

Supporting information with:

Mapping of the binding site on pseudoazurin in the transient 152 kDa complex with nitrite reductase

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Protocol for the production of deuterium labelled PAZ in *Escherichia coli*.

Part of the PAZ gene coding for the mature protein was subcloned in pET-28a(+), creating a plasmid for expression in the cytoplasm of *Escherichia coli*. Protein was produced in *E. coli* strain HMS174 in a M9 minimal medium containing 0.7 g/L $^{15}\text{NH}_4\text{Cl}$ and 5 g/L Na-acetate- d_3 . Cultures were incubated at 37°C with a shaking speed of 250 rpm. *E. coli* was adapted for growth in D_2O by increasing the percentage of D_2O in consecutive 5 ml cultures from 0% to 50%, 80%, 95% and 99.9%. The cultures were used for inoculation (at a ratio 1:5) when their OD_{600} was 0.4. In this way cells slowly adapted first to the deuterated carbon source and then to the deuterated medium. The final preculture was diluted several times to a ratio 1:5. Each dilution to a larger volume was done upon reaching $\text{OD}_{600} = 0.4$. The final volume was 1 litre. In this way, the bacteria remained in the exponential growth phase during the dilution steps. In the final culture, expression was induced at $\text{OD}_{600} = 0.6$ with 0.5 mM IPTG, and 100 μM copper citrate was added. Cultures were harvested at $\text{OD}_{600} = 0.9$ by centrifugation, 10 h after induction. From the first dilution step until harvest took 7 days. After centrifugation, the cell pellet was resuspended in 20 mM phosphate buffer pH 7.0 containing 500 mM NaCl, 1 mM PMSF, DNase, 0.5 mM CuCl_2 and lysed using a French pressure cell (15.000 PSIG). After centrifugation for 15 min at 10.000 rpm supernatant was dialysed against 20mM phosphate buffer pH 7.0 and loaded onto a CM column equilibrated with the same buffer. PAZ eluted at circa 90 mM using a gradient of 0-250mM NaCl. The fractions containing PAZ were concentrated and purified further on a Superdex 75 FPLC gel filtration column. The 277/595 absorbance ratio of PAZ was 1.9 indicating a purity >95%. The yield was 7.5 mg/L and the deuteration level of the aliphatic protons was determined by mass spectrometry to be 93%.

NMR samples containing 100 μM ^2H - ^{15}N -PAZ with or without 23 μM T2D-NiR were left for 8 h at room temperature and 2 days at 4 °C in a buffer solution of 90% D_2O / 10% H_2O to allow for equilibration of the amide exchange process.

^1H - ^{15}N TROSY-SPECTRUM of ^2H - ^{15}N PAZ Cu (I) 1mM
in 10% H_2O /90% $^2\text{H}_2\text{O}$ potassium phosphate buffer 20 mM pH 6.5

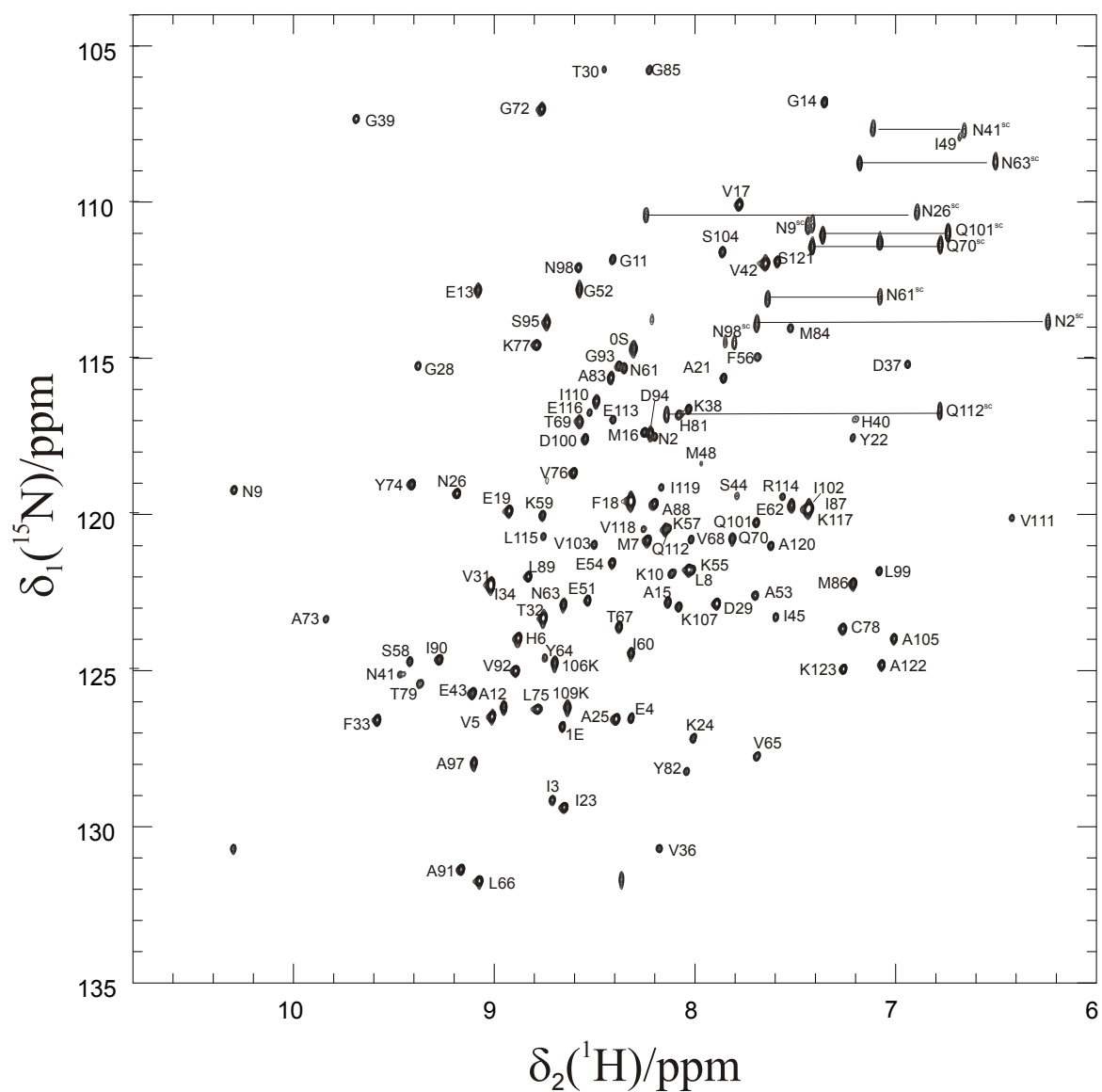


Figure 1 is a scatter plot showing the correlation between $\delta_2(^1\text{H})/\text{ppm}$ (x-axis, ranging from 6 to 10) and $\delta_1(^{15}\text{N})/\text{ppm}$ (y-axis, ranging from 105 to 135). The plot displays data points for 100 proteins, each labeled with its name. A dashed line represents the linear fit to the data. Horizontal bars extending from the right side of each data point indicate the $1\text{-}\sigma$ error for the $\delta_1(^{15}\text{N})$ value. The plot shows a clear negative correlation between the two chemical shift parameters.

