

PROTEOMICS

Supporting Information for Proteomics

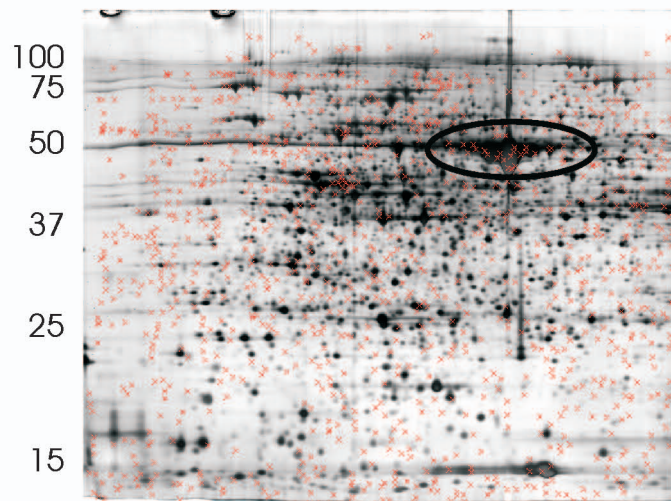
DOI 10.1002/pmic.200800293

Ivy Widjaja, Kai Naumann, Udo Roth, Noreen Wolf, David Mackey,
Jeffery L. Dangl, Dierk Scheel and Justin Lee

**Combining subproteome enrichment and Rubisco depletion enables
identification of low abundance proteins differentially regulated
during plant defense**

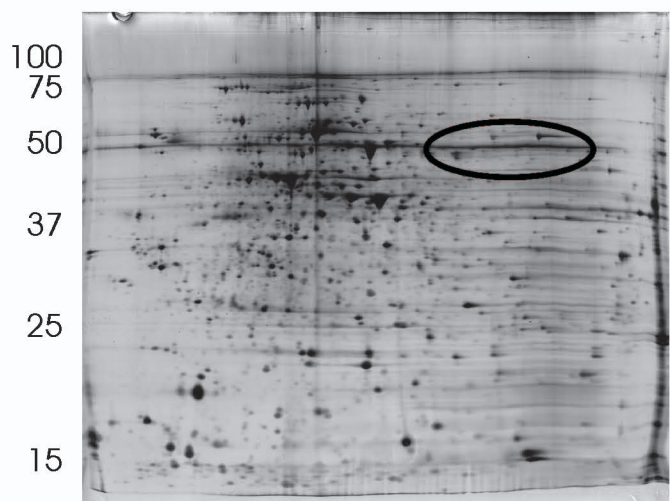
A

pl 4 - 7 Total Protein

MW
(kDa)

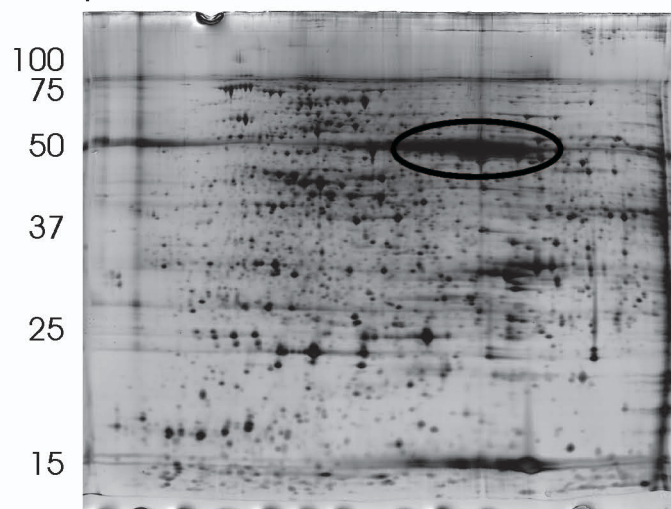
B

pl 4 - 7 10% PEG Pellet

MW
(kDa)

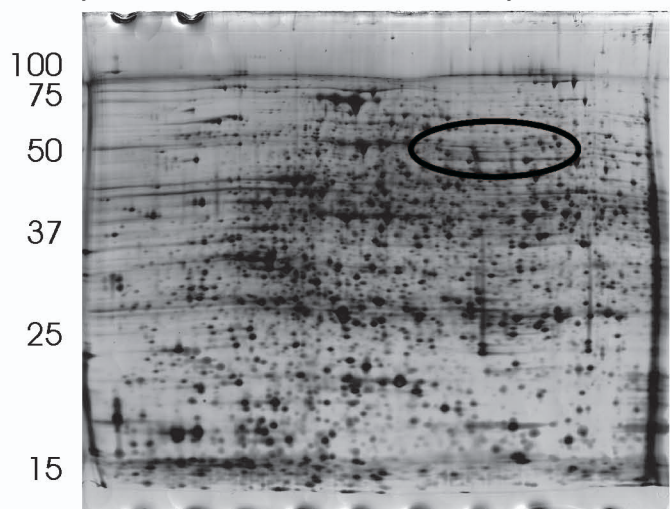
C

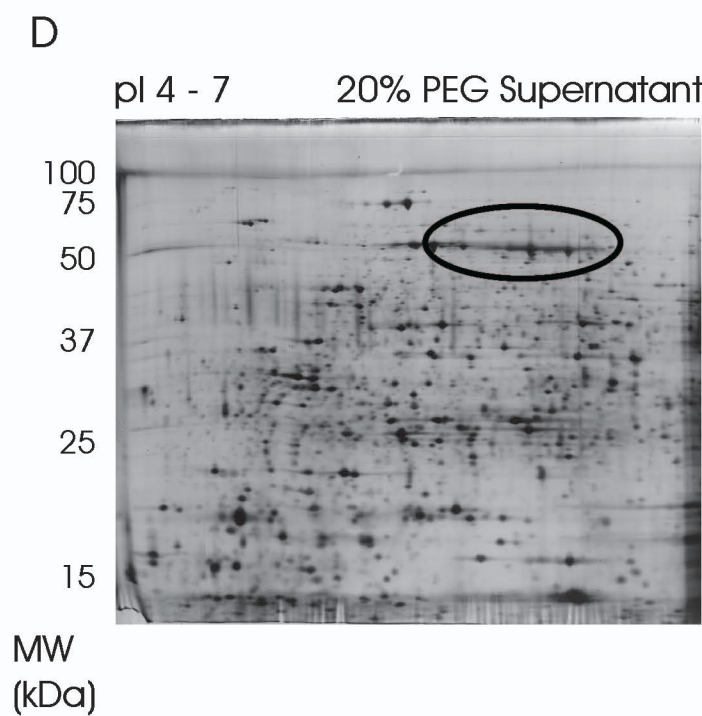
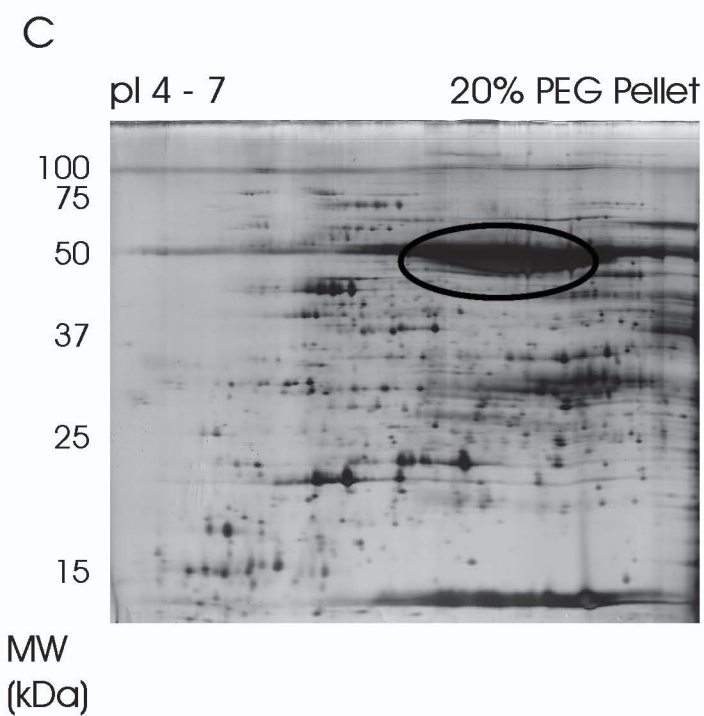
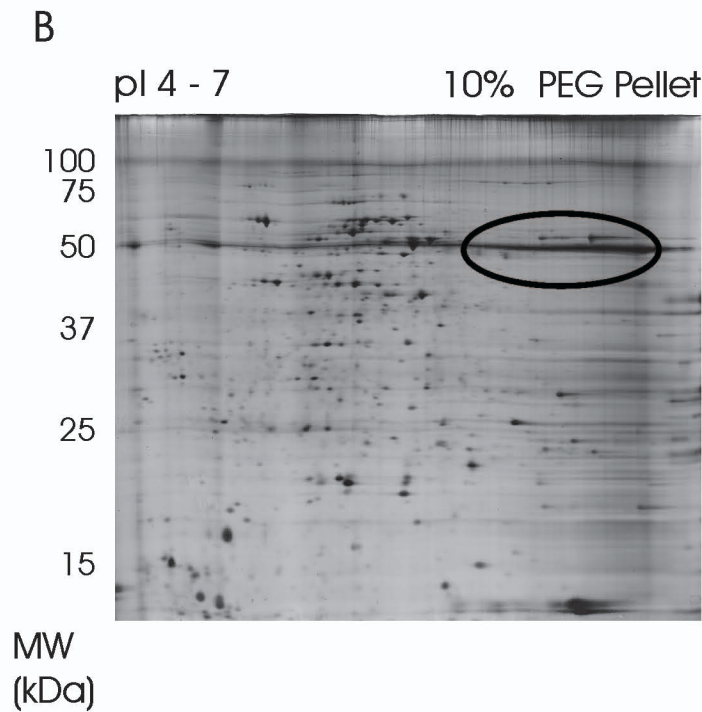
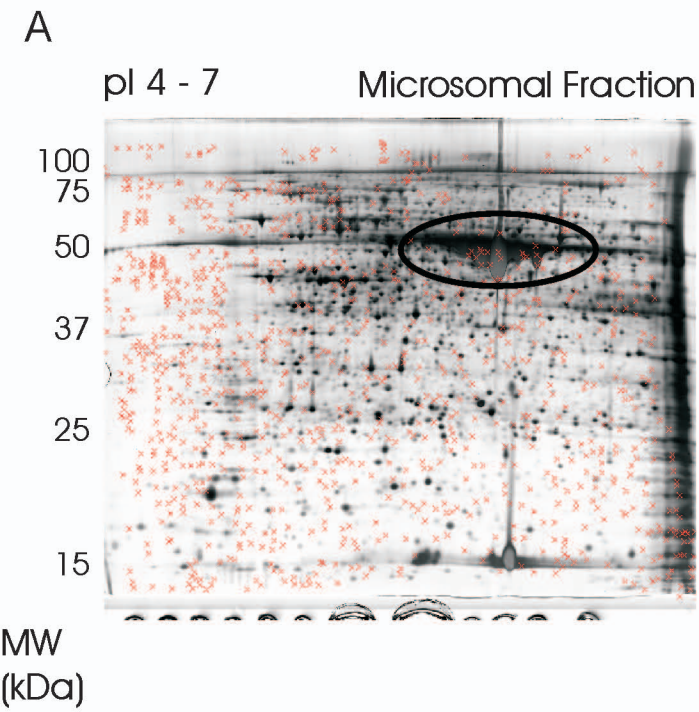
pl 4 - 7 20% PEG Pellet

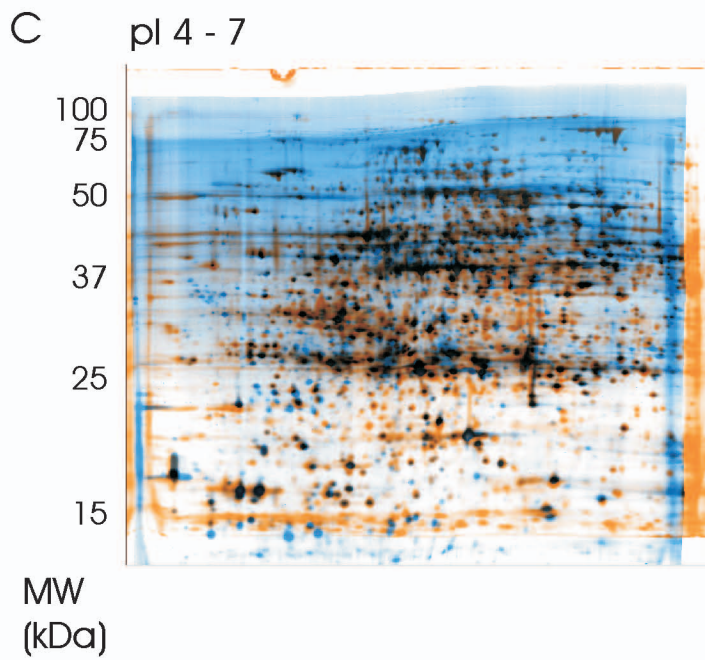
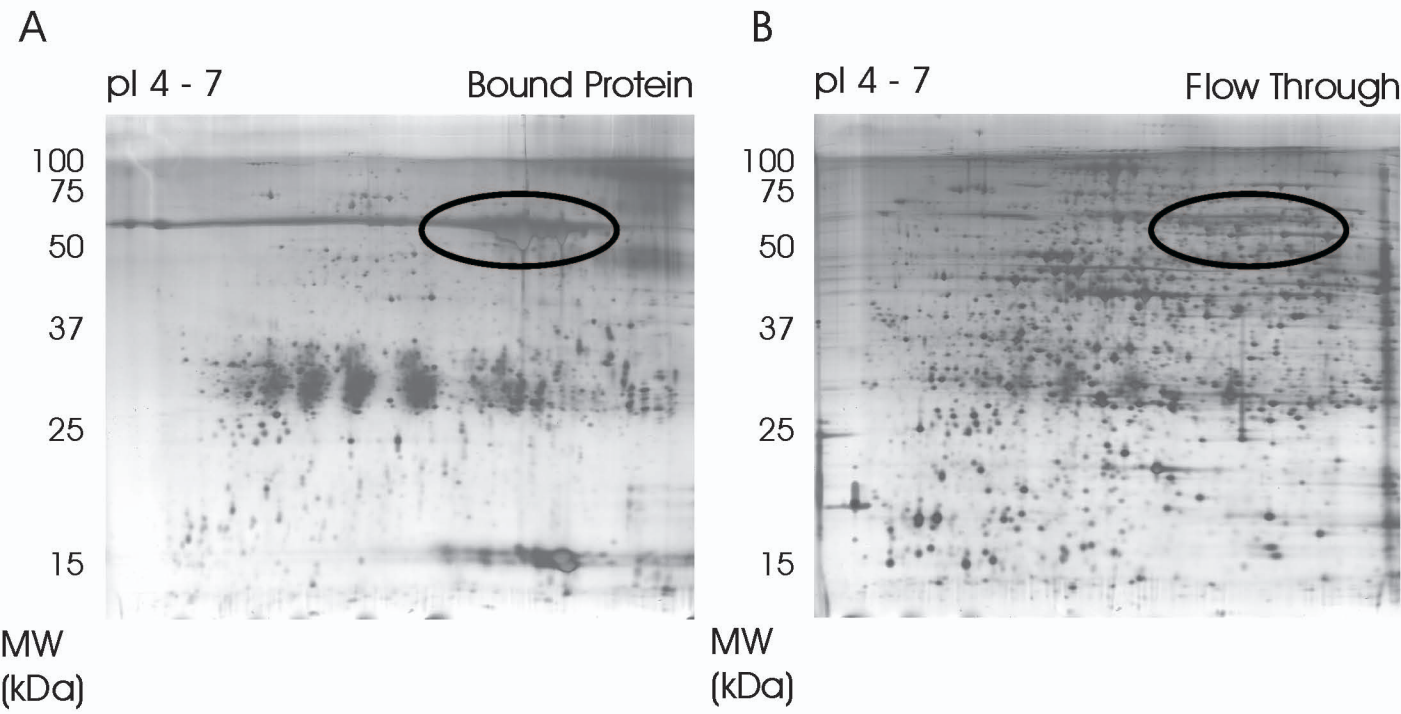
MW
(kDa)

D

pl 4 - 7 20% PEG Supernatant

MW
(kDa)





Legend for Supporting Information

Fig. S1. Silver-stained 2-DE gels of total proteins and Rubisco-depleted total proteins. (A) total protein, (B) 10% PEG pellet, (C) 20% PEG pellet, (D) 20% PEG supernatant. The circled area indicates the location of the abundant Rubisco large subunit. The crosses in “A” indicate positions of protein spots that are newly present or more than three fold increased in spot intensity, both in 10% PEG pellet and supernatant fractions compared to total protein.

Fig. S2. Silver-stained 2-DE gels of microsomal protein and Rubisco-depleted microsomal protein. (A) microsomal protein, (B) 10% PEG pellet, (C) 20% PEG pellet, (D) 20% PEG supernatant. The circled area indicates the location of Rubisco. The crosses in Gel A indicate the positions of protein spots that are newly present or more than three fold increased in spot intensity, both in 10% PEG pellet and supernatant fractions compared to microsomal protein.

Fig. S3. Silver-stained 2-DE gels from Rubisco depletion using Seppro® IgY Rubisco Spin Column. Proteins that bound to the IgY columns (A) and the flow through fraction (B) were analyzed by 2-DE. (C) An overlay image between the Flow Through from Seppro® IgY Rubisco Spin Column (Blue) and supernatant from 20% PEG supernatant fraction (Orange, cf. Fig. S1D). Note that the many orange spots indicate protein spots that were not visible before fractionation.

Table S1. Summary of MALDI-TOF ID of the candidate proteins.

Table S2. Summary of nano-LC-MS² analysis of Remorin isoforms.