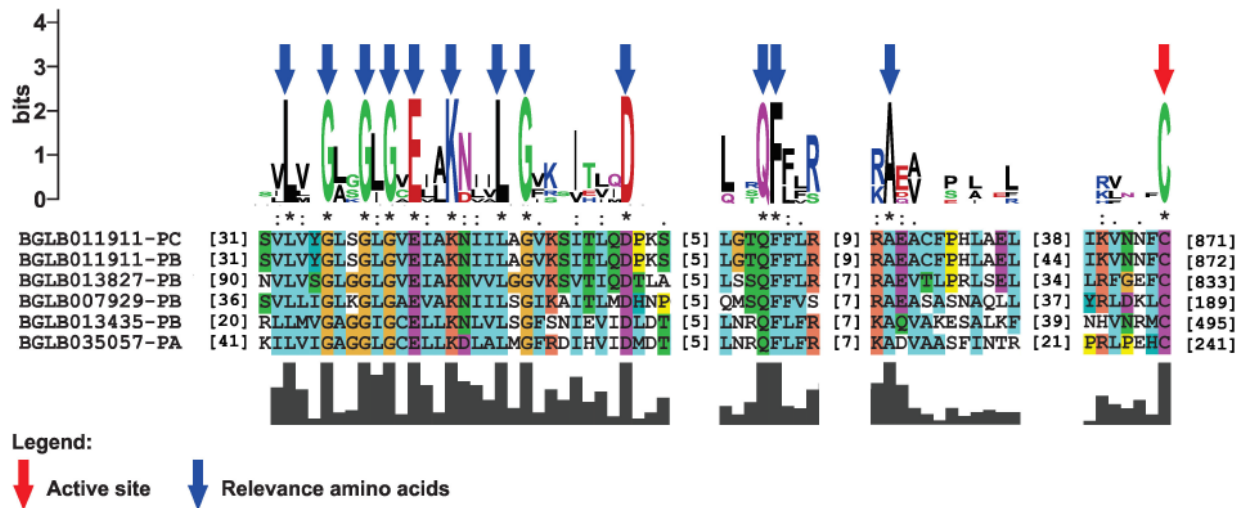


Figure 3. Phylogenetic distribution of the E1 sequences found in *B. glabrata* data against their orthologous organisms.

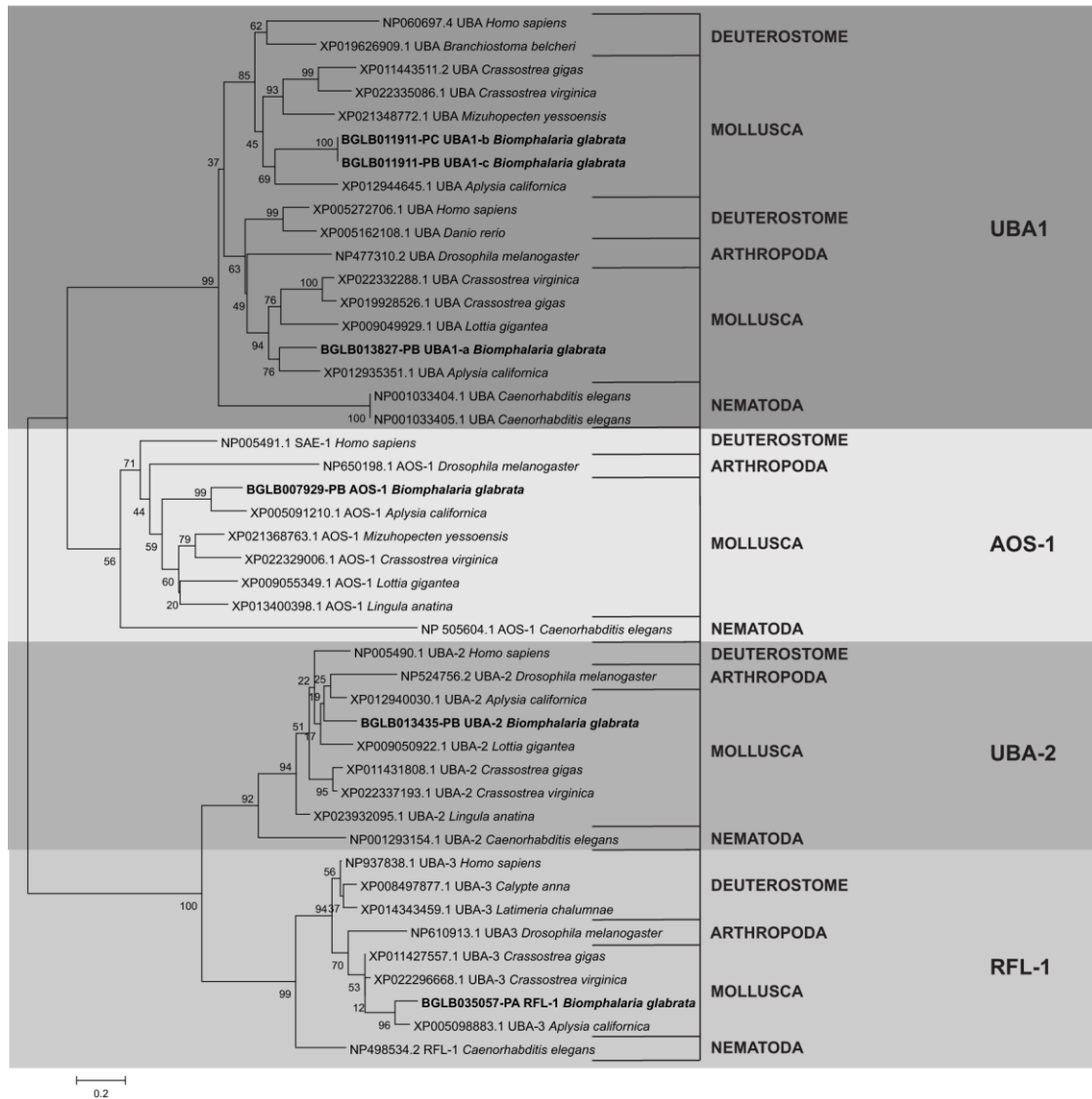


Figure 4. Location and distribution of the Proteasome domain identified in the sequences of the PAS group of *B. glabrata*.

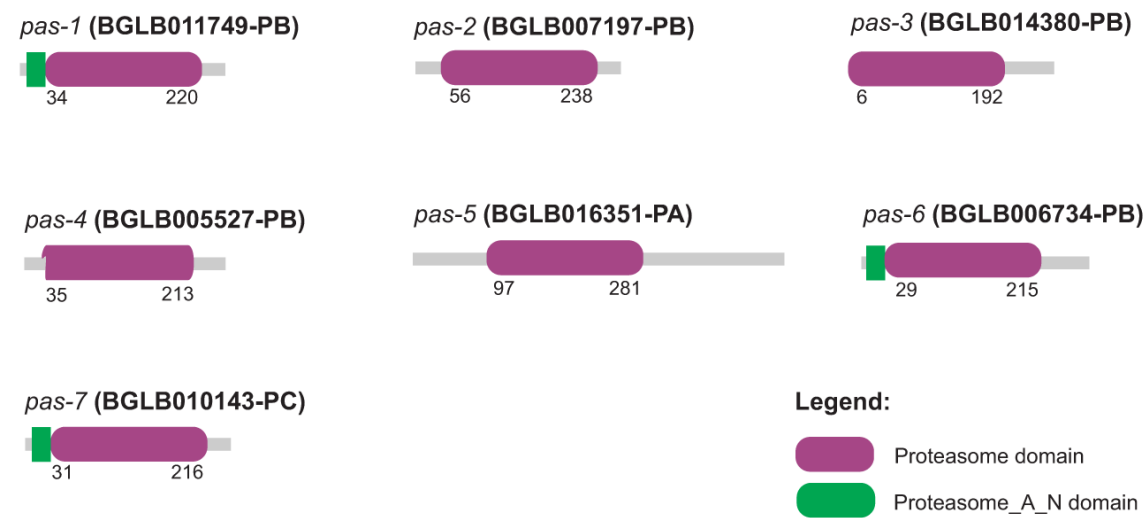


Figure 5. Active site found in the sequences participating in the PAS group of the *B. glabrata* data. The residues involved in the formation of the site are indicated by the red arrows.

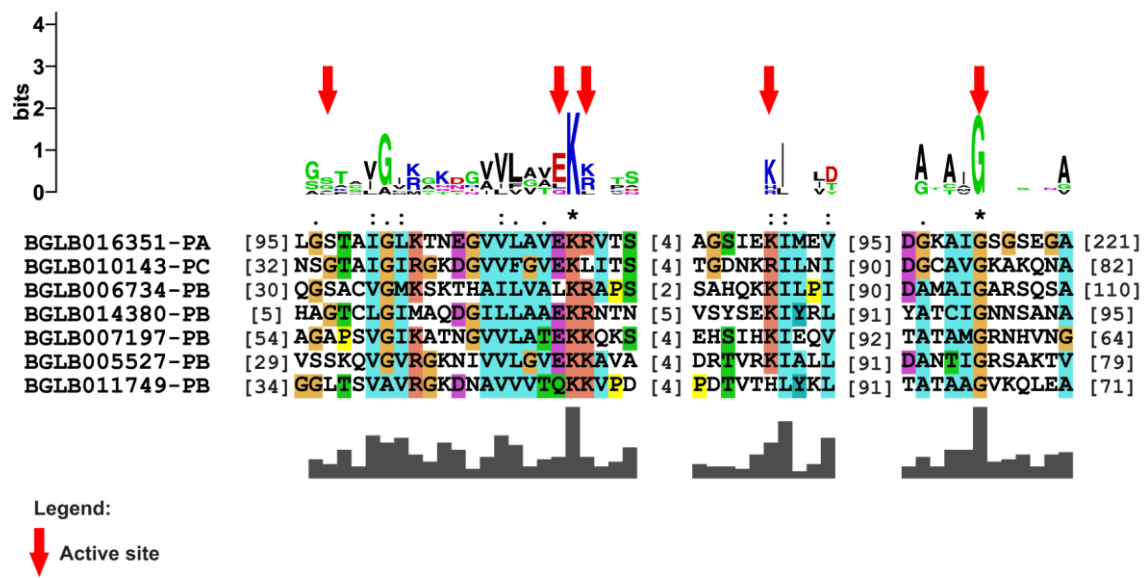


Figure 6. Phylogenetic tree generated by the analyzes using the sequences identified as PAS of mollusk versus model organisms and their orthologs.

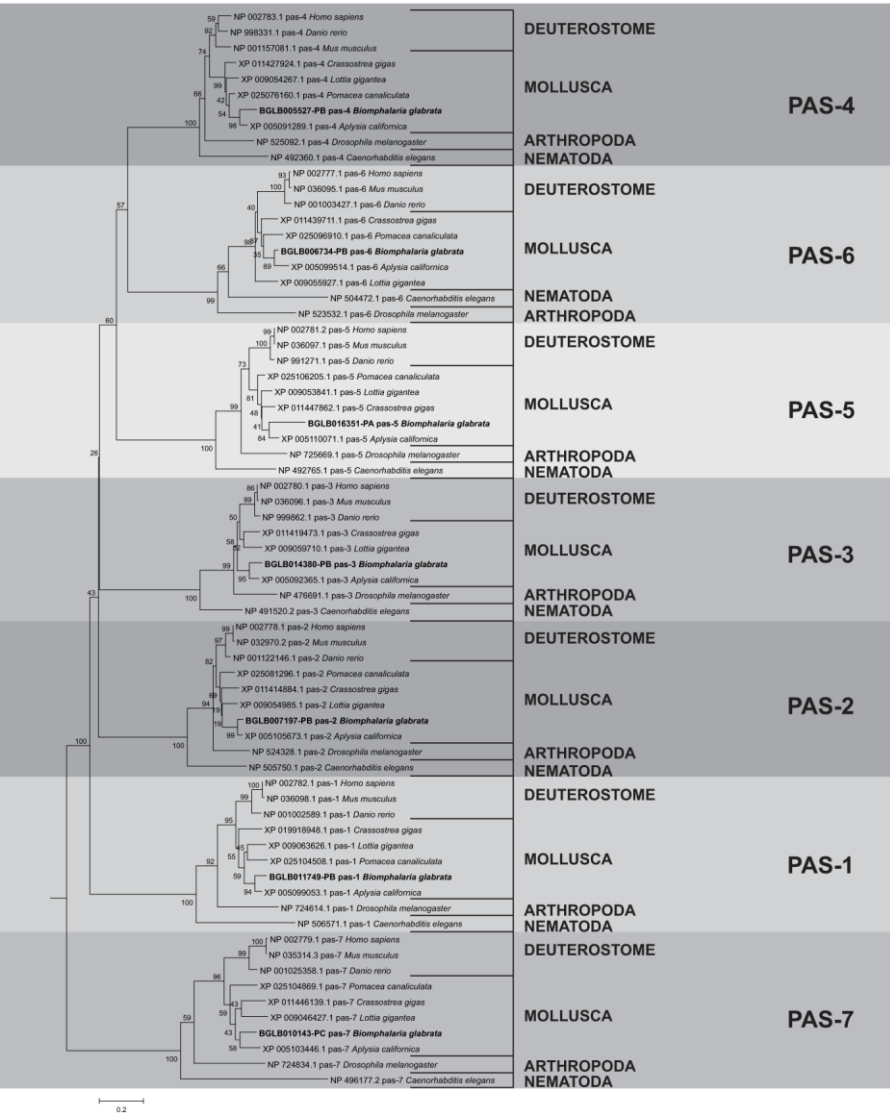


Figure 7. Expression profile of the genes involved in UPS in 12 different tissues of the adult snail.

