

## **Figure 1, Supplemental**

Annotated alignment of SCPL proteins.

The 51 Arabidopsis SCPL proteins and CPY were aligned in AlignX and subsequently annotated in Microsoft Excel. The proteins are arranged from top to bottom in ascending order according to the numbering system provided in Figure 1A. The dashed horizontal line partitions the Clade IA from the Clade IB SCPL proteins, and the solid horizontal line further separates Clade I from Clades II-VI. Cysteine residues forming disulfide bridges in CPY are indicated by yellow connecting lines. Amino acid residues found within the S1 and S1' binding pockets of CPY are labeled in red and blue, respectively. The first page of the figure provides additional color codes used for conserved amino acid residues and important sequence characteristics.