

Supporting Information for

**Biochemical insight into redox regulation of plastidial 3-phosphoglycerate dehydrogenase
from *Arabidopsis thaliana***

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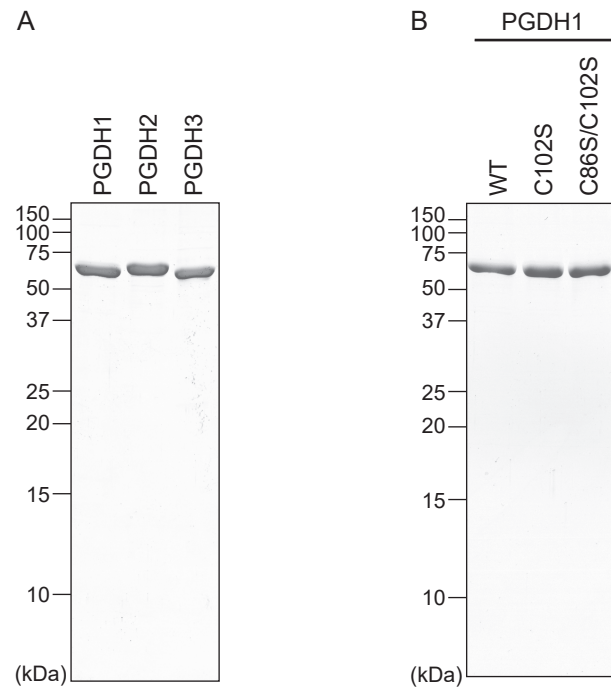


Figure S1. The SDS-PAGE profiles of *Arabidopsis* PGDH used in this study. Equal amounts of the proteins (1 μ g each) were loaded into each lane. (A) PGDH1, PGDH2, and PGDH3. (B) PGDH1 wild type (WT) and Cys-substituted mutants (C102S and C86S/C102S).

Organism	Accession	Sequence
A. thaliana	PGDH1	-----MSA TAAASSIAV ATR-----
	PGDH2	-----MAF SSSSCSVAV NSWTSPPSPS
O. sativa	XP_015650533	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_015634449	-----MAF SSSSCSVAV NSWTSPPSPS
N. tabacum	XP_016448968	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_016445835	-----MAF SSSSCSVAV NSWTSPPSPS
S. oleracea	XP_021860405	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_021839839	-----MAF SSSSCSVAV NSWTSPPSPS
P. trichocarpa	XP_002313870	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_024381540	-----MAF SSSSCSVAV NSWTSPPSPS
P. patens	XP_024389046	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_024381029	-----MAF SSSSCSVAV NSWTSPPSPS
M. polymorpha	XP_024377615	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_024381029	-----MAF SSSSCSVAV NSWTSPPSPS
V. carteri	XP_002950373	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
C. reinhardtii	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
Anabaena 7108	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
S. elongatus 7942	XP_001694402	-----MAF SSSSCSVAV NSWTSPPSPS
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Figure S2. Alignment of PGDH amino acid sequences in photosynthetic organisms. PGDH from *Arabidopsis thaliana*, *Oryza sativa*, *Nicotiana tabacum*, *Spinacia oleracea*, *Populus trichocarpa*, *Physcomitrella patens*, *Marchantia polymorpha*, *Volvox carteri*, *Chlamydomonas reinhardtii*, *Anabaena* sp. PCC 7108, *Synechococcus elongatus* sp. PCC 7942, and *Synechocystis* sp. PCC 6803 are shown. An arrow indicates the predicted cleaved site of the transit peptide. Asterisks indicate the redox-active Cys residues revealed in this study.

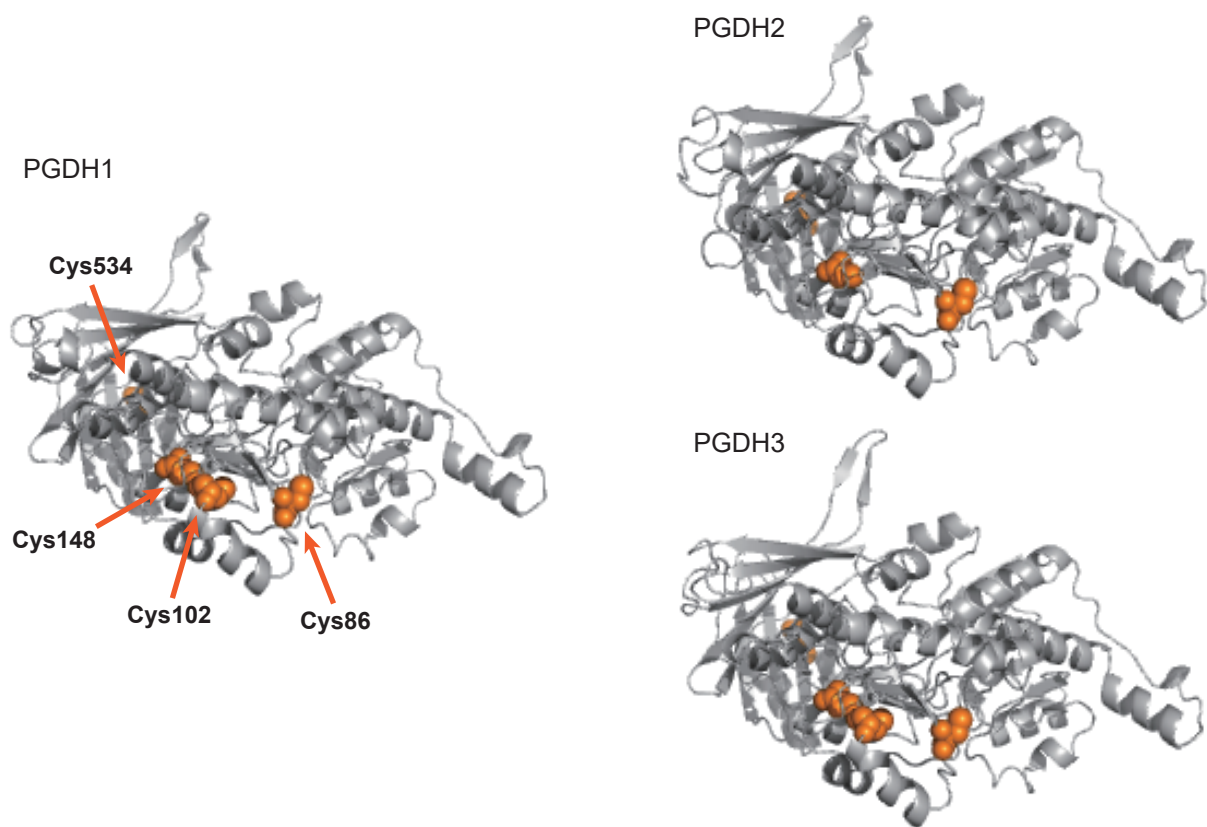


Figure S3. Three-dimensional structure model of *Arabidopsis* PGDH. The model was obtained as a homotetrameric form, but one chain is shown. For PGDH1, four Cys residues are shown by the orange spheres. For PGDH2 and PGDH3, only Cys residues common to PGDH1 are shown in the same way.

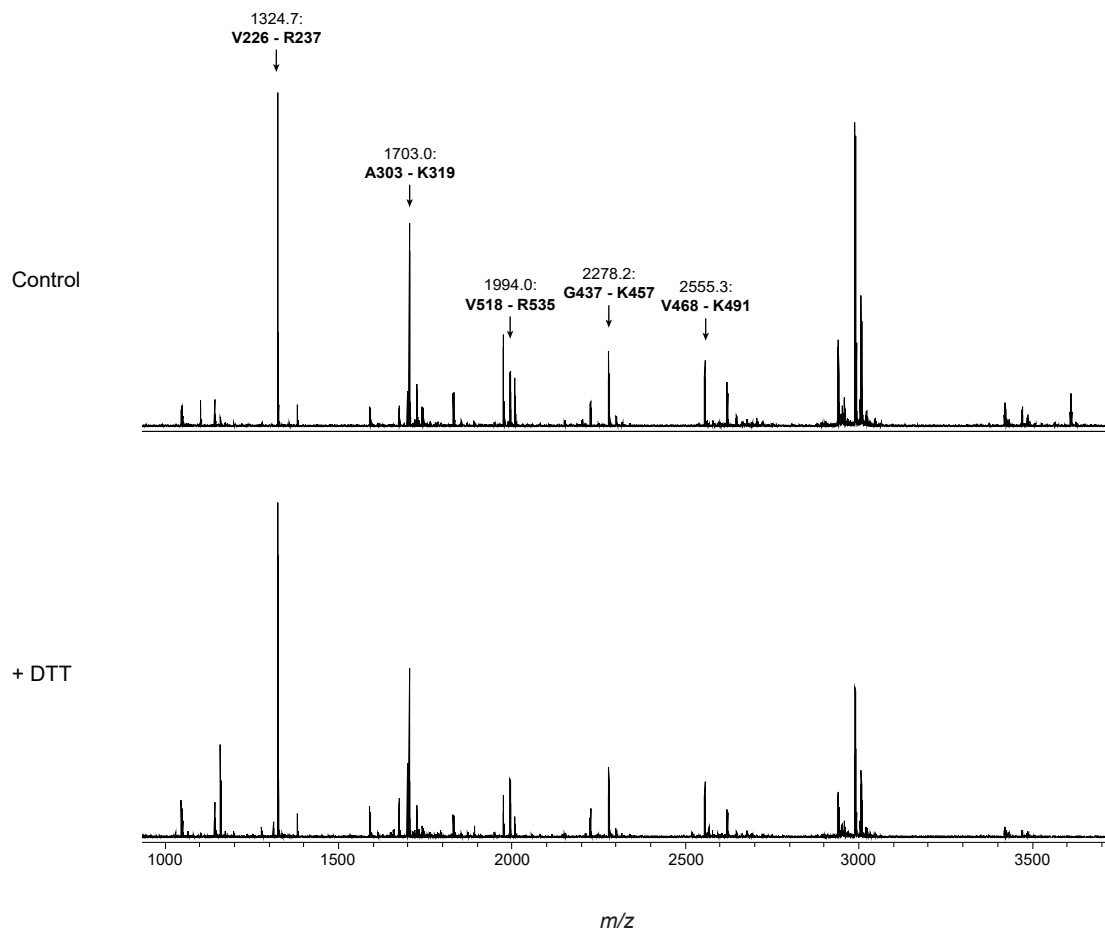


Figure S4. Overall mass spectra of PGDH1 tryptic peptides. Before the Cys alkylation and following in-gel digestion with trypsin, the protein sample was incubated in the absence (control) or presence of 10 mM DTT. The masses of several major peaks are shown with the corresponding peptides.

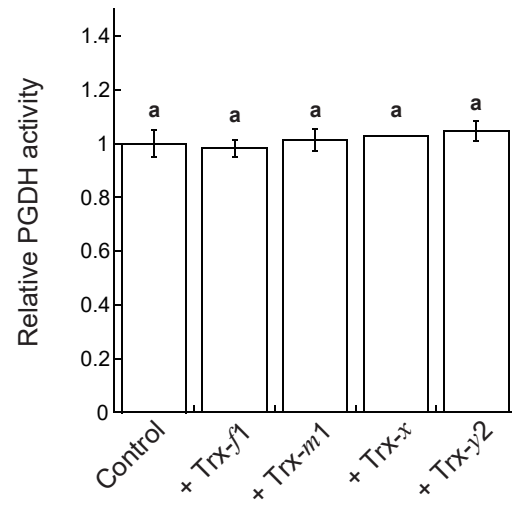


Figure S5. Enzyme activity measurement of PGDH1. PGDH1 (1.2 μM) was incubated with Trx-f1, Trx-m1, Trx-x, or Trx-y2 (0.1 μM each) in the absence of DTT for 30 min. PGDH1 activity was then monitored. Each activity is expressed as the relative value. Data are shown as the mean \pm SD ($n = 3-4$). Statistical analyses were performed using the Tukey-Kramer multiple comparison test, but significant difference was not observed (denoted as same letters, $P > 0.05$).

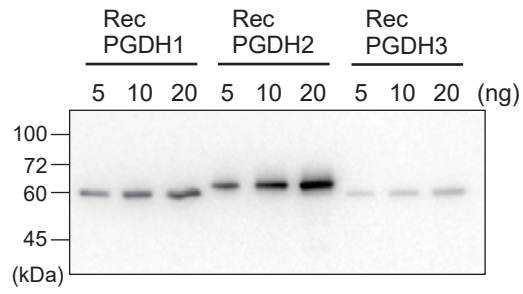


Figure S6. Specificity of PGDH antibody. The indicated amount of recombinant PGDH1, PGDH2, or PGDH3 protein was subjected to SDS-PAGE, followed by immunoblotting analysis using a PGDH antibody.