
**Appendix 2. Prediction of membrane topology of three xlProminin homologs**

(*xlProminin-1, 2 and 3*) using the **TMHMM software**. The X axes represent linear sequences of the proteins, while Y axes indicate probabilities of transmembrane domain formation at a given position. Predicted transmembrane domains are indicated with red, predicted cytosolic domains are indicated with blue, predicted extracellular domains are indicated with pink. All three xlProminins are predicted to have five or six high hydrophobicity peaks that may represent transmembrane domains or signal peptide (if the peak is located at the N-terminus of the sequence). xlProminin-1 and 2 are predicted to have signal peptides, but no conventional signal peptide is predicted for xlProminin-3.