

## NIH Public Access

Author Manuscript

*Biochemistry*. Author manuscript; available in PMC 2013 September 11

Published in final edited form as:

Biochemistry. 2012 September 11; 51(36): 7202–7208. doi:10.1021/bi300911d.

### Quantitative Measurement of Solvent Accessibility of Histidine Imidazole Groups in Proteins

Vennela Mullangi<sup>†,§</sup>, Xiang Zhou<sup>§</sup>, David W. Ball<sup>§</sup>, David J. Anderson<sup>§</sup>, and Masaru Miyagi<sup>†,⊥,#,\*</sup>

<sup>†</sup>Case Center for Proteomics and Bioinformatics, Case Western Reserve University, 10900 Euclid Ave, Cleveland, OH 44106

<sup>⊥</sup>Department of Pharmacology, Case Western Reserve University, 10900 Euclid Ave, Cleveland, OH 44106

<sup>#</sup>Department of Ophthalmology and Visual Sciences, Case Western Reserve University, 10900 Euclid Ave, Cleveland, OH 44106

<sup>§</sup>Department of Chemistry, Cleveland State University, Cleveland, OH 44115

#### Abstract

We report a method to express the solvent accessibility of histidine imidazole groups in proteins. The method is based on measuring the rate of hydrogen exchange (HX) reaction of the imidazole  $C^{e1}$ -hydrogen. The rate profile of the HX reaction as a function of pH gives a sigmoidal curve, which reaches the maximum rate constant ( $k^{\text{max}}$ ) on the alkaline side of the sigmoidal curve. To quantitatively describe the solvent accessibility of imidazole groups in proteins, it is necessary to compare the  $k^{\max}$  of the imidazole groups with their intrinsic  $k^{\max}$  ( $^{i}k^{\max}$ ), the maximum rate constants for the given imidazole groups when they are fully exposed to the bulk solvent. However, the mechanism of HX reaction suggests that the  ${}^{i}k^{max}$  of an imidazole group differs depending on its p $K_a$ , and no systematic study has been conducted to clarify how the  ${}^{i}k^{max}$  is affected by  $pK_a$ . We therefore investigated the relationship between <sup>i</sup> $k^{max}$  and  $pK_a$  using four imidazole derivatives at three different temperatures. The experimentally determined  $pK_{a}$ specific  ${}^{i}k^{max}$  values allowed us to derive a general formula to estimate the  ${}^{i}k^{max}$  value of any given imidazole group exhibiting a specific  $pK_a$  at a specific temperature. Using the formula, the protection factors (PF), the ratio of  ${}^{i}k^{max}$  to  $k^{max}$ , of five imidazole groups in dihydrofolate reductase were obtained and used to express the magnitude of their solvent accessibility. In this definition, the smaller the PF value, the higher the solvent accessibility, and a value of 1 indicates full exposure to the bulk solvent. The solvent accessibility expressed by the PF values agreed well with the solvent accessible surface areas (ASA) obtained from the X-ray diffraction data.

#### INTRODUCTION

It was found more than four decades ago that the imidazole  $C^{e1}$ -proton can be exchanged with deuteron by incubation in deuterium oxide (D<sub>2</sub>O) (1). The Scheme 1 shows the reaction mechanism of the hydrogen exchange (HX) reaction. The HX reaction has been shown to follow pseudo-first-order kinetics, in which the abstraction of the C<sup>e1</sup>-proton from the

<sup>&</sup>lt;sup>\*</sup>Corresponding author: Masaru Miyagi, Ph.D. Case Center for Proteomics and Bioinformatics, Case Western Reserve University, 10900 Euclid Ave., BRB 928, Cleveland, OH 44106-4988, Phone: (216) 368-5917, Fax: (216) 368-6846, masaru.miyagi@case.edu. SUPPORTING INFORMATION AVAILABLE

Temperature effect on the pH\* of D<sub>2</sub>O buffers, and structures of histamine, Ac-His-NHMe, Ac-His-OH, and IPA. This material is available free of charge via the Internet at http://pubs.acs.org.

cationic imidazolium by OD<sup>-</sup> to form a ylide or a carbene intermediate is the ratedetermining step (2–4). The rate profile of the HX reaction as a function of pD yields a sigmoidal curve, which exhibits a progression from the acidic side that accelerates and approaches the plateau on the alkaline side of the sigmoidal curve (Figure 1) (2–6). The rate profile provides two useful parameters that indicate the local environment of the given imidazole group in a protein. The one is the p $K_a$  of the imidazole N-H group, which coincides with the inflection point of the sigmoidal curve, because the rate of the reaction depends on both the concentrations of the conjugate acid of imidazole and OD<sup>-</sup> as can be seen below in the rate equation for this reaction (Equation 1). The other useful parameter is the maximum pseudo first-order rate constant,  $k^{max}$ , which corresponds to the upper plateau of the sigmoidal curve.

Because of the importance of imidazole groups in proteins such as enzyme catalysis and pHdependent structural changes, there has been considerable interest in HX of imidazole groups in proteins (7). Until recently, proton nuclear magnetic resonance (<sup>1</sup>H NMR) spectroscopy was the technique of choice to monitor HX reactions of imidazole groups in proteins (8). However, mass spectrometry (MS) is gaining popularity in recent years, because MS provides higher sensitivity and straightforward signal assignment, and is capable of analyzing membrane proteins and complex protein mixtures (7, 9–12). The MS method has been referred to as histidine hydrogen-deuterium exchange mass spectrometry (His-HDX-MS) (9–11) in order to distinguish it from the amide-HDX-MS (13).

Because the  $pK_a$  value of an imidazole group is sensitive to neighboring charged groups, experimentally obtained  $pK_a$  values are useful indicators of the electrostatic environment of imidazole groups in the proteins (11). On the other hand,  $k^{max}$  values have been used to indicate the solvent accessibilities of imidazole groups (7, 9, 11, 14, 15), because the HX rates at individual imidazole groups are affected significantly by the extent of accessibilities of these groups to the bulk solvent. However, the relationship between the HX rate and solvent accessibility is not straightforward. According to the kinetic studies of the HX reaction (2–4, 6), the reaction rate is expressed by Equation 1:

rate=
$$k[\text{Im}_{\text{total}}]=k_2[\text{Im}^+][\text{OD}^-]$$
 1)

where k is the pseudo first-order rate constant;  $k_2$  is the second order rate constant for the rate-determining step of the HX reaction;  $[Im_{total}]$  and  $[Im^+]$  represent the concentrations of total imidazole and the charged form of imidazole, respectively; and  $[OD^-]$  is the concentration of deuteroxyl ions. Because

$$[Im^+] = \frac{[Im_{total}][D^+]}{(K_a + [D^+])}$$

the expression of *k* can be simplified to Equation 2.

$$k = \frac{k_2 k_{\rm w}}{K_a + [\rm D^+]} \quad 2)$$

where  $K_a$  is the dissociation constant of the imidazolium cation and  $K_W$  is the ion product of heavy water ( $K_W = [D^+][OD^-] = 10^{-14.95}$  at 25°C) (16). The equation indicates that the magnitude of the *k* value is influenced by the  $K_a$  of a given imidazole group and the pD at which the HX reaction takes place. At high pD, however,  $[D^+]$  is negligibly smaller than the  $K_a$ ; therefore, Equation 2 reduces to Equation 3.

$$k^{\max} = \frac{k_2 K_w}{K_a}$$
 3)

where  $k^{\text{max}}$  is the maximum k obtained from the upper plateau of the sigmoidal curve in Figure 1. As Equation 3 implies, the  $k^{\text{max}}$  is independent of pD, and is therefore a more straightforward indicator of solvent accessibility than is k. The value of  $k^{\text{max}}$  is proportional to  $k_2$  and inversely proportional to  $K_a$ ; therefore, it increases 10-fold with a p $K_a$  increase of one pH unit, if the  $k_2$  value remains the same (which is not actually the case). This means that we cannot simply assume that a high value of  $k^{\text{max}}$  is due to greater accessibility of an imidazole group in the protein, because it may be simply due to a high value of  $pK_a$ . Therefore, to quantitatively express the solvent accessibility of a given imidazole group in a protein, it is necessary to know its intrinsic  $k^{\text{max}}$  ( ${}^{i}k^{\text{max}}$ ) value, which is the  $k^{\text{max}}$  value when it is fully exposed to the bulk solvent, and the value is specific to its  $pK_a$  value. Such an  ${}^{i}k^{\text{max}} - pK_a$  relationship for the HX method has not been investigated in a systematic manner, although some studies for the closely related hydrogen-tritium exchange (HTX) method have been done (17).

We report here the relationship between  ${}^{i}k^{max}$  and  $pK_{a}$  obtained with four imidazole derivatives. Based on the study, we derived a general formula that allows us to estimate the  ${}^{i}k^{max}$  value of an imidazole group in a protein exhibiting a specific  $pK_{a}$ . The formula was used to obtain the protection factors (PF), which is defined as the ratio of  ${}^{i}k^{max}$  to  $k^{max}$  of a given imidazole group, to express the solvent accessibility of imidazole groups in a protein.

#### EXPERIMENTAL PROCEDURES

#### Materials

Deuterium oxide (D<sub>2</sub>O, 99%) was purchased from Cambridge Isotope laboratories (Andover, MA). Histamine,  $N^{\alpha}$ -acetyl-DL-histidine (Ac-His-OH), and 1H-imidazole-5-propanoic acid (IPA) were from Sigma-Aldrich (St. Louis, MO).  $N^{\alpha}$ -acetyl-L-histidine methylamide (Ac-His-NHMe) was from Bachem (Torrance, CA). All other chemicals and materials used were either reagent grade or of the highest quality commercially available.

#### Buffer Solutions in D<sub>2</sub>O

Buffers in D<sub>2</sub>O contained 100 mM pyridine (pH\* 4.82–6.51) and 100 mM Nethylmorpholine (pH\* 6.62–9.39). The pH\* of the buffer was adjusted with diluted monodeuteroacetic acid (CH<sub>3</sub>COOD, 99%) at 25°C with a Solution Analyzer model 4603 (Amber Science, Eugene, OR) equipped with a glass AgCl electrode (model 476086, Nova Analytics, Woburn, MA). The reported pH\* values are direct pH meter readings of the D<sub>2</sub>O buffer solutions calibrated with standard buffer solutions made with H<sub>2</sub>O and are uncorrected for the isotope effect at the glass electrode. The pH\* of the D<sub>2</sub>O buffers at different temperatures were estimated as described in the Supporting Information.

#### **Deuteration of Imidazole Derivatives**

One nanomole of histamine, Ac-His-NHMe, Ac-His-OH, or IPA was incubated nµL buffer in D<sub>2</sub>O with different pH\* values (4.82–9.39) at 25, 31, and 37°C for 192, 106, and 50 hr, respectively (see the Supporting Information for the structures of these four model compound). The reaction was stopped by the addition of 5 µL formic acid, and the samples were dried in a Speed Vac. Note that the reaction is negligibly slow at the acidic pH\* (see Figure 1). Prior to MS analysis, the dried samples were redissolved in 50 µL of 0.1% formic acid/50% methanol in H<sub>2</sub>O, which promotes deuterium to proton exchange at rapidly

exchangeable sites (the amino, amide NH and carboxyl groups). The samples are then subjected to flow injection MS analysis as described below.

#### Mass Spectrometry

The samples prepared above were analyzed using a QStar Elite quadrupole/time-of-flight mass spectrometer equipped with a TurboIonSpray® ion source (AB Sciex, Framingham, MA, USA). A 10- $\mu$ L aliquot of each sample was injected into a flowing carrier stream consisting of 0.1% formic acid/50% methanol at 40  $\mu$ L/min, which was directly introduced into the ion source of the mass spectrometer. A Shimadzu LC-20AD pump (Columbia, MD, U.S.A.) was used to deliver the carrier solvent. Mass spectra (from m/z 100 to 300) were acquired in the time-of-flight mass analyzer with 1 sec accumulation time. Analyst QS software (version 2.0, AB Sciex) was used for instrument control, data acquisition, and data processing.

#### Measurement of HX Rate Constant (k) and pKa

The pseudo-first-order rate constant (k) of the HX reaction was determined by monitoring changes in the ratios of the M+1/M isotopic peak of a given imidazole derivative before (time = 0) and after (time = t) the HX reaction as described previously (11). The p $K_a$  values of imidazole derivatives were obtained from the sigmoid titration curve of k versus pH\* using Origin Graphing software (version 8.5, OriginLab, Northampton, MA) using the following equation.

$$y=A_2+\frac{A_1-A_2}{1+e^{(x-x_0)/\delta_x}}$$

where  $A_1$  is the minimum rate constant at the lowest pH\*,  $A_2$  is the maximum rate constant at the highest pH\*,  $x_0$  is the point of inflection, and  $\delta_x$  is the change in *x* corresponding to the most significant change in *y* values.

#### **RESULTS AND DISCUSSION**

#### Relationship between <sup>ikmax</sup> and pK<sub>a</sub>

Figure 2a shows the rate profiles of the HX reactions of histamine, Ac-His-NHMe, Ac-His-OH, and IPA at 25°C as a function of pH\*. The p $K_a$  values of these four model compounds obtained from the inflection point of the sigmoidal curves were: 5.42 for histamine, 6.35 for Ac-His-NHMe, 7.38 for Ac-His-OH, and 7.77 for IPA. This suggests that a neighboring amino group lowers the p $K_a$  of imidazole group as in the case of histamine, whereas a neighboring carboxyl group raises the p $K_a$  as in the case of Ac-His-OH and IPA. This result is consistent with the well-established fact that neighboring electron-withdrawing groups (e.g., RNH<sub>3</sub><sup>+</sup>, GdnH<sup>+</sup>, ImH<sup>+</sup>) lower the p $K_a$  of the imidazole group, whereas neighboring electron-donating groups (e.g., RCOO<sup>-</sup>, RO<sup>-</sup>, RS<sup>-</sup>) raise it (18). The p $K_a$  of Ac-His-NHMe is considered to be the intrinsic p $K_a$  of the imidazole group in proteins that have no adjacent dissociable groups.

The rate profiles in Figure 2a also provide the maximum k values ( $k^{max}$ ) for the imidazole derivatives. The obtained values were 0.0016, 0.0029, 0.0057, and 0.0104 (hr<sup>-1</sup>) for histamine, Ac-His-NHMe, Ac-His-OH, and IPA, respectively. As expected from the reaction mechanism (2–4, 6), the  $k^{max}$  increased with increasing p $K_a$  in these four model compounds. Because the imidazole groups of these compounds are fully exposed to the bulk solvent, these  $k^{max}$  values can be considered to be their intrinsic  $k^{max}$  ( $ik^{max}$ ) values. In the base-catalyzed reaction, the plot of the common logarithm of the reaction rate constant,

## General formula to calculate the $pK_a$ -specific ${}^{i}k_{max}$ values of imidazole groups at a specific temperature

Although the equation obtained above can be used to find the  $pK_a$ -specific  $\log^i k^{\max}$  values of imidazole groups at 25°C, the HX reaction may be carried out at a different temperature. To obtain a general formula to calculate the  $pK_a$ -specific  $\log^i k^{\max}$  values of imidazole groups at any specific temperature, we determined the  ${}^{i}k^{max}$  values for the four model compounds at 31 and 37 °C as well (Table 1). The  ${}^{i}k^{max}$  values of the model compounds at each temperature were converted to  $\log^{i} k^{\max}$  and plotted against their pK<sub>a</sub> values (Figure 3a). The magnitude of the  $\log^{i} k^{\max}$  values increased as the temperature increased; however, as can be seen, the slopes of the three linear regression lines remained unchanged. We therefore averaged the three slope values, yielding a value of 0.3159, and used this in the general formula given below. In addition to the common slope value, the general formula requires the temperature-specific y-intercept values. The relationship between the yintercept and temperature was obtained by plotting the y-intercept values at  $pK_a = 7.0$  from the three linear regression lines against the temperature, as shown in Figure 3b. Note that the y-intercept values at  $pK_a = 7.0$  were used, because they are much closer to the  $pK_a$  values of typical imidazole groups in proteins than those at  $pK_a = 0$ , and are thus expected to provide more accurate  $\log^{i} k^{\max}$  values around typical p $K_{a}$  values of imidazole groups. From the plot, the relationship between the y-intercept at  $pK_a = 7.0$  and temperature (T) was found to be:

 $y=0.0576 \times T - 3.7467$ 

where y is the y-intercept value at  $pK_a = 7.0$  and T is the temperature in Celsius. Thus, the general formula to calculate the  $pK_a$  specific  $\log^i k^{\max}$  value of an imidazole group at a specific temperature was derived to be:

 $log^{i}k^{max} = 0.3159 \times (pK_{a} - 7) + (0.0576 \times T - 3.7467)$ 

and, inverting the logarithm function gives us  ${}^{i}k^{max}$  value.

#### Quantitative analysis of solvent accessibilities of five histidine imidazole groups in DHFR

We recently reported the  $pK_a$  and  $k^{max}$  of five histidine imidazole groups in dihydrofolate reductase (DHFR) (11). The data was obtained at 37°C. The experimentally determined  $pK_a$ and  $k^{max}$  values of the five imidazole groups in apo-DHFR, and their  ${}^{i}k^{max}$  values at 37°C calculated using the general formula are shown in Table 2. On the basis of solely the  $k^{max}$ values, the most reactive residue is His141 and the reactivity decreases in the following order: His141 > His45 > His149 > His 124 > His114. However, we cannot simply assume that the decreasing order of reactivity is same as the decreasing order of solvent accessibility, because the magnitude of their intrinsic reactivities (rate constants),  ${}^{i}k^{max}$ , are influenced significantly by their  $pK_a$  values. Therefore, in order to accurately describe the solvent accessibilities of the histidine imidazole groups, we propose to use the protection factors (PF) defined as the ratio of the HX rate of a given histidine imidazole group when it is in a fully solvent-exposed state ( ${}^{i}k^{max}$ ) to the HX rate in the protein ( $k^{max}$ ) as shown below.

 $PF = \frac{{^ik}^{max}}{{k^{max}}}$ 

In this definition, the smaller the value, the higher the solvent accessibility, and a value of 1 indicates full exposure to the bulk solvent. Now it is evident in the table that the true solvent accessibility decreases in the following order: His45  $\approx$  His149 > His141 > His 124 > His114, which is different from the order obtained based solely on the reactivity of these residues (log $k^{max}$  values) described above. Analogous PF concepts are used in amide-HX, especially in NMR studies (19).

The straight line in Figure 4 shows the relationship between  $\log^{i} k^{\max}$  and  $pK_{a} (\log^{i} k^{\max} - pK_{a} \text{ plot})$  at 37°C produced using the general formula. In the figure, the  $\log k^{\max}$  values of the five imidazole groups in DHFR are plotted. The solvent accessibilities of the five imidazole groups are indicated by the distance from the straight line of the plot to the plotted individual  $k^{\max}$  values. On the plot, the shorter the distance, the higher the solvent accessibility, and the presence of any plotted point on the straight line indicates that the corresponding imidazole group is fully exposed to the bulk solvent. For easy understanding, the PF values for these histidine residues from Table 2 are also shown. We found that this type of plot with the PF values is convenient to visually indicate the solvent accessibility of imidazole groups in proteins.

Figure 5 shows how the solvent accessibilities of five imidazole groups in apo-DHFR (black circles) change upon folate and NADP<sup>+</sup> binding. The experimentally determined  $pK_a$  and  $k^{max}$  values of the five imidazole groups in DHFR-folate-NADP<sup>+</sup> are shown in Table 2. It is clearly seen in the plot that the solvent accessibilities of His114 and His124 decrease upon ligand binding, whereas the solvent accessibility of His45 increases, accompanied by an increased  $pK_a$ . Thus, the  $\log^i k^{max} - pK_a$  plot is useful to visualize the changes of solvent accessibility and  $pK_a$  of imidazole groups in proteins.

It is worth mentioning that one can carry out an experiment measuring the  ${}^{i}k^{max}$  values of imidazole groups in a completely unfolded protein, and compares the values with the  $k^{\text{max}}$ values in the folded protein to obtain the PF values. Such approaches are effective in estimating the intrinsic HX rates for backbone amide N-H groups (20), which are significantly influenced by the two adjacent side chains even in the absence of folded structure (21). This is because the two adjacent side chains have different degrees of steric hindrance and inductive effects to the amide N-H group between them. However, in case of His-HX the values obtained by such experiments do not accurately reflect the  ${}^{i}k^{max}$  values of these imidazole groups because of the following two reasons. First, the  $pK_a$  of imidazole groups in the unfolded protein are different from those in the folded protein due to the loss of electrostatic effect by the neighboring side chains and other structural elements in the three dimensional geometry, which exists only in the folded state. Second, in contrary to the amide HX, no steric hindrance by the adjacent side chains to the imidazole groups in unfolded structure is expected, though they may elicit inductive effect. Such inductive effect, however, should alter the  $pK_a$  of the imidazole ring, and therefore is taken into account in the pKa specific  ${}^{i}k^{max}$  values. Thus, the  ${}^{i}k^{max}$  values of imidazole groups need to be determined by the model compounds with different  $pK_a$  values whose imidazole groups are fully solvent exposed.

## Correlation of the PF values with solvent accessible surface areas obtained from X-ray diffraction data

The solvent accessible surface areas of the  $C^{e1}$  atom of five histidine imidazole groups in apo-DHFR and DHFR-folate-NADP<sup>+</sup> complex are shown in Table 2. Note that the smaller the PF values, the higher the solvent accessibility; while the larger the ASA values, the higher the solvent accessibility. On the basis of the PF values for the histidine residues in apo-DHFR, the solvent accessibility decreases in the following order: His45  $\approx$  His149 > His141 > His 124 > His114, while ASA data suggests the following order: His45 > His141 > His 124 > His114  $\approx$  His149. The only difference is His149, for which the PF value indicates that the residues is quite accessible to the bulk solvent, yet the ASA data indicates that His149 is the least solvent accessible residue. This discrepancy may be reflecting the difference in protein structures in the solution and crystal. We performed a two-sample Wilcoxon rank-sum test (22) for assessing whether the solvent accessibility ranked by the PF and ASA are statistically different. The analysis for the two rankings gave the Pearson's Correlation Coefficient of 0.53 with the *p*-value for the Wilcoxon rank-sum test of 0.84 (the null hypothesis was that the distributions of PF and ASA are the same), indicating that the difference between the two rankings is not significantly different. Likewise, the solvent accessibility ranking of these histidine residues by the PF and ASA in DHFR-folate-NADP+ complex appeared quite similar to each other as can be seen in Table 2 in the following order: His45 > His141  $\approx$  His149 > His124 > His114. The statistical analysis for the two rankings gave the Pearson's Correlation Coefficient of 0.93 with the p-value for the Wilcoxon rank-sum test of 0.15. Thus, the solvent accessibilities indicated by the PF values appear to agree well with ASA data. It should be noted, however that the ASA values we used were for only the  $C^{e1}$  atom of imidazole group. When we used the ASA values for entire imidazole ring we did not find good correlation with the FA values. The finding suggests that it is not necessary for an imidazole group to be entirely exposed to the bulk water for the HX to occur. Further accumulation of His-HX data will clarify this point.

Even though the data size is small, the decent correlation between the PF and SAS value suggests that the PF value reflects the solvent accessibility of imidazole groups in proteins. This is contrary to amide HX, in which the critical event that allows exchange is hydrogenbond separation and exposure, not solvent access to the amide N-H group (23). More data on PF will be needed to confirm the positive correlation between the PF and SAS.

#### Temperature dependence of the <sup>i</sup>k<sup>max</sup>

The <sup>i</sup> $k^{max}$  values for the four model compounds at different temperatures presented in Table 1 were used to generate Arrhenius plots (Figure 6). From the plots the activation energies of the HX reaction for histamine, Ac-His-NHMe, Ac-His-OH, and IPA were estimated to be 104, 106, 102, and 99 kJ/mol, respectively. These values agree well with the value of 104 kJ/mol obtained with L-histidine at pH\* 9 (6), at which the obtained rate constant can be considered to be <sup>i</sup> $k^{max}$ .

In summary, we have described a method to measure the solvent accessibility of histidine imidazole groups in proteins. The key assumption underlying the analysis is that the structure and solvent accessibility does not change over the pH range investigated. It can easily be tested whether the assumption holds by comparing the experimentally obtained titration curves with the theoretical curves. For example, the titration curves of the four model compounds can be superimposed perfectly on their theoretical curves, suggesting no cooperative conformational rearrangement occurred on these compounds over the pH range investigated. However, it may not be unusual to find imidazole groups in proteins whose titration curves are not superimposed on the theoretical ones. Such non superimposable titration curves are indicative of the pH dependent changes of local electrostatic or

hydrophobic environment, or both, of the given imidazole group. Apparently, the PF values cannot be given to the buried non titratable imidazole groups. However, based on the analytical limit of the measurement, the data can provide information on "how slow the HX rates are" by providing the half-lives ( $t_{1/2}$ ) of their HX reactions (9, 11). The measure of solvent accessibility expressed as PF value is an independent value and can be compared with the values of other imidazole groups in the same protein or in other proteins. The present method is intended to be used for the data obtained by mass spectrometry, however could also be used for the HX data obtained by <sup>1</sup>H NMR spectroscopy. The log<sup>i</sup> $k^{max} - pK_a$  plot is useful to show visually the solvent accessibilities of imidazole groups in proteins.

#### **Supplementary Material**

Refer to Web version on PubMed Central for supplementary material.

#### Acknowledgments

The authors wish to thank Drs. Takashi Nakazawa (Nara Women's University) and Chris Dealwis (Case Western Reserve University) for helpful discussion and Dr. Jean-Eudes Dazardfor (Case Western Reserve University) for performing the statistical analysis on PF and ASA data.

FUNDING: This study was supported by NIH grant P30EY-11373 (Visual Sciences Research Center of Case Western Reserve University) and funds from Case Western Reserve University and the Cleveland Foundation.

#### Abbreviations

Ac-His-OH	N <sup>a</sup> -acetyl-DL-histidine
Ac-His-NHMe	$N^{\alpha}$ -acetyl-L-histidine methylamide
ASA	solvent accessible surface areas
DHFR	dihydrofolate reductase
НХ	hydrogen exchange
IPA	1H-imidazole-5-propanoic acid
MS	mass spectrometry
NADP <sup>+</sup>	nicotinamide-adenine dinucleotide phosphate
NMR	nuclear magnetic resonance
PF	protection factor

#### References

- Olofson RA, Thompson WR, Michelman JS. Heterocyclic nitrogen ylides. J Am Chem Soc. 1964; 86:1865–1866.
- Vaughan JD, Mughrabi ZE, Wu C. The kinetics of deuteration of imidazole. J Org Chem. 1970; 35:1141–1145.
- Bradbury JH, Chapman BE, Pellegrino FA. Hydrogen-deuterium exchange kinetics of the C-2 protons of imidazole and histidine compounds. J Am Chem Soc. 1973; 95:6139–6140. [PubMed: 4733837]
- 4. Amyes TL, Diver ST, Richard JP, Rivas FM, Toth K. Formation and stability of N-heterocyclic carbenes in water: the carbon acid pKa of imidazolium cations in aqueous solution. J Am Chem Soc. 2004; 126:4366–4374. [PubMed: 15053626]
- Harris TM, Randall JC. Deuterium exchange reactions at the C2-position of imidazoles. Chem Ind. 1965; 41:1728–1729. [PubMed: 5842032]

- Bradbury HJ, Chapman BE, Crompton MW, Norton RS, Teh JS. Hydrogen–deuterium exchange of the C-2 protons of histidine and histidine peptides and proteins. Journal of the Chemical Society, Perkin Transactions II. 1980:693–700.
- 7. Miyagi M, Nakazawa T. Determination of pKa values of individual histidine residues in proteins using mass spectrometry. Anal Chem. 2008; 80:6481–6487. [PubMed: 18665614]
- Markley, JL.; Cheung, SM. Differential exchange of the C2-hydrogens of histidine side chains in native proteins: proposed general technique for the assignment of histidine NMR peaks in proteins. Proc. Int. Conf. Stable Isot. Chem. Biol. Med., 1st; 1973. p. 103-118.
- Lodowski DT, Palczewski K, Miyagi M. Conformational Changes in the G Protein-Coupled Receptor Rhodopsin Revealed by Histidine Hydrogen-Deuterium Exchange. Biochemistry. 2010; 49:9425–9427. [PubMed: 20939497]
- Wimalasena DS, Janowiak BE, Lovell S, Miyagi M, Sun J, Zhou H, Hajduch J, Pooput C, Kirk KL, Battaile KP, Bann JG. Evidence that histidine protonation of receptor-bound anthrax protective antigen is a trigger for pore formation. Biochemistry. 2010; 49:6973–6983. [PubMed: 20672855]
- Miyagi M, Wan Q, Ahmad MF, Gokulrangan G, Tomechko SE, Bennett B, Dealwis C. Histidine hydrogen-deuterium exchange mass spectrometry for probing the microenvironment of histidine residues in dihydrofolate reductase. PLoS One. 2011; 6:e17055. [PubMed: 21359214]
- Tran DT, Bannerjee S, Alayash AI, Crumbliss AL, Fitzgerald MC. Slow Histidine H/D Exchange Protocol for Thermodynamic Analysis of Protein Folding and Stability using Mass Spectrometry. Anal Chem. 2011
- Konermann L, Pan J, Liu YH. Hydrogen exchange mass spectrometry for studying protein structure and dynamics. Chem Soc Rev. 2011; 40:1224–1234. [PubMed: 21173980]
- Markley JL. Correlation proton magnetic resonance studies at 250 MHz of bovine pancreatic ribonuclease. I. Reinvestigation of the histidine peak assignments. Biochemistry. 1975; 14:3546– 3554. [PubMed: 240382]
- Shindo H, Cohen JS. Nuclear magnetic resonance titration curves of histidine ring protons. Ribonuclease S-peptide and S-proteins. J Biol Chem. 1976; 251:2648–2652. [PubMed: 4455]
- Haynes, WM., editor. CRC Handbook of Chemistry and Physics. 92. CRC Press/Taylor and Francis; Boca Raton, FL: 2011. (Internet Version 2012)
- Minamino, N.; Matsuo, H.; Narita, K. Tritium exchange titration of imidazole derivatives Factors affecting on pKa and reactivity of imidazole ring. In: Shiba, T., editor. Peptide Chemistry-1977. Protein Research Foundation; Osaka: 1978. p. 85-90.
- Barlin, GB.; Perrin, DD. Dissociation constants in the elucidation of structure. In: Bentley, KW.; Kirby, GW., editors. Elucidation of Organic Structures by Physical and Chemical Methods. Vol. Part I. Wiley; New York: 1972. p. 611-677.
- Pan Y, Briggs MS. Hydrogen exchange in native and alcohol forms of ubiquitin. Biochemistry. 1992; 31:11405–11412. [PubMed: 1332757]
- 20. Buck M, Radford SE, Dobson CM. Amide hydrogen exchange in a highly denatured state. Hen egg-white lysozyme in urea. J Mol Biol. 1994; 237:247–254. [PubMed: 8145239]
- Bai Y, Milne JS, Mayne L, Englander SW. Primary structure effects on peptide group hydrogen exchange. Proteins. 1993; 17:75–86. [PubMed: 8234246]
- 22. Wilcoxon F. Individual Comparisons by Ranking Methods. Biometrics Bulletin. 1945; 1:80-83.
- Chetty PS, Mayne L, Lund-Katz S, Stranz D, Englander SW, Phillips MC. Helical structure and stability in human apolipoprotein A-I by hydrogen exchange and mass spectrometry. Proc Natl Acad Sci U S A. 2009; 106:19005–19010. [PubMed: 19850866]



#### Figure 1.

A hypothetical rate profile of the HX reaction of the imidazole C<sup>e1</sup>-hydrogen, plotting the pseudo first-order rate constant (*k*) against pD. The rate profile was produced by computing the *k* against varying pD using the equation,  $k = k_2 K_W / (K_a + [D^+])$ , where  $k_2$  is the second order rate constant for the rate-determining step of the HX reaction;  $K_W$  is the ion product of heavy water, and  $K_a$  is the dissociation constant of the imidazolium cation. The  $k_2$ ,  $K_W$  and  $K_a$  were set to be 1 (mol<sup>-1</sup>•hr<sup>-1</sup>), 10–14 (mol<sup>2</sup>/L) and 10<sup>-7</sup> (mol/L), respectively, in this simulation. The  $pK_a$  of the imidazole group can be obtained from the inflection point of the sigmoidal curve, and the maximum pseudo first-order rate constant,  $k^{max}$ , from the upper plateau of the sigmoidal curve.



#### Figure 2.

pH\* and p $K_a$  dependence of HX reaction at the C<sup>e1</sup>-position of imidazole groups. (a) pH\* dependence of the *k* for HX at the imidazole group in histamine (red), Ac-His-NHMe (blue), Ac-His-OH (green), and IPA (black). The experimentally obtained p $K_a$  and the intrinsic  $k^{\text{max}}$  (<sup>i</sup> $k^{\text{max}}$ ) for the four imidazole derivatives are shown. (b) log<sup>i</sup> $k^{\text{max}} - pK_a$  plot for the HX reaction at the C<sup>e1</sup>-position of imidazole at 25°C in 1, histamine; 2, Ac-His-NHMe; 3, Ac-His-OH; and 4, IPA. The equation and the correlation coefficient ( $r^2$ ) of the linear regression line are presented.

Mullangi et al.



#### Figure 3.

 $\log^{i} k^{\max} - pK_{a}$  plots at different temperatures for the HX reaction at the C<sup>e1</sup>-position of imidazole. (a) 1, histamine; 2, Ac-His-NHMe; 3, Ac-His-OH; and 4, IPA. The linear regression analyses for 25, 31, and 37°C plots yielded slope values of 0.3255, 0.3129, and 0.3094, and y-intercept values (at  $pK_{a} = 7.0$ ) of -2.3001, -1.9723, -and -1.6097, respectively. (b) The relationship between the y-intercept value and temperature is shown. The y-intercept values at  $pK_{a} = 7.0$  were obtained from Figure 4a. The equation and the correlation coefficient ( $r^{2}$ ) of the linear regression line are presented.



#### Figure 4.

 $\log k^{\max}$  values of five histidine imidazole groups in apo-DHFR, plotted on the  $\log^i k^{\max} - pK_a$  plot at 37°C. The straight line in the figure was produced using the formula:  $\log^i k^{\max} = 0.3159 \times (pK_a - 7) + (0.0576 \times 37 - 3.7467)$ . The black circles are  $\log k^{\max}$  values of five histidine imidazole groups in apo-DHFR. The numbers in the parentheses are PF values for the imidazole groups.



#### Figure 5.

Changes in solvent accessibilities of five histidine imidazole groups in apo-DHFR upon folate and NADP<sup>+</sup> binding. The log $k^{max}$  values of five histidine imidazole groups in apo-DHFR (circles) and DHFR-folate-NADP<sup>+</sup> complex (triangles) are plotted on the log<sup>i</sup> $k^{max} - pK_a$  plot at 37°C. The straight line in the figure was produced using the formula: log<sup>i</sup> $k^{max} = 0.3159 \times (pK_a - 7) + (0.0576 \times 37 - 3.7467)$ .

Mullangi et al.



#### Figure 6.

Arrhenius plots of the HX reaction at the C<sup>e1</sup>-position of the imidazole groups of 1, histamine; 2, Ac-His-NHMe; 3, Ac-His-OH; and 4, IPA.





#### Table 1

 $^{i}K^{max}$  values of imidazole derivatives at different temperatures

			<sup>i</sup> k <sup>max</sup> (hr <sup>-1</sup> )	
	$a_{\mathbf{p}K_{\mathbf{a}}}$	25°C	31°C	37°C
Histamine	5.42 (±0.11)	0.0016 (±0.0001)	0.0036 (±0.0002)	0.0082 (±0.0009)
Ac-His-NHMe	6.35 (±0.03)	0.0029 (±0.0001)	0.0065 (±0.0002)	0.0153 (±0.0003)
Ac-His-OH	7.38 (±0.02)	0.0057 (±0.0001)	0.0124 (±0.0003)	0.0278 (±0.0005)
IPA	7.77 (±0.01)	0.0104 (±0.0001)	0.0208 (±0.0003)	0.0483 (±0.0011)

<sup>*a*</sup>The p $K_a$  values were values obtained at 25°C from the pH\* dependence of the measured exchange rate.

\_

# Table 2

Solvent accessibilities of five imidazole groups in apo-DHFR and DHFR-folate-NADP+

 $\mathbf{p}K_{\mathbf{a}} = k^{\max}(\mathbf{hr}^{-1})^{\mathbf{d}} = \mathbf{i}k^{\max}(\mathbf{hr}^{-1})^{\mathbf{b}} = \mathbf{PF}^{\mathbf{c}} = \mathbf{ASA}^{\mathbf{d}}$ 

s45         6.99         0.0131         0.0241         1.8         46.0           i14         6.84         0.0017         0.0216         12.4         16.4           i124         7.60         0.0083         0.0375         4.5         25.1           i141         8.04         0.0178         0.0316         2.9         38.7           i149         6.51         0.0087         0.0170         1.9         16.1 <b>IFR-folate-NADP+</b> 0.0170         1.9         16.1         51.5           s45         7.30         0.0265         0.0301         1.1         51.5           s45         7.30         0.0265         0.0374         31.5         17.0           s114         7.17         0.0009         0.0274         31.5         17.0           s124         7.61         0.00274         31.5         17.0           s124         8.14         0.02033         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	HQ-0	FR				
I14         6.84         0.0017         0.0216         12.4         16.4           s124         7.60         0.0083         0.0375         4.5         25.1           s141         8.04         0.0178         0.0316         2.9         38.7           s149         6.51         0.0087         0.0170         1.9         16.1 <b>FFR-folate-NADP+</b> 0.0170         1.9         16.1         31.5           s149         6.51         0.0087         0.0301         1.1         51.5           s144         7.17         0.0009         0.0274         31.5         17.0           s124         7.61         0.0047         0.0378         8.1         26.2           s144         8.14         0.0203         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	is45	6.99	0.0131	0.0241	1.8	46.0
s124         7.60         0.0083         0.0375         4.5         25.1           s141         8.04         0.0178         0.0516         2.9         38.7           s149         6.51         0.0087         0.0170         1.9         16.1           HFR-folate-NADP+         0.0170         1.9         16.1         51.5           s144         7.17         0.00265         0.0301         1.1         51.5           s144         7.17         0.0009         0.0274         31.5         17.0           s141         8.14         0.02031         0.0378         8.1         26.2           s144         8.14         0.02033         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	s114	6.84	0.0017	0.0216	12.4	16.4
sill         8.04         0.0178         0.0516         2.9         38.7           sild         6.51         0.0087         0.0170         1.9         16.1 <b>HFR-folate-NADP+</b> 0.0170         1.9         16.1         1.5           sild         7.30         0.0265         0.0301         1.1         51.5           sild         7.17         0.0009         0.0274         31.5         170           sild         7.17         0.00047         0.0378         8.1         26.2           sild         8.14         0.10203         0.0555         2.7         35.7           sild         6.0111         0.0216         1.9         35.1	s124	7.60	0.0083	0.0375	4.5	25.1
si 49         6.51         0.0087         0.0170         1.9         16.1 <b>HFR-folate-NADP+</b>	s141	8.04	0.0178	0.0516	2.9	38.7
<b>HFR-folate-NADP+</b> is45         7.30         0.0265         0.0301         1.1         51.5           s114         7.17         0.0009         0.0274         31.5         17.0           s124         7.61         0.0047         0.0378         8.1         26.2           s141         8.14         0.0203         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	s149	6.51	0.0087	0.0170	1.9	16.1
is45         7.30         0.0265         0.0301         1.1         51.5           s114         7.17         0.0009         0.0274         31.5         17.0           s124         7.61         0.0047         0.0378         8.1         26.2           s141         8.14         0.0203         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	HFR-f	olate-NA	+4C			
\$114         7.17         0.0009         0.0274         31.5         17.0           \$124         7.61         0.0047         0.0378         8.1         26.2           \$141         8.14         0.0203         0.0555         2.7         35.7           \$149         6.84         0.0111         0.0216         1.9         35.1	is45	7.30	0.0265	0.0301	1.1	51.5
s124         7.61         0.0047         0.0378         8.1         26.2           s141         8.14         0.0203         0.0555         2.7         35.7           s149         6.84         0.0111         0.0216         1.9         35.1	s114	7.17	0.0009	0.0274	31.5	17.0
silt         8.14         0.0203         0.0555         2.7         35.7           silt9         6.84         0.0111         0.0216         1.9         35.1	s124	7.61	0.0047	0.0378	8.1	26.2
s149 6.84 0.0111 0.0216 1.9 35.1	s141	8.14	0.0203	0.0555	2.7	35.7
	s149	6.84	0.0111	0.0216	1.9	35.1

<sup>a</sup>Calculated from the reported  $t_1/2$  (day) values using the equation:  $K^{\text{IIIAX}} = \ln 2/t_1/2/24$ .

 $b_{\text{Calculated using the formula: } i_{k}\text{max} = 10^{\text{Alog}i_{k}\text{max}}$ .

cCalculated using the formula: PF =  $i k^{\text{maX}}/k^{\text{maX}}$ .

<sup>d</sup>Solvent accessible surface area; the structural data of apo-DHFR (PDB code number: 5DFR) and DHFR-folate-NADP<sup>+</sup> (PDB code number: 1RX2) were used to obtain the ASA for the C<sup>e1</sup> atom of the five histidine residues.