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Dissecting Molecular Interactions Involved in Recognition of Target Disulfides by the barley Thioredoxin System

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Supporting Information

ABSTRACT: Thioredoxin reduces disulfide bonds, thus regulating activities of target proteins in various biological systems, e.g., inactivation of inhibitors of starch hydrolases and proteases in germinating plant seeds. In the three-dimensional structure of a complex with barley α-amylase/subtilisin inhibitor (BASI), two loops in barley thioredoxin h2 (HvTrxh2), containing an invariant cis-proline (86EAMP89) and a conserved glycine (104VGA106), surround the active site cysteines (45WCGPC49) and contribute to binding of BASI through backbone–backbone hydrogen bonds [Maeda, K., Hägglund, P., Finnie, C., Svensson, B., and Henriksen, A. (2006) Structure 14, 1701–1710]. This study involves mutational analysis of key amino acid residues from these two loops in reactions with three protein disulfide substrates, BASI, barley glutathione peroxidase, and bovine insulin as well as with NADPH-dependent barley thioredoxin reductase. HvTrxh2 M88G and M88A adjacent to the invariant cis-proline lost efficiency in both BASI disulfide reduction and recycling by thioredoxin reductase. These effects were further pronounced in M88P lacking a backbone NH group. Remarkably, HvTrxh2 E86R in the same loop displayed overall retained catalytic properties, with the exception of a 3-fold increased activity toward BASI. From the 104VGA106 loop, a backbone hydrogen bond donated by A106 appears to be important for target disulfide recognition as A106P lost 90% activity toward BASI but was efficiently recycled by thioredoxin reductase. The findings support important roles in target recognition of backbone–backbone hydrogen bond and electrostatic interactions and are discussed in relation to earlier structural and functional studies of thioredoxins and related proteins.

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and with the proteins arsenate reductase and 3′-phosphoadenosine-5′-phosphosulphate (PAPS) reductase. In the recently determined structure of yeast Trx2 in complex with methionine sulfoxide reductase, the similarity is striking as three fully analogous antiparallel backbone—backbone hydrogen bonds are found. The interactions in the HvTrxh2–BASI complex therefore appear to be characteristic of disulfide target recognition by Trxs.

The barley Trx system is here used as a model to study the molecular interactions involved in target disulfide recognition. A comparison of the detailed characteristic of the interactions at the proteins interfaces observed in the structures of the HvTrxh2–BASI complex and EcTrx1 linked to E. coli NTR (EcNTR) and PAPS reductase, respectively (Table 2), motivated the mutational analysis of the functional roles of HvTrxh2 E86, M88, and A106 in reactions with three targets proteins, BASI, barley glutathione peroxidase, and bovine insulin, and with barley NTR (HvNTR2). The importance of backbone hydrogen bonds between Trx and target proteins was probed by mutational elimination of backbone amide hydrogens in HvTrxh2 M88P and A106P. Notably, while the M88P mutant was deficient in all assays performed, A106P showed reduced activity toward BASI and no loss of HvNTR2-mediated recycling. Engineering a hypothesized electrostatic attraction between E86R\textsubscript{HvTrxh2} and E168\textsubscript{BASI} conferred a remarkable activity increase toward BASI.

### EXPERIMENTAL PROCEDURES

**Site-Directed Mutagenesis.** HvTrxh2 E86R, M88G, M88A, M88P, M88L, A106G, A106S, A106P, and A106Y were generated using Quikchange (Stratagene) and the HvTrxh2 gene cloned in pET-15b (Novagen), providing an N-terminal His tag and thrombin cleavage site, as a template. For mutagenesis primers, see Table S1 of the Supporting Information. Mutagenesis was confirmed by bidirectional DNA sequencing, and plasmids were transformed into E. coli Rosetta DE3 cells (Novagen) for expression.

**Protein Production and Quantification.** Wild-type (wt) HvTrxh2 and mutants, BASI, and HvNTR2 were produced as described, purified (His-Trap HP column, GE Healthcare), dialyzed against 30 mM Tris-HCl (pH 8.0), concentrated (Amicon Ultra Centrifugal Filter Device, Millipore), and further purified by gel filtration (HiLoad 26/60 Superdex 75 column, GE Healthcare) in 30 mM Tris-HCl (pH 8.0) and 0.2 M NaCl. Eluted proteins were dialyzed against 30 mM Tris-HCl (pH 8.0), concentrated as described above, and stored at −80 °C. All proteins migrated as single bands via sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE). EcTrx1 and EcNTR were obtained by the same procedure using expression plasmids with the corresponding genes inserted in pET14a and pET15b, respectively, purchased from Eurofins MWG Operon (Ebersberg, Germany).

BASI C144S was conjugated with 2-nitro-5-thiobenzoate (TNB) as reported previously. Yields were 10–20 mg of wt and mutant proteins obtained from 1 L of bacterial culture, except that HvTrxh2 M88G was obtained in 10-fold smaller amounts. Protein production and quantification.

| Table 1. Sequence Alignment of Trxs with Respect to the Substrate Recognition Loop Motif |

<table>
<thead>
<tr>
<th>PDB</th>
<th>45–49</th>
<th>86–89</th>
<th>104–106</th>
</tr>
</thead>
<tbody>
<tr>
<td>HvTrxh2</td>
<td>2VLL</td>
<td>WCGPC</td>
<td>EAMPF</td>
</tr>
<tr>
<td>HvTrxh1</td>
<td>2VM2</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td>AtTrxh1</td>
<td>1XFL</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td>PtTrxh1</td>
<td>1T13</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td>HsTrx1</td>
<td>3TRX</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td>ScTrx1</td>
<td>3F3Q</td>
<td>------</td>
<td>------</td>
</tr>
<tr>
<td>EcTrx1</td>
<td>1SRX</td>
<td>------</td>
<td>------</td>
</tr>
</tbody>
</table>

“Seven selected Trxs with known three-dimensional structures were aligned according to the substrate recognition loop motif in HvTrxh2 as defined in the complex with BASI. The two loops EAMP and VGE are named the cis-proline and glycine loop, respectively, after the invariant residues (italics). Mutagenized residues in HvTrxh2 are underlined, and sequence identities are marked (−) to six other Trxs from Hordeum vulgare (barley) (Hv), Arabidopsis thaliana (At), Populus trichocarpa (Pt), Homo sapiens (Hs), Saccharomyces cerevisiae (Sc), and E. coli (Ec). Residue numbering for HvTrxh2 and EcTrx1 is shown above and the sequences, respectively.

Intermolecular backbone—backbone hydrogen bond is seen between A106\textsubscript{HvTrxh2} NH and D146\textsubscript{BASI} O (Figure 1). A106 follows an invariant glycine residue found in Trxs and glutaredoxins in the loop between β5 and α4, here termed the glycine loop (Table 1). A106 is well-conserved among Trxs of diverse origin, although HvTrxh1 noticeably has glycine at this position (Table 1). Hydrogen bonding patterns similar to those of the HvTrxh2–BASI complex are found in disulfide-bonded complexes between Trx and short synthetic peptide fragments derived from transcription factors NF-κB and ref-1.
### Table 2. Pairs of Atoms Forming Intermolecular Contacts in Three Trx Complexes

<table>
<thead>
<tr>
<th>HvTrxh2–BASI (PDB entry 2IWT)</th>
<th>EcTrx1–PAPS reductase (PDB entry 208V)</th>
<th>EcTrx1–NTR (PDB entry 1F6M)</th>
</tr>
</thead>
<tbody>
<tr>
<td>HvTrxh2</td>
<td>EcTrx1</td>
<td>EcTrx1</td>
</tr>
<tr>
<td>M88 N</td>
<td>175 O</td>
<td>175 N</td>
</tr>
<tr>
<td>M88 O</td>
<td>148 O</td>
<td>1239 N</td>
</tr>
<tr>
<td>A106 N</td>
<td>149 O</td>
<td>139 O</td>
</tr>
<tr>
<td>E86 CB, CD</td>
<td>R73 NH1</td>
<td>R73 N</td>
</tr>
<tr>
<td>E86 CB, CD</td>
<td>R73 NE</td>
<td>R73 NE</td>
</tr>
<tr>
<td></td>
<td>R73 NH2</td>
<td>R73 NH2</td>
</tr>
<tr>
<td></td>
<td>R73 NH2†</td>
<td>R73 NH2</td>
</tr>
</tbody>
</table>

*Unless stated otherwise, the contacts represent hydrogen bond interactions in the HvTrxh2–BASI, EcTrx1–PAPS reductase, and EcTrx1–NTR complexes involving residues corresponding to HvTrxh2 E86, M88, and A106. The information about hydrogen bonds and hydrophobic contacts was obtained from the Protein Data Bank and processed with the tool sum (http://www.ebi.ac.uk/thornton-srv/databases/pdbsum/). For a three-dimensional image of the three H-bonds in the HvTrxh2–BASI complex, see Figure 3B of ref 7. In the structure of the EcTrx1–NTR complex containing four pairs of Trx–NTR chains, hydrogen bonds refer to interactions between chains A–C and E–G. Between chains B–D and F–H, there are some deviations that involve the side chain of R73<sub>E<sub>E</sub>T<sub>Trxh2</sub></sub>—van der Waals contacts.*

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**Spectrophotometric Assays of HvTrxh2 Mutants.** In assays toward BASI, HvNTR2, and HvGpx2, activity was determined as the (turnover) number of disulﬁdes reduced per second per molecule of Trx. In assays of activity toward BASI and HvGpx2, the consumption of NADPH was recorded using 0.2 μM HvNTR2, found to be saturating. To obtain the background levels, NADPH1 consumption (ε<sub>340</sub> = 6200 M<sup>−1</sup> cm<sup>−1</sup>) or, in NTR assays, release of the TNB anion (ε<sub>412</sub> = 13600 M<sup>−1</sup> cm<sup>−1</sup>) was monitored in the absence of Trx for 5 min. At least 45 s was used for evaluation of reduction rates in BASI and NTR assays. Activity toward BASI (final concentrations of 50 and 100 μM) was measured using 0.2 mM NADPH in 0.1 M Tris-HCl (pH 7.5), 2 mM EDTA, and 2.0 μM Trx (except 26 ± 10 μM for mutant M88P of very low activity) in a 100 μL quartz cuvette, in at least duplicate. Disulﬁde reduction activities were linearly proportional to concentrations of both BASI and Trx and reported as second-order rate constants (M<sup>−1</sup> s<sup>−1</sup>). Mutants were screened for deficient recycling by HvNTR2 (0.1 μM) in 0.1 M Tris-HCl (pH 7.5), 2 mM EDTA, and 0.2 mM NADPH, including BSA (0.1 mg/mL) and using 0.2 mM 5,5'-dithiobis(nitrobenzoic acid) (DTNB) as final electron acceptor (1 mM plastic cuvettes) the formation of TNB anion above a background level of 0.005 ΔA<sub>412</sub> min<sup>−1</sup> in the absence of Trx. At a minimum, triplicate experiments were performed. To determine k<sub>cat</sub> for HvNTR2 and k<sub>cat</sub> for Trx as the substrate, 50 nM HvNTR2 was used with 0.25–10 μM Trx in 0.1 M potassium phosphate (pH 7.5), 2 mM EDTA, BSA (0.1 mg/mL), 0.2 mM NADPH, and 0.2 mM DTNB. The Michaelis–Menten equation was fit to the data (Kaleidagraph, Synergy Software, Reading, PA). Activity against HvGpx2 was assayed (100 μL microtiter plate format) for 25 min with (subsaturation) 1.0 μM Trx (15 μM HvTrxh2 M88P) using 0.2 μM HvNTR2, 0.2 μM HvGpx2, and 0.2 mM NADPH in 0.1 M potassium phosphate (pH 7.5), 2 mM EDTA, and 0.1 mg/mL BSA. Reactions were initiated by addition of tert-butyl peroxide to a final concentration of 1.0 mM; three independent duplicate assays were performed. Controls with and without wt HvTrxh2 were included in each microtiter plate. Under these conditions, the turnover number of wt HvTrxh2 (0.045 s<sup>−1</sup>) was defined as 100% activity. An assay for reduction of disulﬁde bonds in bovine insulin was adapted to the microtiter plate format and performed essentially as described previously.27 The reaction was initiated by adding DTT (final concentration of 0.33 mM) to 1.0 μM Trx and 1 mg/mL bovine insulin in 100 mM potassium phosphate (pH 7.0), 0.2 mM EDTA (250 μL). Turbidity was monitored at 650 nm, and the rate of absorbance change in the interval of 0.1–0.2 absorbance unit was determined. The values obtained were compared to a standard curve of the rates from 0.2 to 1.0 μM wt HvTrxh2 (Figure S1 of the Supporting Information).

**DTT Reduction Kinetics.** Assumed pseudo-first-order reaction mixtures of Trx (7 μM) and DTT (100 μM) in reaction buffer [0.1 mM sodium phosphate and 0.2 mM EDTA (pH 7.0)] were incubated at room temperature. Reactions (188 μL) were quenched at appropriate time points with 40% acetic acid (from 38 to 54%) in 0.1% trifluoroacetic acid. Their relative amounts were obtained from the peak areas at 215 nm after integration with Chromeleon (Dionex). Reduced and oxidized proteins were separated by a gradient of acetonitrile (from 38 to 54%) in 0.1% trifluoroacetic acid. Their relative amounts were obtained from the peak areas at 215 nm after integration with Chromeleon (Dionex).

**Circular Dichroism Spectroscopy.** Trx (10 μM) was dialyzed against 20 mM sodium phosphate (pH 7.0) (Slide-A-Lyzer cassettes, Pierce). CD spectra were recorded (Jasco J-600 CD spectrometer) at 25 °C using a 1.0 mm quartz cuvette (300 μL). Five scans from 250 to 190 nm were recorded per sample, and resulting spectra were smoothed and corrected for buffer blank.

**Complete Reduction of Trx.** Trx was reduced by 10 mM DTT in 1 mM EDTA for at least 30 min in the dark. Excess DTT was removed by gel filtration (NAP-5 column, GE Healthcare) using argon-purged reaction buffer [0.1 mM sodium phosphate and 0.2 mM EDTA (pH 7.0)], and the samples were stored on ice, protected from light, and used within the same day. The SH:Trx molar ratio was confirmed (2.0 ± 0.2) using 0.2 mM DTNB with 0.2 mM cystamine as a mediator in 3.0 M guanidine HCl and 0.1 M Tris-HCl (pH 8.0).29

**Determination of the HvTrxh2 M88P Redox Potential (E'<sup>°</sup>) by Equilibrium with EcTrx1.** Using equilibrium reactions with the NADPH/NADP<sup>+</sup> couple catalyzed by EcNTR, we first verified that the redox potential of the Histagged version of EcTrx1 was −270 ± 1 mV. This “classical method” was performed according to Krause et al.,<sup>30</sup> employing the reaction buffer as stated above. EcTrx1 was then used as the reference protein in direct protein–protein equilibrium (in reaction buffer) with HvTrxh2 M88P according to the method developed by Åslund et al.<sup>31</sup> The redox reaction (in 100 μL) was initiated by mixing one protein in the reduced state with 27.
the other protein in its oxidized state in a 1:1 ratio at ~50 μM (and vice versa). The reaction mixture was allowed to equilibrate overnight (16 h) before the reaction was quenched by phosphoric acid (0.67 M, 100 μL) to a final pH of ~2.0, and the mixture (150 μL) was loaded onto the C18 RP-HPLC column, equilibrated in 5% (v/v) acetonitrile and 0.1% (v/v) trifluoroacetic acid. The four protein species were eluted by a gradient of acetonitrile (from 40.5 to 62%) in 0.1% (v/v) trifluoroacetic acid over 25 min at a flow rate of 1 mL/min. The equilibrium constant was calculated in the direction of the reference being reduced (eq 1).

\[
K = \frac{[M88P]_{ox}[EcTrx_{red}]}{[M88P]_{red}[EcTrx_{ox}]} \tag{1}
\]

To gauge the loss of reducing equivalents to molecular oxygen during the aerobic incubation, samples with reduced protein only were included as controls.

**Reduction of BASI Visualized by PEG Maleimide Incorporation.** TMM(PEG)\(_{12}\) (Thermo Scientific), an ethylmaleimide derivative linked to a trimethylated branched polyethylene glycol of 2.4 kDa (apparent shift in SDS–PAGE of >2.4 kDa), was used to label thiol groups. BASI and reduced M88H\(_{\text{HvTrxh2}}\) O and A106 HvTrxh2 NH, respectively, in the HvTrxh2 NTR complex, where I75 EcTrx1 NH forms bonds involving I75 EcTrx1 O and A93 EcTrx1 NH, corresponding to the so-called "substrate recognition loop motif" in HvTrxh2 and are both diluted to 20 μL. Incorporation of TMM(PEG)\(_{12}\) an ethylmaleimide derivative linked to a trimethylated branched polyethylene glycol of 2.4 kDa (apparent shift in SDS–PAGE of >2.4 kDa), was used to label thiol groups. BASI and reduced Trx (or DTT) was added in a 2-fold molar excess over BASI C144S-TNB (24 and 12 μM), and aliquots (20 μL) removed at appropriate intervals were reacted with TMM(PEG)\(_{12}\) (5 μL) to a final concentration of 1 mM. After 2 h, the remaining TMM(PEG)\(_{12}\) was quenched by 50 mM DTT. The samples were diluted in SDS sample buffer, and 2 μg of BASI was loaded in each lane for SDS–PAGE.

**Reduction of BASI C144S-TNB.** BASI C144S-TNB was diluted in reaction buffer (100 μL quartz cuvette), and the baseline absorbance at 412 nm was recorded for 30 s at room temperature. Reduced Trx (or DTT) was added in a 2-fold molar excess over BASI C144S-TNB (24 and 12 μM), and the reaction (100 μL) was monitored at 10 s intervals. To obtain second-order reaction rate constants, the progress curve was linearly fit by Microsoft Excel to eq 2.

\[
k_t = \frac{1}{[\text{Trx}]_0 - [\text{BASI}^*]_0} \ln \frac{[\text{Trx}][\text{BASI}^*]_0}{[\text{BASI}^*][\text{Trx}]_0} \tag{2}
\]

BASI* denotes the TNB activated form, BASI C144S-TNB.

**RESULTS**

**Comparison of Intermolecular Contacts in Structures of Trx Complexes.** Interacting atoms involving residues corresponding to the so-called "substrate recognition loop motif" in HvTrxh2 are compared in two Trx–target complexes, HvTrxh2–BASI and EcTrx1–PAPS reductase, and the EcTrx1–NTR complex (Figure 1 and Table 2). It should be noted that the EcTrx1–PAPS reductase and EcTrx1–NTR complexes have three and two additional hydrogen bond interactions, respectively (not included in Table 2). In comparison, the HvTrxh2–BASI complex appears to be a complex of lower affinity, possibly reflecting a fine-tuned regulation of α-amylase/subtilisin inhibition.

In the EcTrx1–PAPS reductase complex, two hydrogen bonds involve I75_{EcTrx1} O and A93_{EcTrx1} NH, corresponding to M88_{HvTrxh2} O and A106_{HvTrxh2} NH, respectively, in the HvTrxh2–BASI complex. These interactions are not observed in the EcTrx1–NTR complex, where I75_{EcTrx1} NH forms hydrogen bonds to D139_{EcNTR} OD1. D139_{EcNTR} was suggested to be an acid/base catalyst influencing the nearby active site cysteines in EcNTR. On the basis of this observation, we predict that residues corresponding to EcTrx1 I75 are important in both target protein and NTR recognition.

E86_{HvTrxh2} from the cis-proline loop makes van der Waals contacts with Q149 and E168 in BASI (Figure 1 and Table 2). The latter residue has a functional role in the inhibition of barley α-amylase as shown using the BASI mutants E168Q and E168T. E86_{HvTrxh2} corresponds to R73_{EcTrx1} that participates in multiple intermolecular interactions in the EcTrx1–PAPS reductase and EcTrx1–NTR complexes. E86_{HvTrxh2} and E168_{BASI} are quite closely spaced in the HvTrxh2–BASI complex, 4.6 Å being the shortest distance between the side chain carboxylate OE atoms. The carboxylate of E86_{HvTrxh2} is ~15 Å from the active site disulfide of HvTrxh2, excluding a direct effect on cysteine reactivity. On the basis of the structure of the HvTrxh2–BASI complex, an E86R_{HvTrxh2} mutant was designed to engineer electrostatic attraction toward BASI.

The comparison of HvTrxh2–BASI, EcTrx1–PAPS reductase, and EcTrx1–NTR complexes highlights possible key roles of E86, M88, and A106 in Trx–target protein and NTR recognition, motivating the mutational analysis presented here.

**Apparent BASI Reduction.** Reduction of BASI by Trx was analyzed in an assay coupled to HvNTR2-dependent NADPH oxidation. The disulfide reduce activity was linearly proportional to the concentration of BASI (Figure 2) and Trx and expressed as second-order rate constants relative to that of wt HvTrxh2 (Δ). Rates of NADPH oxidation in Δ340 s\(^{-1}\) were converted to rates of turnover (s\(^{-1}\)) of mutant or wt HvTrxh2.

![Figure 2](https://example.com/figure2.png)
Table 3. Activity of HvTrxh2 Mutants

<table>
<thead>
<tr>
<th>HvTrxh2 mutant</th>
<th>BASI</th>
<th>DTNB/NTR</th>
<th>Gpx</th>
<th>insulin</th>
</tr>
</thead>
<tbody>
<tr>
<td>E86R</td>
<td>3.01 ± 0.18</td>
<td>0.83 ± 0.02</td>
<td>0.53 ± 0.02</td>
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</tr>
<tr>
<td>M88G</td>
<td>0.06 ± 0.01</td>
<td>0.15 ± 0.002</td>
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<tr>
<td>M88A</td>
<td>0.30 ± 0.01</td>
<td>0.31 ± 0.01</td>
<td>0.25 ± 0.03</td>
<td>0.60 ± 0.05</td>
</tr>
<tr>
<td>M88P</td>
<td>ndb</td>
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<td>0.010 ± 0.005</td>
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<tr>
<td>M88L</td>
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<tr>
<td>A106G</td>
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<tr>
<td>A106S</td>
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<tr>
<td>A106P</td>
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<td>0.90 ± 0.10</td>
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<tr>
<td>A106Y</td>
<td>0.27 ± 0.02</td>
<td>1.29 ± 0.09</td>
<td>0.70 ± 0.06</td>
<td>0.81 ± 0.07</td>
</tr>
</tbody>
</table>

“*The activity is normalized to the wt value, and 1.0 represents 550 M M−1 s−1 for the apparent reduction rate of BASI, 1.2 DTNB disulfides Trx−1 s−1 in the DTNB–NTR assay, and 0.045 Gpx disulfide Trx−1 s−1, respectively. For insulin, an activity of 1.0 relates to the rate of absorbance change at 650 nm in the interval between 0.1 and 0.2 of wt HvTrxh2 (see Experimental Procedures and Figure S1 of the Supporting Information). Reduction of BASI is based on the average of two measurements. aActivity with HvTrxh2 M88P was not detectable.

The kinetics of selected HvTrxh2 mutants revealed that the low catalytic efficiency toward M88G stemmed from an increased $k_{cat}$ of 8.4 ± 1.7 μM compared to a value of 1.75 ± 0.075 μM for wt HvTrxh2 (Figure 4A). The apparent $k_{cat}$ of HvNTR2 (12.5 s−1) was not affected, although the M88HvTrxh2 side chain is close to the active site cysteines. A linear dependence on the concentration of M88P was observed in contrast to the substrate saturation curves found for wt HvTrxh2 and its mutants (Figure 4A,B). The catalytic efficiency for M88P decreased 300-fold to 2.2 × 10^4 M M−1 s−1 (from 7.1 × 10^6 M M−1 s−1 for wt HvTrxh2), and the curve demonstrates the deficient binding to HvNTR2.

Apparent Reduction of Glutathione Peroxidase (Gpx).

Gpxs from plants are Trx-dependent thioredoxins that exhibit sequence homology to classical glutathione-dependent mammalian Gpxs. Briefly, the catalytic cycle of Trx-dependent Gpx is initiated when the so-called peroxidatic cysteine is oxidized to a sulfenic acid concomitant with peroxide reduction. This sulfenic acid is then attacked by a second “resolving” cysteine in Gpx, resulting in the formation of an intramolecular disulfide that is reduced by Trx to regenerate Gpx. wt HvTrxh2 and mutants were analyzed for specific activity with barley HvGpx2 as a catalytic disulfide target in the presence of HvNTR2/NADPH as the Trx recycling system. The M88P mutant was the least active as in the BASI assay and probably influenced by inefficient recycling by HvNTR2 (Table 3). Furthermore, the activities of mutants M88G, M88A, and M88L of 13, 25, and 70%, respectively, followed the trend as in the BASI and HvNTR2 assays. Overall, the A106 mutants showed only minor decrease in activity toward HvGpx2, and the 52% activity of A106P was much higher than that toward BASI (Figure 2). HvTrxh2 E86R had reduced activity toward HvGpx2 (53% of wt), as opposed to its 3-fold increased activity toward Basi.

Reduction of Insulin. HvTrxh2 mutants were analyzed for NTR-independent activity using insulin as a substrate in the presence of DTT, a widely used Trx assay. Insulin is a good substrate, giving a second-order rate constant of 2.4 × 10^7 M−1 s−1 for HvTrxh2, which is more than 1 order of magnitude higher than that with BASI as the substrate. In agreement with the other three steady state assays, HvTrxh2 M88P had the
lowest activity (10%), other M88 mutants displayed 50−70% of the wt activity, and the activity of E86R and A106 mutants was essentially unaffected (Table 3). The higher residual activity of mutant M88P against insulin compared to those against BASI, Gpx2, and HvNTR2 may reflect the fact that negative effects on the NTR interaction are bypassed by using DTT as a reductant.

Reduction by DTT. As HvTrxh2 M88P gave very low activity in assays using HvNTR2/NADPH, the reactivity of its dithiol/disulfide active site should be assessed using an approach not involving protein−protein interactions. In the case of EcTrx1, single-turnover reduction by DTT was monitored by the redox-dependent fluorescence change, but HvTrxh2 is lacking the equivalent of W28 in EcTrx1 and shows no such transition signal. Here, the rate of reduction of HvTrxh2 by DTT was determined using acid quenching followed by HPLC quantification of reduced and oxidized forms (Figure S2 of the Supporting Information). DTT reduced mutant M88P with a rate constant of 21 M⁻¹ s⁻¹, which is approximately 5-fold slower than for wt (Figure 5).

CD Spectroscopy. The mutants having very low or no activity in the various assays were subjected to CD spectroscopy to probe changes in secondary structure. Only slight differences in CD spectra are observed among wt HvTrxh2, M88G, M88P, and A106P, verifying that the proteins are properly folded (Figure S3 of the Supporting Information).

Redox Potential of HvTrxh2 M88P. The redox potential of HvTrxh2 M88P was determined by direct protein−protein equilibrium with EcTrx1 and separation of reduced and oxidized forms by HPLC according to the method developed by Åslund et al. During the aerobic overnight incubation, control samples of reduced HvTrxh2 M88P were less stable than those of EcTrx1 and retained 92 and 96% of the reduced form, respectively (data not shown). This loss of reducing equivalents to molecular oxygen did not rule out observations of reliable equilibria (Figure 6), and an equilibrium constant (K) of 1.25 ± 0.12 was determined. This corresponds to a difference of 3 ± 1 mV, with HvTrxh2 M88P as the more reducing species. Using a kinetic approach, the redox potential of wt HvTrxh2 was previously determined to be very close to that of EcTrx1. It can therefore be concluded that the redox potential of HvTrxh2 M88P is essentially unchanged.

Single-Turnover Reduction of BASI. Chemically reduced wt HvTrxh2, M88P, and A106P were incubated with BASI (20 μM) at a 1:1 molar ratio to analyze disulfide reduction in BASI, in a manner independent of NTR recycling, by modifying released BASI thiol groups with TMM(PEG)₁₂. SDS−PAGE analyses demonstrated that wt HvTrxh2 and the two mutants partially reduced BASI (Figure S4 of the Supporting Information). To quantify the reductive capacity of HvTrxh2 mutants on the BASI C₁₄₄−C₁₄₈ disulfide, an activated single-cysteine BASI C₁₄₄S mutant was employed in which the lone exposed cysteine residue (C₁₄₈) is disulfide-bonded to TNB (C₁₄₄S−TNB). The second disulfide, C₄₄−C₉₃, in BASI is...
known to be very poorly reduced by HvTrxh2. The release of TNB anion from the BASI C144S−TNB complex with a 2-fold molar excess of fully reduced wt HvTrxh2, M88P, A106P, and E86R or DTT was measured at 412 nm (Figure 7A). In contrast to the reduction of wt BASI, as indicated by incorporation of TMM(PEG)12, reduction of the activated BASI C144S−TNB complex was driven to completion and the efficiencies of wt HvTrxh2 and the mutant (and of DTT) were given by the second-order rate constants (Figure 7B). It is important to point out that only the initial nucleophilic attack by Trx is monitored in this single-turnover assay. Noticeably, HvTrxh2 E86R gave higher reactivity with a $k = 2500 \text{ M}^{-1} \text{s}^{-1}$ as compared to a $k = 1550 \text{ M}^{-1} \text{s}^{-1}$ for wt (Figure 7B). By contrast to the behavior in the HvNTR2-dependent BASI assay, mutants A106P and M88P lost reactivity to the same extent ($k = 300–350 \text{ M}^{-1} \text{s}^{-1}$). Both mutants were more reactive than DTT ($k = 100 \text{ M}^{-1} \text{s}^{-1}$) in the reduction of the BASI C144S−TNB complex.

**DISCUSSION**

The dithiol active site WCGPC sequence in Trxs has been thoroughly investigated. This study concerns two neighboring Trx loops called the $\text{cis}$-proline and the glycine loop (Figure 1) contributing intermolecular hydrogen bonds in the HvTrxh2−BASI complex, which appear to be central for the rapid reduction of the BASI C144−C148 disulphide. Mutant A106P, not able to act as a hydrogen bond donor, showed only 10% apparent reduction of the BASI disulphide. Different replacements of A106 indicate that the side chain may also contribute to the reactivity toward BASI. Importantly, mutant A106P was not efficiently recycled by HvNTR2 and also reacted fairly efficiently with insulin and HvGpx2. Together, these data provide strong evidence that the formation of hydrogen bonds between HvTrxh2 A106 NH and the substrate does not represent a universal requirement essential for Trx function and...
recycling by NTR. The A106 NH hydrogen bond may be important for reduction of PAPS reductase and methionine sulfoxide reductase because homologues of A106 in Trx complexes with these target proteins participate in similar intermolecular backbone—backbone hydrogen bonds as observed in the HvTrxh2—BASI complex.7,8,10 While the role of this highly conserved alanine residue was not previously investigated by mutagenesis, the invariant preceding glycine residue (G92 of EcTrx1) has previously been identified as being critical for interactions with EcNTR and bacteriophage T7 DNA polymerase.37

The side chain of HvTrxh2 M88 is important for efficient target disulfide reduction as demonstrated by the same order of decreasing activity found for HvTrxh2 (wt > M88L > M88A > M88G) toward BASI, Gpx, and HvNTR2 (Table 3). The results are consistent with observed favorable van der Waals contacts involving the M88 side chain in the HvTrxh2—BASI complex.7 One can speculate that these interactions are less relevant for the exceptionally fast Trx-catalyzed reduction of disulfides in insulin. For mutant M88P, the effect of the loss of one of the three backbone hydrogen bonds to BASI was not conclusively demonstrated because the mutant was severely deficient in recycling by NTR. Moreover, it was affected in terms of the chemical reactivity of its active site cysteines (Figure 5), although it has an essentially unperturbed redox potential (Figure 6). The shortcomings of HvTrxh2 M88P thus appear to be of a kinetic nature. The M88P substitution perhaps induces strain transmitted to the neighboring cis-proline [P89 (Table 1)], an invariant key residue of the Trx superfamily.21,36 The position of M88 in HvTrxh2 corresponds to an isoleucine residue in EcTrx1 (Table 1), and a comprehensive mutational analysis, including determination of the structure of EcTrx1 I75T, demonstrated that this “cisPro minus 1 residue” is a general activity regulator of Trx fold proteins.38 EcTrx1 I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively affected than mutants with charged side chains (K, R, H, E, and D), and I75P, however, was not generally more negatively opposed to M88P toward BASI, Gpx, and HvNTR2 (Table 3). The comparison thus suggests different roles of the cis-Pro minus 1 residue NH group for the HsNTR1 recycling, the loss of the hydrogen bond to BASI is not the EcTrx1 complex resembles the HvTrxh2—BASI complex and not the EcTrx1—NTR complex, in which I75EcTrx1 NH is hydrogen bonded to the side chain of D139HsNTR involved in acid/base catalysis. The comparison thus suggests different roles of the cis-Pro minus 1 residue NH group for interactions with low- and high-molecular weight NTR.

The side chain of R73EcTrx1 Protrudes at the protein surface and appears to play central roles in stabilizing the EcTrx1—PAPS and EcTrx1—NTR complexes (Table 2). The importance of R73EcTrx1 for NTR recognition was suggested by Slaby and Holmgren in 1979 on the basis of the observation that tryptic cleavage at R73 in EcTrx1 [R^GG (Table 1)] impaired activity toward EcNTR.41 These findings were corroborated in a recent study in which EcTrx1 R73D and R73G had 0.6 and 3.8% activity, respectively, with EcNTR but retained the insulin disulfide reductase activity.42 In HvTrxh2, and in most of the known plant h-type Trx, a glutamic acid (HvTrxh2 E86) corresponds to R73EcTrx1. In yeast Trx, the position is occupied by a serine residue (Table 1). Mutant E86R retained almost full activity with barley HvNTR2, indicating that a strong determinant of the interaction between NTR and Trx evolved differently in plants, yeast, and bacteria. In this context, bacteriophage T4 glutaredoxin, the specific hydrogen donor of phage ribonucleotide reductase (originally called T4 thioredoxin), remains an intriguing example of molecular evolution by having leucine at the position corresponding to R73EcTrx1. T4 glutaredoxin is efficiently reduced by glutathione as well as by EcNTR, and viral replication is therefore supported by both cellular reduction systems.43,44 The strikingly 3-fold increased activity of E86R toward the BASI disulfide is possibly a result of an electrostatic contact to E168BASI. In contrast to R73EcTrx1, E86HvTrxh2 seems not to be restricted by NTR interaction, and this residue may thus evolve and modulate activities toward target disulfides.

In conclusion, mutational analysis highlights the importance of key residues at the active site surface of Trx for interactions with target proteins and the NTR in recycling, as demonstrated by remarkable changes in activity profiles of single-amino acid variants. These findings add novel insight into the molecular basis of Trx target recognition that is relevant for other Trx fold oxidoreductases, e.g., glutaredoxins, and facilitates the development of catalysts with altered substrate specificities.

**ASSOCIATED CONTENT**

5 Supporting Information
One table and four figures. This material is available free of charge via the Internet at http://pubs.acs.org.

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ABBREVIATIONS
BASI, barley α-amylase/subtilisin inhibitor; CD, circular dichroism; DTNB, 5,5′-dithiobis(2-nitrobenzoic acid); EcTrx1, E. coli thioredoxin 1; EcNTR, E. coli NAPDH-dependent thioredoxin reductase; HvGpx2, barley glutathione peroxidase 2; HvNTR2, barley NADPH-dependent thioredoxin reductase 2; HvTrxh1, barley thioredoxin h1; HvTrxh2, barley thioredoxin h2; PAPS, 3′-phosphoadenosine 5′-phosphosulfate; PDB, Protein Data Bank; TNB, 2-nitro-5-thiobenzoate; wt, wild-type.

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