Supporting information:

Electrochemical and structural properties of a protein system designed to generate tyrosine Pourbaix diagrams

Melissa C. Martínez-Rivera[‡], Bruce W. Berry^{t§}, Kathleen G. Valentine[‡],

Kristina Westerlund[§], Sam Hay[§] and Cecilia Tommos^{t§}*

[‡]Graduate Group in Biochemistry & Molecular Biophysics and Department of Biochemistry & Biophysics, University of Pennsylvania, Philadelphia, Pennsylvania 19104-6059, and [§]Department of Biochemistry & Biophysics, Arrhenius Laboratories for Natural Sciences, Stockholm University, SE-106 91 Stockholm, Sweden



Fig. S1. Electrochemical properties of $\alpha_3 Y$ *and control samples.* (A) Cyclic voltammogram of 210 μ M $\alpha_3 Y$ in 20 mM sodium acetate, 20 mM potassium phosphate, 40 mM KCl, pH 5.43; scan rate 200 mV/s, iR-compensation 103 ohm, temperature 23° C. (B) Differential pulse voltammograms of buffer containing 20 mM sodium acetate, 20 mM potassium phosphate, 40 mM KCl, pH 5.52 (red) and 200 μ M α_3 C in 20 mM sodium acetate, 20 mM potassium phosphate, 40 mM KCl, pH 5.46 (orange); interval time 0.1 s, step potential 1.05 mV, scan rate 10.5 mV s⁻¹, modulation time 5 ms, modulation amplitude 50 mV, temperature 23° C.



Fig. S2. Stick and backbone representations of the $\alpha_3 W$ solution NMR structure (1LQ7.pdb; Dai *et al.*, J. Am. Chem. Soc. 124, 10952–10953, 2002). Helices 1, 2 and 3 are colored yellow, blue and purple, respectively. The high-quality structure of $\alpha_3 W$ (average RMSD from mean coordinates: 0.22 Å (backbone atoms helical residues), 0.33 Å (backbone atoms all residues), 0.76 Å (heavy atoms helical residues)) was used as a guide to engineer Y32/His interactions in the $\alpha_3 Y$ protein. $\alpha_3 Y$ is a single-site W32Y variant of $\alpha_3 W$.



Fig. S3. Probing for Y32/His interactions in single-site α_3 Y-His variants by absorption spectroscopy. (A) Absorption spectra of α_3 Y (orange) and N-acetyl-tyrosinamide (NAYA; black) dissolved in 10 mM potassium phosphate, 30 mM KCl, pH 7.0. (B) Absorption spectra of α_3 Y-E13H (purple) and α_3 Y-I62H (green) in 10 mM Tris, 15 mM KCl, pH 9.0. The data were collected at room temperature.



Fig. S4. Probing for Y32/His interactions in single-site α_3 Y-His variants by fluorescence spectroscopy. Introducing a histidine at position 13, 33 or 58 did not give rise to any significant shift in the Y32 fluorescence emission spectrum. The orange spectra represent α_3 Y while the dashed black spectra represent three different α_3 Y-His variants at pH 5.0 (panels A, B and C) and at pH 8.5 (panels D, E and F. The pH 5.0 samples were prepared in 15 mM sodium acetate and 30 mM KC1. The pH 8.5 samples were prepared in 15 mM Tris and 30 mM KC1. The spectra were obtained at room temperature and have been smoothened for clarity.



Fig. S5. Probing for Y32/His interactions in single-site α_3 Y-His variants by fluorescence spectroscopy. Introducing a histidine at position 9, 12, 29, 36 or 62 gave rise to a perturbation of the Y32 fluorescence excitation (panels A, B and C) and/or emission (panels D, E and F) spectra. Samples conditions were as follows: (A) α_3 Y (orange) and α_3 Y-V9H (green) in 15 mM sodium acetate, 30 mM KCl, pH 5.0; (B) α_3 Y (orange) and α_3 Y-K29H (blue) in 10 mM sodium acetate, 30 mM KCl, pH 5.5; (C) α_3 Y (orange) in 15 mM sodium acetate, 30 mM KCl, pH 5.5; (D) α_3 Y (orange) and α_3 Y-L12H (cyan) in 10 mM Tris, 15 mM KCl, pH 8.2; (E) α_3 Y (orange) in 15 mM sodium acetate, 30 mM KCl, pH 5.5; (D) α_3 Y (orange) and α_3 Y-L12H (cyan) in 10 mM Tris, 15 mM KCl, pH 8.2; (E) α_3 Y (orange) in 15 mM sodium acetate, 30 mM KCl, pH 5.5; (F) α_3 Y (orange) and α_3 Y-L58H (black) in 15 mM Tris, 30 mM KCl, pH 8.5. The spectra were obtained at room temperature and have been smoothened for clarity.



Fig. S6. Absorption spectrum of $\alpha_3 Y$ as a function of pH. Spectra recorded on $\alpha_3 Y$ at pH 7.0 (orange; λ_{max} 277.8 nm) and 12.3 (blue; λ_{max} 293.2 nm). $\alpha_3 Y$ was dissolved in 10 mM potassium phosphate, 10 mM HEPES, 10 mM sodium borate, 10 mM CAPS and the spectra collected at room temperature.



Fig. S7. One-dimensional NMR spectrum of $\alpha_3 Y$ -K36H *as a function of pH*. NMR spectra recorded on $\alpha_3 Y$ -H36H at pH 5.0 (left panel), 7.0 (middle) and 9.2 (right). The pH-sensitive resonance of the histidine $\varepsilon 1$ ring proton shifts more than 1 ppm across the titrated pH range. $\alpha_3 Y$ -H36H was dissolved in D₂O containing a buffer cocktail of deuterated sodium acetate, sodium phosphate, sodium borate and 30 mM KCl. The spectra were collected at 25° C.



Fig. S8. Chemical denaturation of $\alpha_3 Y$ and histidine variants. Panel (A) displays urea-induced unfolding/folding transitions of $\alpha_3 Y$ (black circles), $\alpha_3 Y$ -V9H (green diamonds), $\alpha_3 Y$ -K29H (blue squares) and $\alpha_3 Y$ -K36H (magenta crosses) while panel (B) displays data obtained on the $\alpha_3 Y$ -L12H (circles) and $\alpha_3 Y$ -I62H (diamonds) proteins. The grey lines in panel (A) represent nonlinear curve fits to determine the stability of the protein in the absence of denaturant (see Table 1 in the main text; Santoro & Bolen, *Biochemistry 27*, 8063–8068, 1988). The proteins were dissolved in 10 mM sodium acetate, 10 mM potassium phosphate, 10 mM sodium borate, pH 8.2 and the data collected at 25° C.



Fig. S9. Gel filtration of $\alpha_3 Y$ *and* $\alpha_3 Y$ -*K29H*. Elution profiles of $\alpha_3 Y$ (solid line) and $\alpha_3 Y$ -K29H (dotted line) on an analytical SuperdexTM 75 gel filtration column equilibrated with 10 mM sodium acetate, 10 mM potassium phosphate, 10 mM sodium borate, 100 mM KCl, pH 7.0. The data were collected at room temperature.



Fig. S10. Two-dimensional ¹⁵N-HSQC NMR spectrum of α_3 Y-K36H as a function of pH. ¹⁵N-HSQC spectra of α_3 Y-K36H obtained at 35° C and (A) pH 8.4, (B) pH 7.0 and (C) pH 5.5. The protein was dissolved in 20 mM deuterated Tris, 20 mM NaCl, 8% D₂O (pH 8.4) or 20 mM deuterated sodium acetate, 20 mM sodium phosphate, 20 mM NaCl, 8% D₂O (pH 7.0 and 5.5).