

Supplementary Files:

Figure S1. Schematic representation of the Substrate Recognition Loop in AtTRXh1, HvTRXh1, PtTRXh1, PtTRXh4, AtTRXo1, AtTRXo2, and SoTRXm. The active site motifs are highlighted in black whereas the cis-Pro and Gly loops are highlighted in gray with conserved and non-conserved residues indicated in cyan and white, respectively. The size of the strings is not proportional to the length in amino acids.

Figure S2. Far-UV CD spectra of reduced and oxidized CrTRXh1 in Tris-HCl buffer (30 mM; pH 7.9).

Figure S3. MALDI-TOF MS analysis of CrTRXh1 after IAM-dependent alkylation. The pre-reduced CrTRXh1 was incubated with 10-fold excess of IAM at pH 5.0, 7.0, and 9.0. At indicated time, an aliquot was withdrawn and subjected to MS analysis as indicated in «Material and Methods».

Figure S4. Kinetic of alkylation of CysN and CysC from CrTRXh1. The pre-reduced CrTRXh1 was incubated with 2-fold **(a)** or 10-fold **(b)** excess of IAM and analyzed by MS. Linear plots are indicative of the reduced (closed circles) or monoalkylated (open circles) state of the protein. Data are reported as mean of three replicates. **(c)** Logarithmic plot of data reported in panel (a) and (b).

Table S1. Interface interactions including salt bridges and hydrogen bonds in the reduced and oxidized CrTRX *h1* (cut-off distance 4.5 Å).

Figure S1

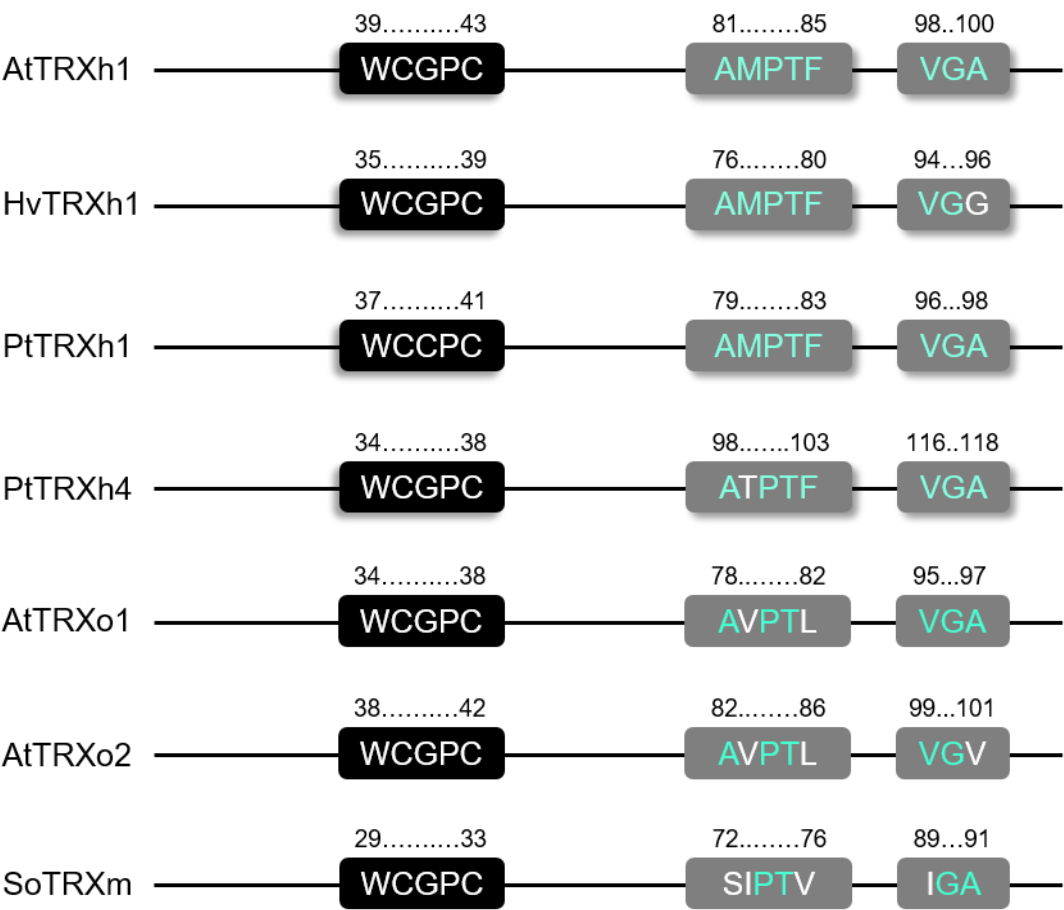


Figure S2

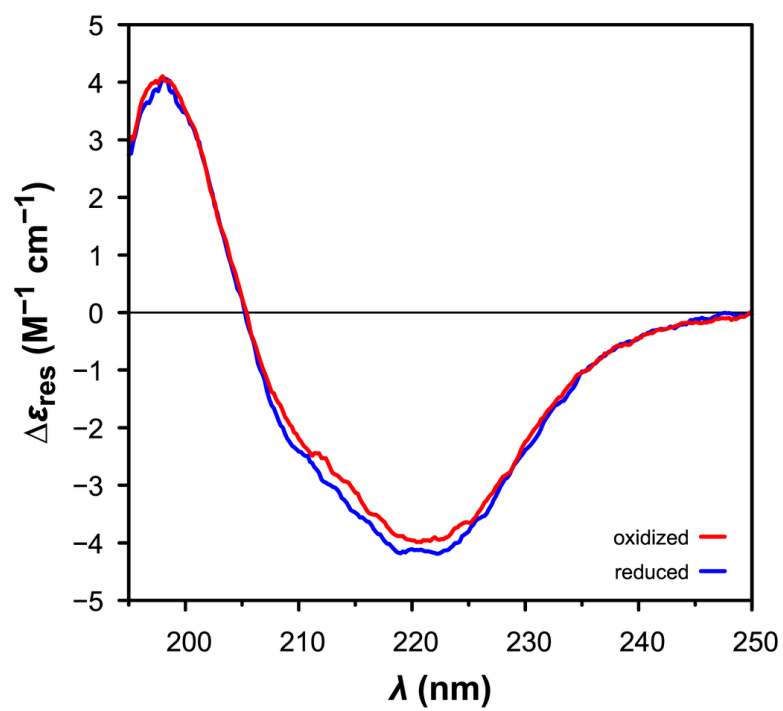


Figure S2.

Figure S3

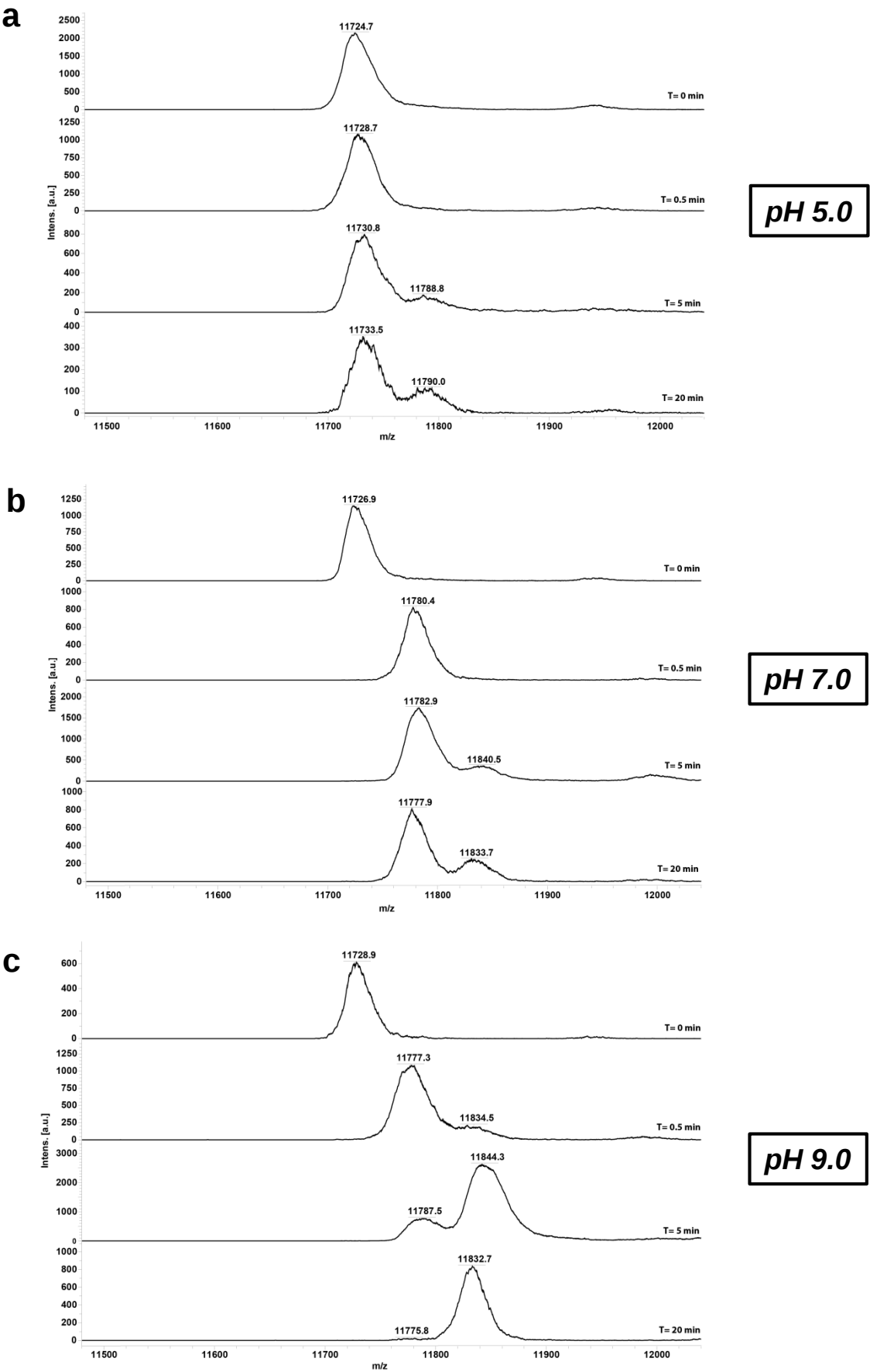


Figure S4

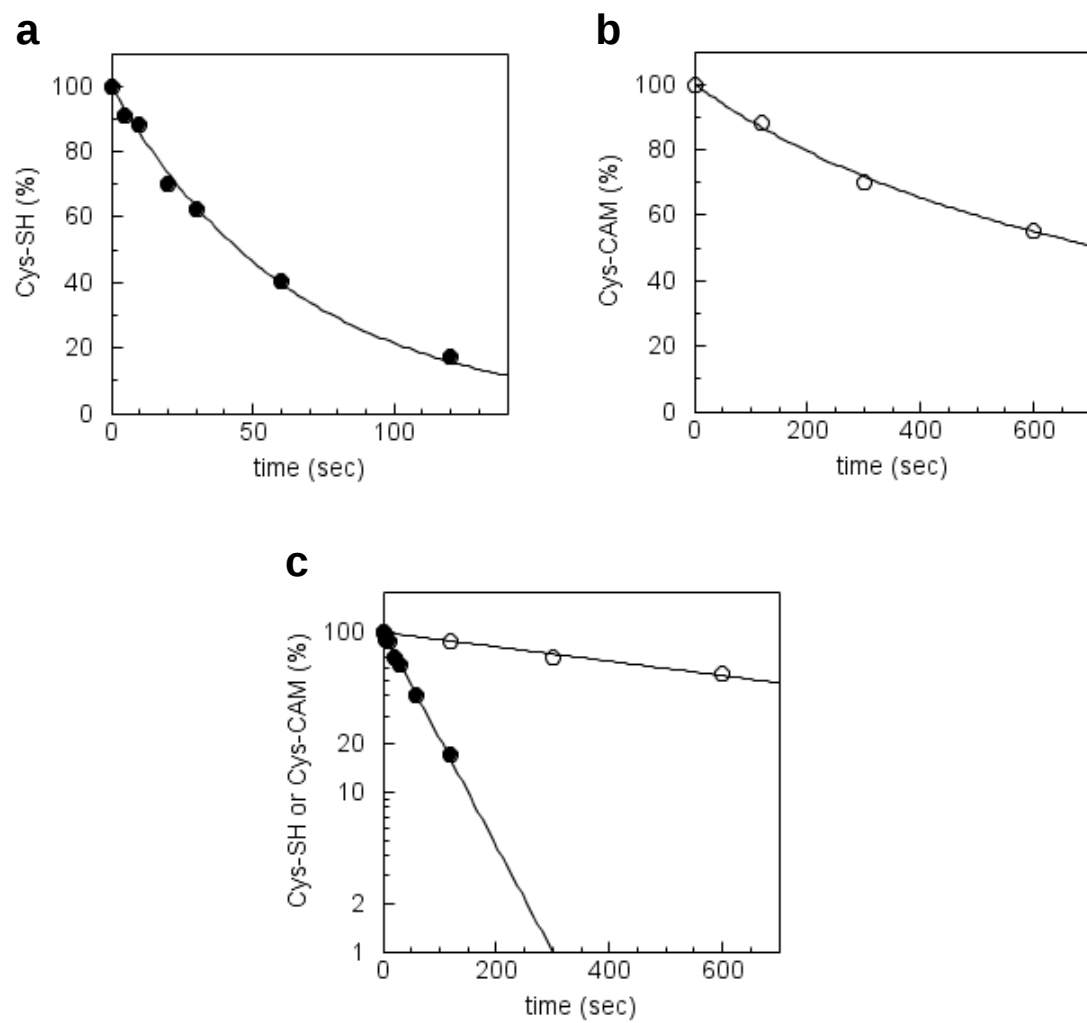


Table S1

Chains		Distance (Å)	
A (atom)	B (atom)	Oxidized	Reduced
Lys40 (NZ)	Glu72 (OE1)	3.5	3.4
Glu72 (OE1)	Lys40 (NZ)	2.5	/
Met79 (N)	Thr77 (O)	2.8	3.0
Thr77 (O)	Met79 (N)	2.9	2.9
Trp35 (NE1)	Val64 (O)	3.6	3.4
Trp35 (NE1)	Asp65 (OD1)	2.9	3.2
Val64 (O)	Trp35 (NE1)	4.0	4.0
Asp65 (OD1)	Trp35 (NE1)	/	4.0