**Fig. S1.** Multiple sequence alignment of *Phytophthora infestans* PnP proteins and *Phytophthora sojae* PsojNIP. Identical amino acids are shaded in black and similar amino acids are shaded in gray. Residue numbers are indicated on the left of the sequences. Signal peptides are underlined. Conserved cysteine residues are highlighted with asterisks. The alignment was conducted using the program ClustalX (Thompson JD, Gibson TJ, Plewniak F, Jeanmougin F, Higgins DG: The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res 1997, 25:4876-4882.) and visualized with BOXSHADE (http://bioweb.pasteur.fr/seqanal/interfaces/boxshade.html).