Supplementary Material

The p*K*_a values of the catalytic residues in the retaining glycoside hydrolase T26H mutant of T4 lysozyme

Jacob A. Brockerman,¹ Mark Okon,^{1,2} Stephen G. Withers,^{1,2,3} and

Lawrence P. McIntosh^{1,2,3*}

¹ Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada V6T 1Z3

² Department of Chemistry, University of British Columbia, Vancouver, BC, Canada V6T 1Z1

³ Michael Smith Laboratories, University of British Columbia, Vancouver, BC, Canada V6T 1Z4

*Correspondence to: Lawrence P. McIntosh

Department of Biochemistry and Molecular Biology, University of British Columbia, Vancouver, BC, Canada V6T 1Z3 phone: 604-822-3341 Email: mcintosh@chem.ubc.ca



Supporting Information Figure S1. The ¹⁵N-HSQC spectrum of T26H-T4L* in 100 mM KCl, 30 mM potassium phosphate, and 5% D₂O at pH 5.5 and 25 °C. Assigned mainchain amide ¹H^N-¹⁵N signals are labeled.



Supporting Information Figure S2. (A) Overlaid ¹⁵N-HSQC spectra of T26H-T4L* (red) and wild-type T4L* (blue) with both samples at pH 5.5 and 25 °C. Signals from amides and arginine sidechains (~ 85 ppm in ¹⁵N) are shown. (B) Histogram of amide chemical shift differences between corresponding amides in the two proteins, calculated¹ as $\Delta \delta = \{(\Delta \delta_H)^2 + \{(0.14\Delta \delta_N)^2\}^{1/2}$. Blank values are for prolines and residues for which assignments were not obtained. (C) When mapped on the structure of T26H-T4L* (1QT8.pdb), amides with the largest perturbed chemical shifts cluster around position 26 (*).



Supporting Information Figure S3. Superimposed ¹⁵N-decoupled ¹³C-HSQC spectra of uniformly ¹³C/¹⁵N-labeled T26H-T4L* showing the ¹H^{82-1³C⁸² signals of (A) His26 and (B) His31 as the protein was titrated between pH 5 and 11 at 25 °C. The ¹³C⁸² signals are doublets due to ¹J_{CC} coupling with the adjacent ¹³C^{γ}. For clarity, only representative titration points are shown, and all data are presented in Fig. 2B. Both neutral histidines adopt the N⁸¹H tautomer (structure shown) based on fit plateau ¹³C⁸² chemical shifts of 126.7 ppm (His26) and 127.2 ppm (His31).}



Supporting Information Figure S4. Assignment of the signals from the guanidinium sidechain of Arg145 in uniformly ¹³C/¹⁵N-labeled T26H-T4L* at pH 6.5 and 25 °C. (A) The ¹H-¹³C plane from a 3D C(CCO)-TOCSY-NH spectrum taken at the ¹⁵N shift of Ala146 (119.2 ppm). This

provided assignments for the ¹³C^{α} (58.8 ppm), ¹³C^{β} (31.2 ppm), ¹³C^{γ} (25.5 ppm) and ¹³C^{δ} (44.8 ppm) of Arg145. (B) The ¹H-¹³C plane at the indicated ¹⁵N shift (84.8 ppm) of a 3D H^eN^eC^{δ} spectrum² yielded the assignment of the ¹H^e (6.86 ppm) and ¹⁵N^e (84.8 ppm) signals of Arg145 by virtue of a scalar correlation to the ¹³C^{δ} (see also Fig. 5). (C) The ¹³C^{ζ} (159.5 ppm) was then assigned from the corresponding ¹H-¹³C plane of a 3D H^eN^eC^{ζ} spectrum.³ (D, E) Finally, ¹⁵N^{η} signals at 75 ppm and ~ 71 ppm were identified from a 2D N^{e/ η}–C^{ζ} correlation spectrum.^{4,5} Panels D and E are from the same ¹³C-detected spectrum, but E is displayed at a higher contour level for clarity. These assignments are similar to those reported for wild-type T4L^{*,4-7} (F) The cartoon summarizes the expected ¹⁵N^{η}, ¹³C^{ζ}, and ¹⁵N^{ϵ} chemical shifts of an arginine sidechain upon titration from its positively charged to neutral form.^{8,9} Under these conditions (pH 6.5), all thirteen arginines in T26H-T4L^{*} have chemical shifts diagnostic of a fully protonated guanidinium group.

Supplementary References

- 1. Williamson MP (2013) Using chemical shift perturbation to characterise ligand binding. Prog Nucl Magn Reson Spectrosc 73:1-16.
- Andre I, Linse S, Mulder FA (2007) Residue-specific pK_a determination of lysine and arginine side chains by indirect ¹⁵N and ¹³C NMR spectroscopy: Application to apo calmodulin. J Am Chem Soc 129:15805-15813.
- 3. Kay LE, Ikura M, Tschudin R, Bax A (1990) 3-dimensional triple-resonance NMR-spectroscopy of isotopically enriched proteins. J Magn Reson 89:496-514.
- 4. Yoshimura Y, Oktaviani NA, Yonezawa K, Kamikubo H, Mulder FA (2017) Unambiguous determination of protein arginine ionization states in solution by NMR spectroscopy. Angew Chem Int Ed Engl 56:239-242.
- 5. Werbeck ND, Kirkpatrick J, Hansen DF (2013) Probing arginine side-chains and their dynamics with carbon-detected NMR spectroscopy: Application to the 42 kDa human histone deacetylase 8 at high pH. Angew Chem Int Ed Engl 52:3145-3147.
- 6. Gerecht K, Figueiredo AM, Hansen DF (2017) Determining rotational dynamics of the guanidino group of arginine side chains in proteins by carbon-detected NMR. Chem Commun (Camb) 53:10062-10065.
- 7. Mackenzie HW, Hansen DF (2017) A ¹³C-detected ¹⁵N double-quantum NMR experiment to probe arginine side-chain guanidinium ¹⁵N^η chemical shifts. J Biomol NMR 69:123-132.
- Platzer G, Okon M, McIntosh LP (2014) pH-dependent random coil ¹H, ¹⁵C, and ¹⁵N chemical shifts of the ionizable amino acids: A guide for protein pK_a measurements. J Biomol NMR 60:109-129.
- 9. Fitch CA, Platzer G, Okon M, Garcia-Moreno BE, McIntosh LP (2015) Arginine: Its pK_a value revisited. Protein Sci 24:752-761.