Title: Differential regulation of monodehydroascorbate reductase (MDAR) and glutathione reductase (GR) by nitration and *S*-nitrosylation

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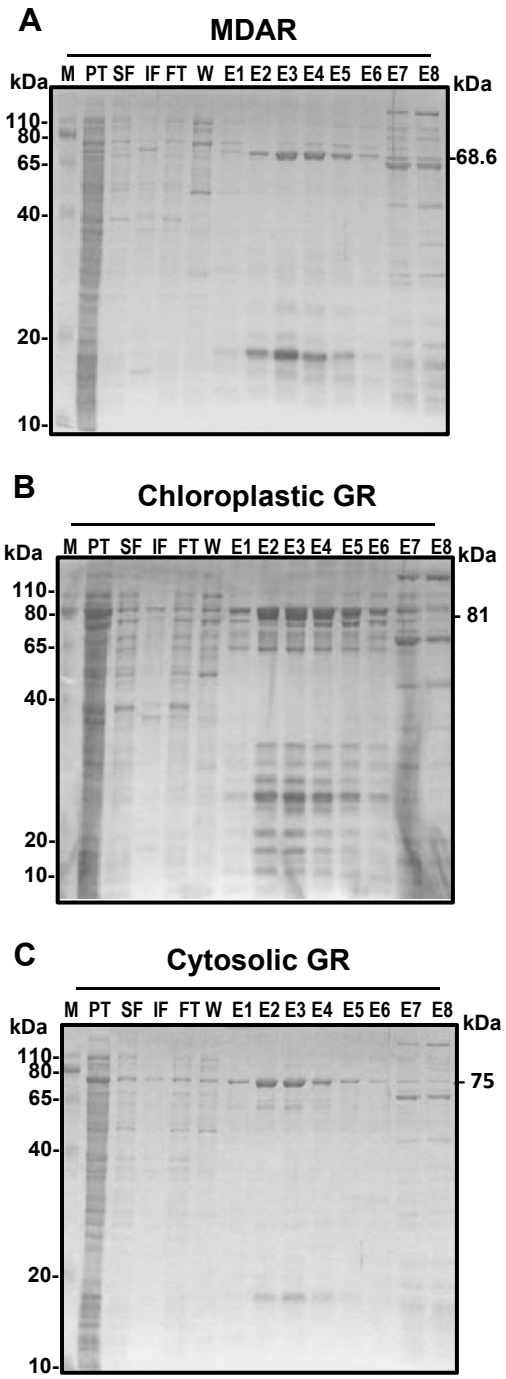
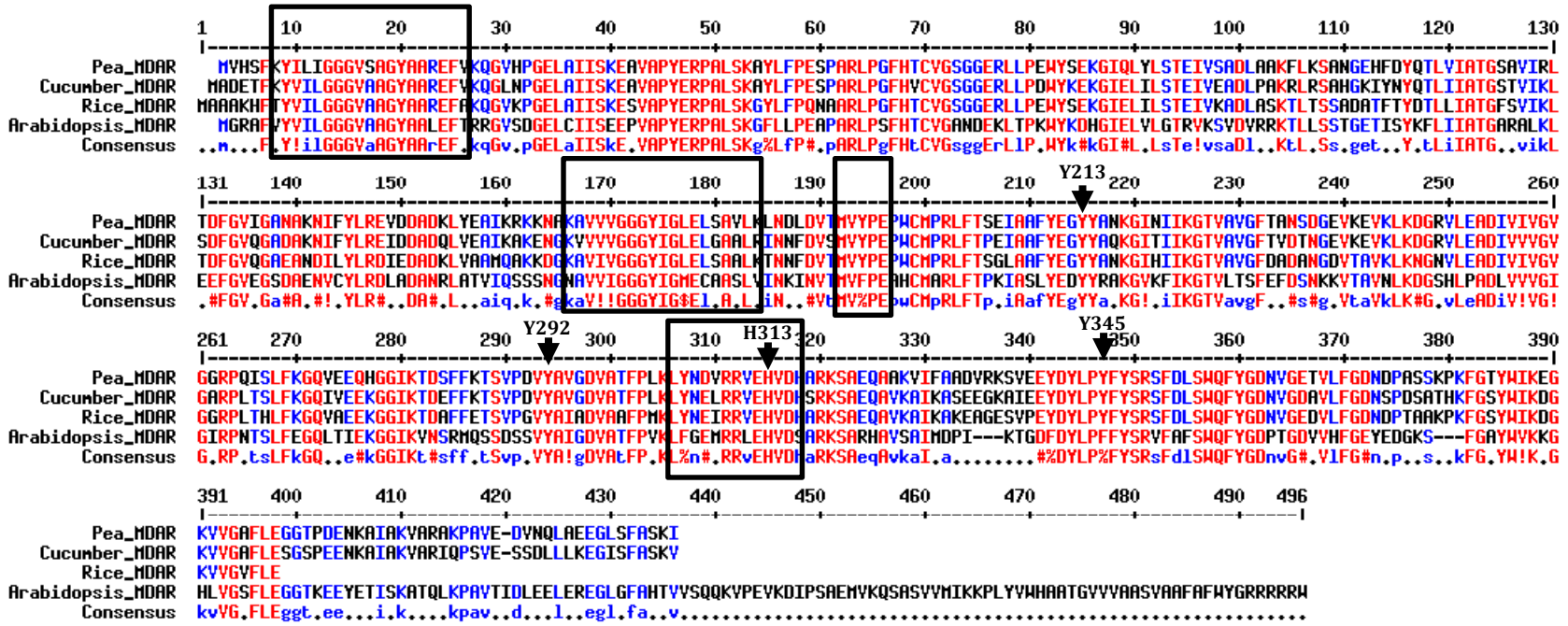
Supplemental Table 1. Characterization in terms of evolutionary conservation (rho score and residue variation in the column of the multiple alignment file), likelihood of tyrosine phosphorylation (phosphorylation score), solvent-accessible surface area (ASA) and estimated pKa of the 3 tyrosine (Y) and 2 cys (C) residues susceptible of being responsible for the modulation of the enzymatic activity of pea MDAR by peroxynitrite and GSNO

Residue	Rho	Variability	NetPhos score	ASA(Å^2)	pKa
Tyr213	3.51	YF	0.564	71	11.13
Tyr292	1.0	Y	0.402	32	9.95
Tyr345	7.14	FY.C	0.040	104	11.99
Cys68	2.58	CA		61	9.09
Cys197	5.04	LFCI		5	13.17



Supplemental Figure 1. SDS-PAGE analysis of the purification of the recombinant proteins. (A) Peroxisomal monodehydroascorbate reductase (MDAR). **(B)** Chloroplastic glutathione reductase. **(C)** Cytosolic glutathione reductase. The gel was stained with Coomasie blue. M, molecular markers; PT, total protein; SF, soluble fraction; IF, insoluble fraction; FT, flow-through; W, wash; E1-E8, elution fractions.



Supplemental Figure 2. Multiple alignment of the deduced amino acid sequences of MDAR in different plant species. Nucleotide binding zones are highlighted within a box. Arrows indicate tyrosines targets of nitration (Y213, Y292 and Y345) and Histidine 313. Alignment was carried out using Multalin (http://multalin.toulouse.inra.fr/multalin/). Pea_MDAR: MDAR from *Pisum sativum* (AAV11490.1); Cucumber_MDAR: MDAR from *Cucumbis sativa* (BAA05408.1); Rice_MDAR: MDAR from *Oryza sativa* (BAA77282.1); Arabidopsis_MDAR: MDAR from *Arabidopsis thaliana* (AEE77367.1).