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Supplementary Materials

Functional Interplay between P5 and PDI/ERp72 to Drive Protein Folding

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This PDF file includes:
Figure S1, Disulfide bond formation of RNase A catalyzed by P5, PDI, or ERp72, related to Figure 2; Figure S2, Aggregation of GAPDH in the presence of P5, PDI, or ERp72, related to Figure 4.

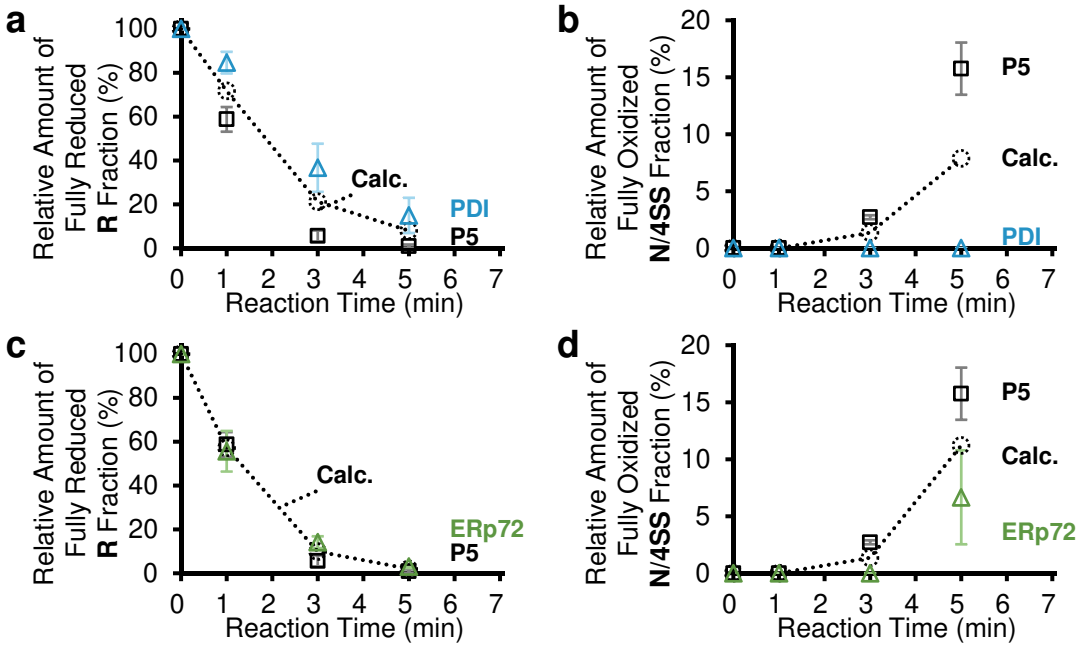

Figure S1. Disulfide bond formation of RNase A catalyzed by P5, PDI, or ERp72, related to Figure 2. (**a**–**d**) Quantification of the relative band intensities of reduced form (**a**,**c**) and oxidized form (**b**,**d**) in Figure 2. Error bars indicate the means ± SEM of three independent experiments. **P5**, results of 1 μM P5 alone; **PDI**, results of 1 μM PDI alone; **ERp72**, results of 1 μM ERp72 alone; **Calc.**, calculated arithmetic means of the results of P5 alone and PDIs alone (dotted line and circle).

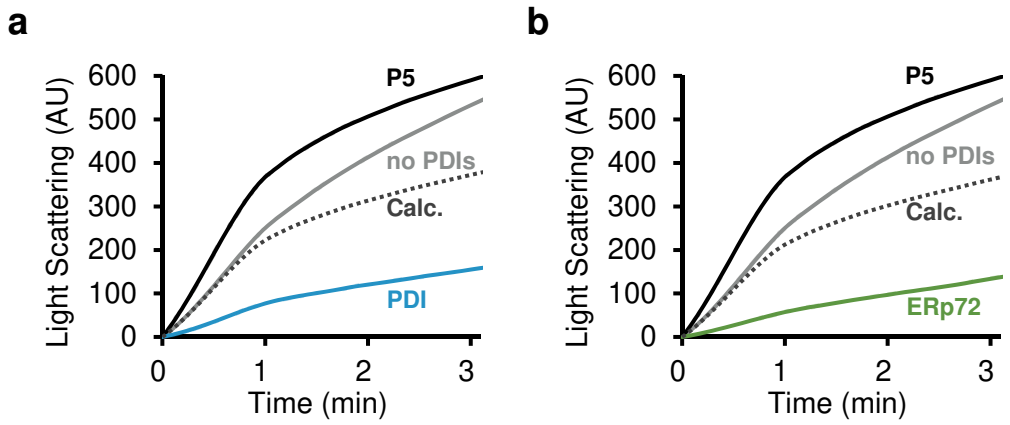

Figure S2. Aggregation of GAPDH in the presence of P5, PDI, or ERp72, related to Figure 4. (**a**,**b**) Reduced and denatured GAPDH (1 μM) was incubated without PDIs (**no PDIs**), with 5 μM P5 alone (**P5**), with 5 μM PDI alone (**PDI**), or with 5 μM ERp72 alone (**ERp72**). GAPDH aggregation was evaluated by measuring 90˚ light scattering at 620 nm over time. AU, arbitrary units; **Calc.**, calculated arithmetic means of the fluorescence intensities of P5 alone and PDIs alone (dotted line).