

SUPPLEMENTAL DATA

FIGURE LEGENDS

Fig. S1. Size estimation and schematic overview of the product bands in Fig. 2A and B. The actual molecular mass with # includes the mass of the (MRGSH₆GS-) tag, 1.4 kDa.

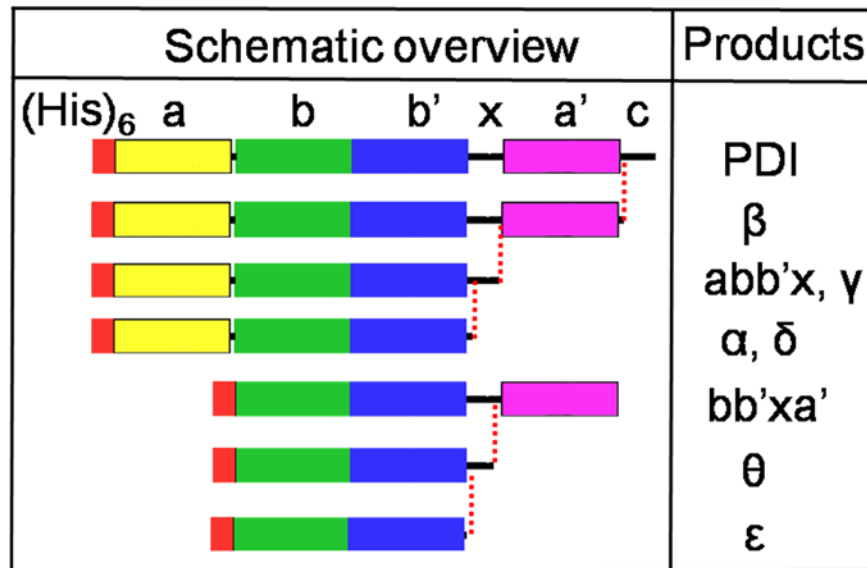
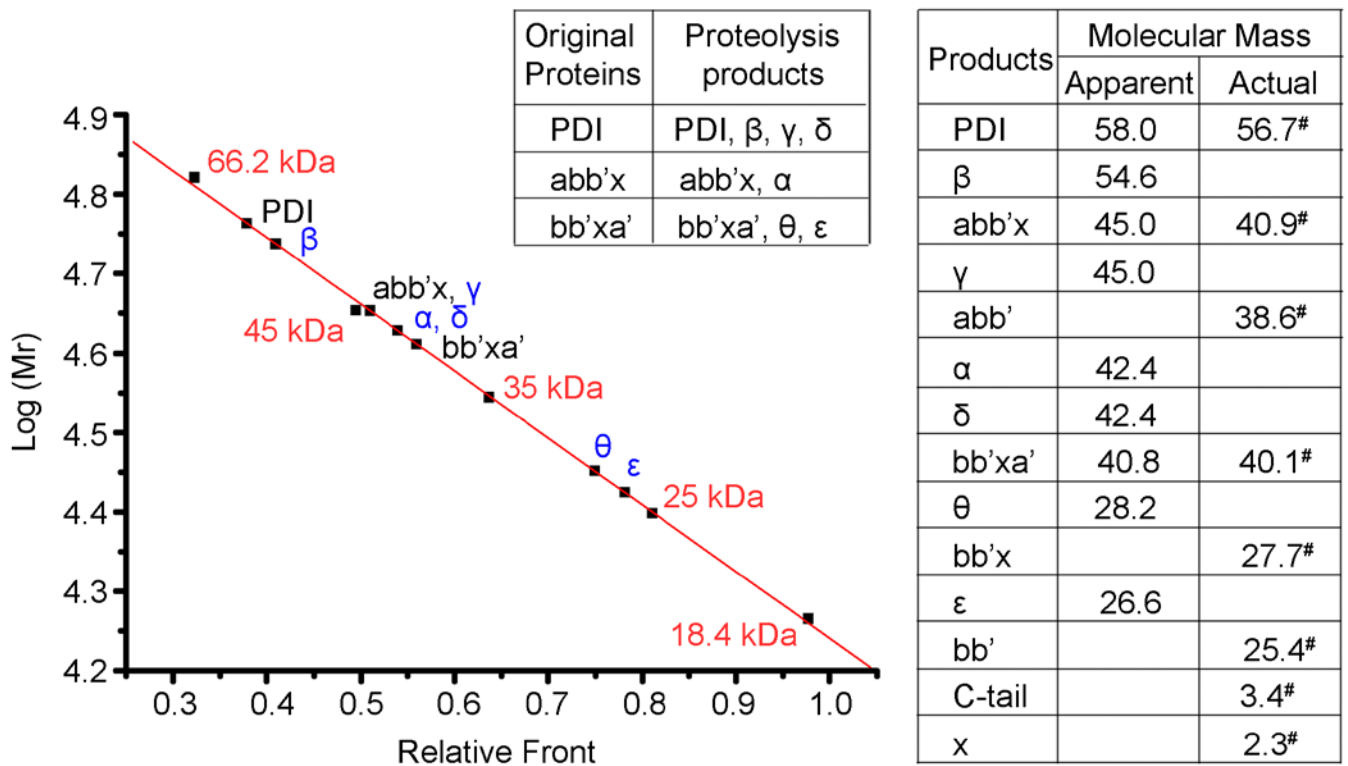
Fig. S2. Proteolysis of alternative (His)₆-tagged constructs for accurate product mass determination. PDI and L343A PDI with N-terminal (MH₆M-) tags at 1 mg/ml (A, B) or 2 mg/ml (C, D) were digested by 0.5 µg/ml proteinase K (A, B) or 0.7 µg/ml chymotrypsin (C, D). Reactions were stopped by 5 mM PMSF at different times as indicated before analysis on SDS-12% PAGE gel. The bands indicated by arrows were cut out and analyzed by tryptic digestion/mass spectrometry.

Fig. S3. Limited digestion profiles of PDI with (His)₆-tag at its C- terminals. 1 mg/ml PDI with a C-terminal (-H₆) tag was digested by 2 µg/ml chymotrypsin (A) at 25 °C for different times as indicated. The reactions were terminated by adding PMSF to a final concentration of 0.5 mM, and analyzed by reducing SDS-15% PAGE for Coomassie blue staining. Digestion profiles of PDI with a N-terminal (MRGSH₆GS-) tag under the same condition (B) was used for comparison. The major products are indicated by arrows.

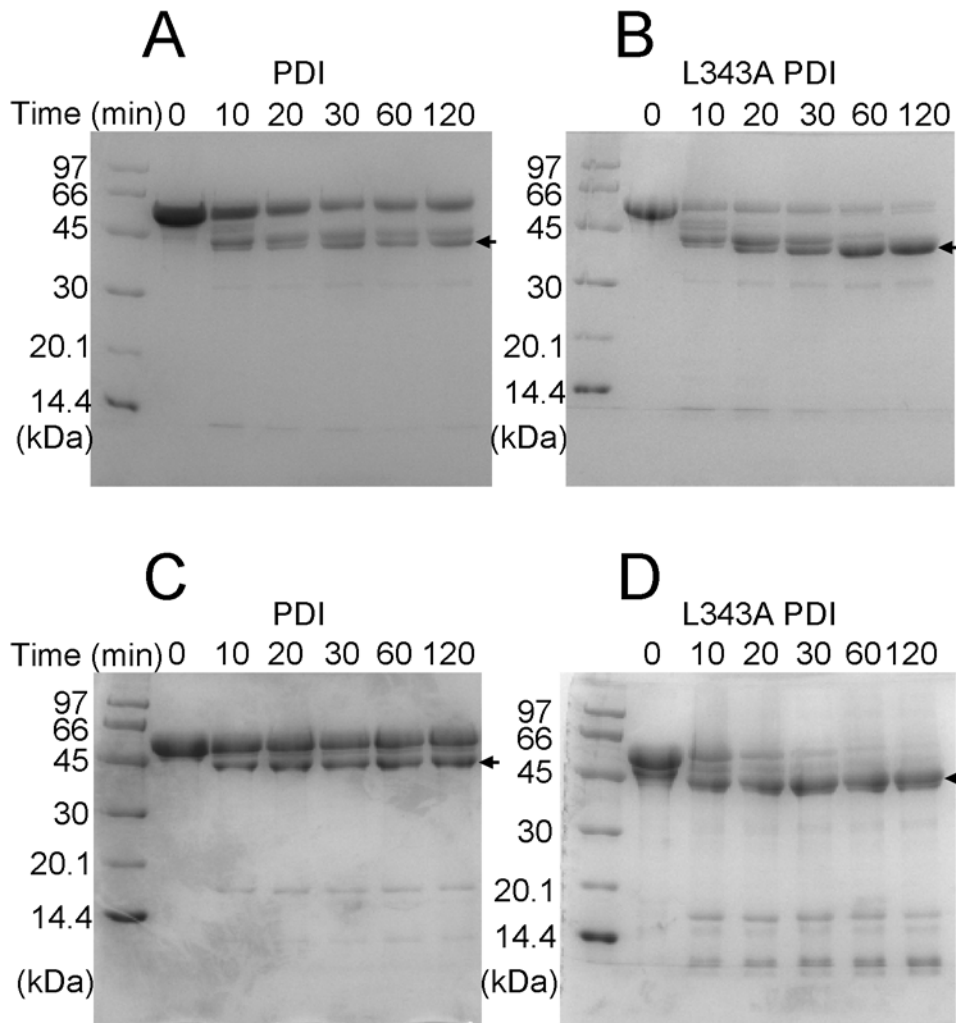
Fig. S4. Stern-Volmer analysis of quenching of intrinsic protein fluorescence by iodide anions. Ksv plots of I272A mutants (○) and L343A mutants (△) in b'x background (■) (A), W111F/W390F background PDI (■) (B) and W111F abb'x background (■) (C).

Fig. S5. Far-UV CD analysis of the effects of the mutations on the secondary structure of PDI and abb'x. Far-UV CD spectra of the mutants in PDI background (A) or **abb'x** background (B) at 2.5 µM in 20 mM sodium phosphate buffer, pH 7.6, at 25 °C.

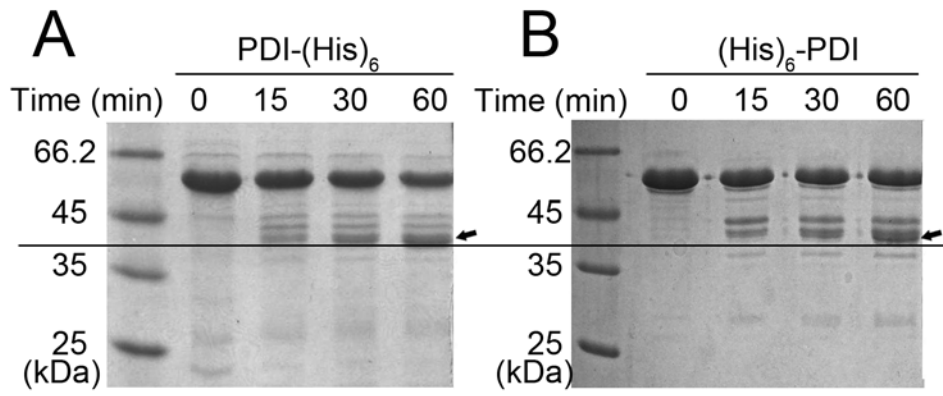
Supplemental figure 1



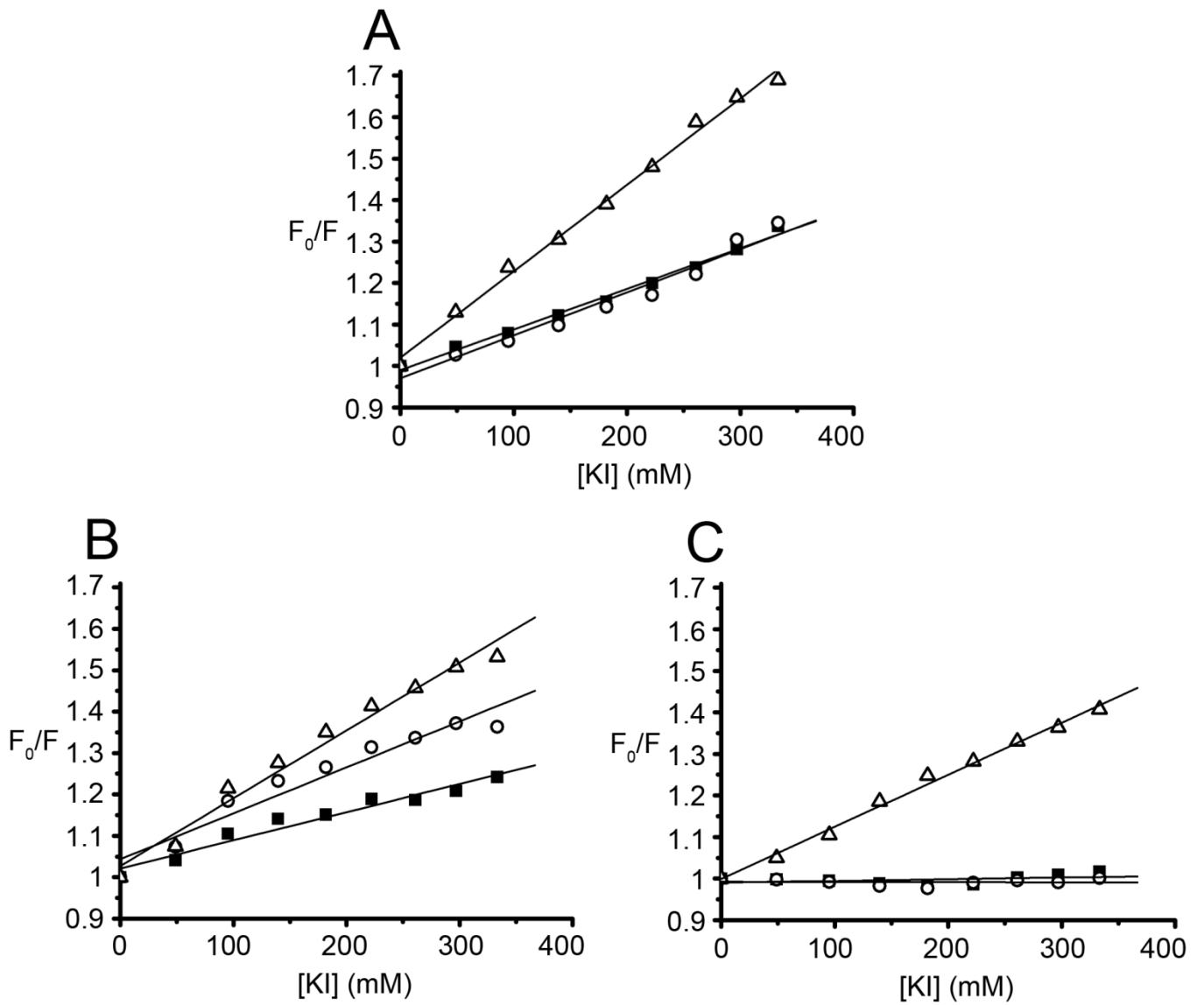
Supplemental figure 2



Supplemental figure 3



Supplemental figure 4



Supplemental figure 5

