

Supplemental figure 1

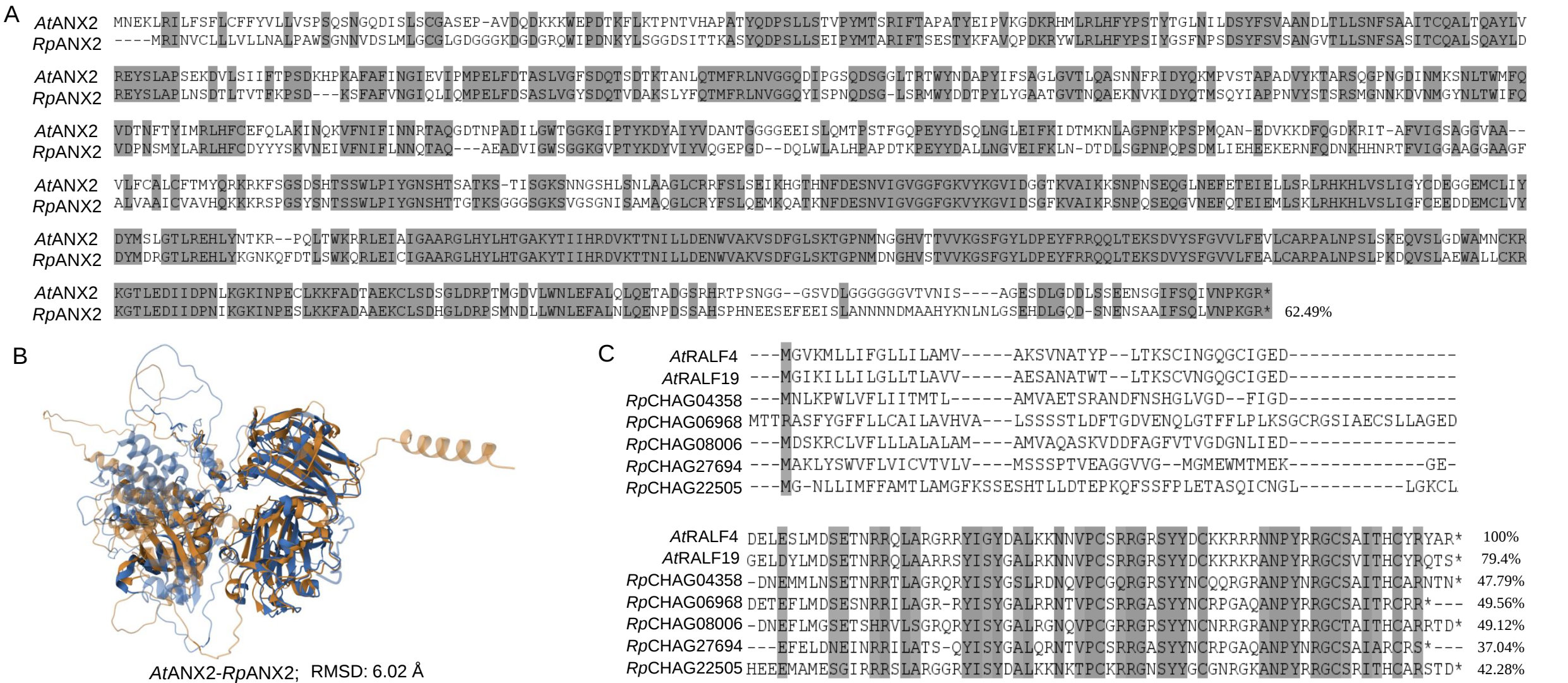


Fig. S1 Sequence and structural conservation of ANX2 and RALF proteins between *A. thaliana* and *R. pseudoacacia*.

(A) Amino acid sequence alignment of ANX2 from *A. thaliana* (*AtANX2*) and *R. pseudoacacia* (*RpANX2*). Gray shading indicates identical residues; the overall sequence identity is 62.49%.

(B) Superposition of the three-dimensional structures of *AtANX2* and *RpANX2* predicted with AlphaFold2 (root mean square deviation, RMSD = 6.02 Å).

(C) Amino acid sequence alignment of *A. thaliana* RALF4 and RALF19 with five putative *R. pseudoacacia* RALF homologs (*RpCHAG04358*, *RpCHAG06968*, *RpCHAG08006*, *RpCHAG22505*, and *RpCHAG27694*). Gray shading indicates identical residues; numbers on the right indicate the percentage identity of each sequence to *AtRALF4*.