Table S1. Identification of the proteins contaminating the ATPS-purified sample[1].

Band [2]	Accession number	Protein name	Size (kDa)
1	gi|384038819	chloroplast PsbO4 precursor	35.4
2	gi|61697113	chloroplast photosynthetic oxygen-evolving protein 23 kDa subunit	28.3
3	gi|511774224	2-Cys peroxiredoxin	25.5
4	gi|58700507	chloroplast oxygen-evolving protein 16 kDa subunit	24.2
5	gi|343174748	pathogenesis-related protein 1	17.7

[1]Method: The acquired spectra were analyzed using the Applied Biosystems GPS Explorer (version 3.6) and the Matrix Science MASCOT algorithm in the NCBI *N. benthamiana* database and the NCBI *N. benthamiana* EST database, as described in Duby et al. (2010).

Reverse phase separation of peptides was completed on an Ultimate 3000 chromatography chain (ThermoFisher Scientific) using a C18 PepMap 100 analytical column (150 mm, 3 µm i.d., 100 Å), (ThermoFisher Scientific). Previously the sample was dissolved in 0.025% (v/v) TFA and 5% (v/v) ACN and desalted using a C18 Pep Map 100 pre-column (10 mm, 5 µm i.d., 100 Å). Peptides were backflushed onto the analytical column with a flow rate of 300 nL/min by a 180 min linear gradient from 8 to 76% (v/v) ACN in water containing 0.1% (v/v) TFA in buffer A and 0.085% (v/v) TFA in buffer B.

The eluted peptides were mixed with a-cyano-4-hydrocinnamic acid (4 mg/mL in 70% ACN/0.1% TFA) and spotted directly onto a MALDI target using a Probot system (ThermoFisher Scientific).

[2]The band numbers correspond to those annotated in Figure 5.