**C:\Users\hornette\Desktop\Bild100.tif**

**Figure S4. Section of the protein alignment for PDS from *Oryza sativa* and cyanobacteria, algae and plants with reported mutations conferring NFZ resistance.**

The following residues are highlighted: 1, Phe162; 2, Arg300; 3, Tyr506; 4, Thr508 5, Leu538. Global sequence alignment was carried out with the Blosum62 matrix. Identical residues are green, similar residues greenish or yellow. Position numbering refers to the immature protein from *O. sativa* (A2XDA1.2) including its N-terminal 87 amino acid transit peptide. Organisms and accession numbers (from top to bottom): *Oryza sativa*, A2XDA1.2; *Arabidopsis thaliana*, Q07356.1; *Chlorella zofingiensis*, ABR20878.1; *Hydrilla verticillata*, AAT76434.1; *Synechococcus elongatus* PCC 7942, CAA39004.1; *Synechocystis sp.* PCC6803, CAA44452.1.