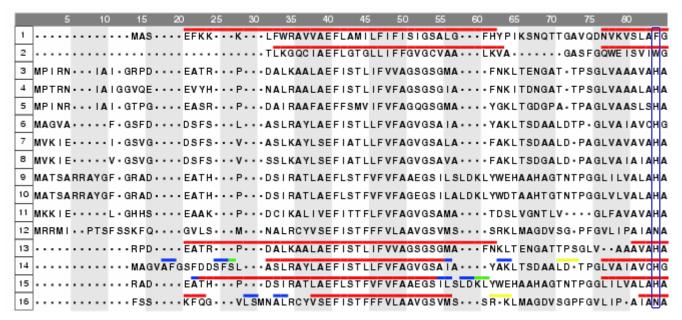
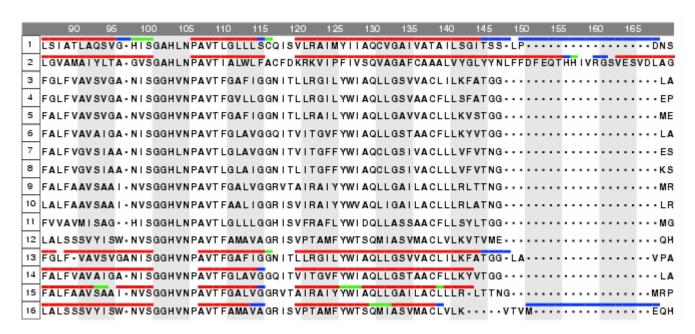
Supplemental Figure 3 Structural alignment of the TIP family with AQP1 and GlpF

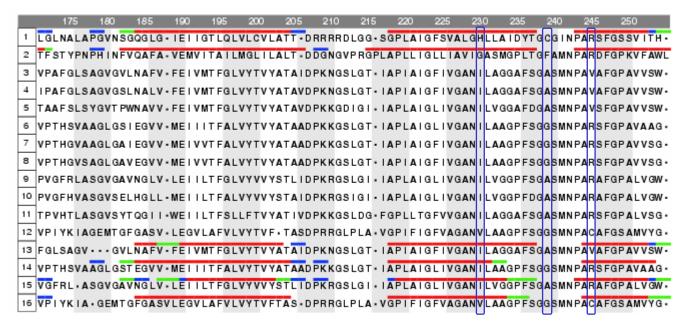
The amino acid sequences of the ten members of the Arabidopsis TIP family were aligned based on sequence and structural similarity with bovine AQP1 and *E. coli* GlpF by using the Multiple Alignment program of the MOE software as described in the Materials and Methods. The sequences are numbered as follows: 1 AQP1, 2 GlpF, 3 Arabidopsis thaliana (At)TIP1;1, 4 AtTIP1;2, 5 AtTIP1;3, 6 AtTIP2;1 7 AtTIP2;2, 8 AtTIP2;3, 9 AtTIP3;1, 10 AtTIP3;2, 11 AtTIP4;1, 12 AtTIP5;1. Also shown are the structurally aligned homology models of 13 AtTIP1;1, 14 AtTIP2;1, 15 AtTIP3;1 and 16 AtTIP5;1. The red bars above the sequences denote the positions of transmembrane and NPA α-helices (as outlined in Fig. 1 in the manuscript text) based on experimental structures (AQP1 and GlpF) and the TIP homology models. The blue and green bars above sequences represent regions of loops that constitute turns. The aligned ar/R residues are highlighted in vertical blue boxes.



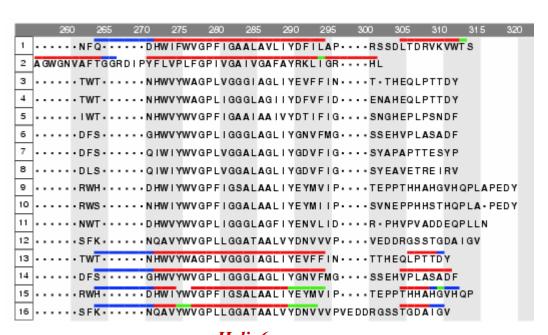
Helix1 Helix2



Helix2 NPA Loop B Helix3



Helix4 Helix5 NPA Loop E



Helix6