Precise Probing of Residue Roles by Post-Translational $\beta,\gamma$-C,N Aza-Michael Mutagenesis in Enzyme Active Sites

Jitka Dadová, ‡ Kuan-Jung Wu, ‡ Patrick G. Isenegger, ‡ James C. Errey, ‡ Gonçalo I. L. Bernardes, ‡,†,‡,∥ Justin M. Chalker,§‖ Lluís Raich,§ Carme Rovira,§,∥ and Benjamin G. Davis§,†,*

‡Chemistry Research Laboratory, Department of Chemistry, University of Oxford, Mansfield Road, Oxford OX1 3TA, U.K. §Departament de Química Inorgànica i Orgànica (secció de Química Orgànica) & Institut de Química Teòrica i Computacional (IQTCUB), Universitat de Barcelona, Martí i Franquès 1, 08028 Barcelona, Spain ∥Institució Catalana de Recerca i Estudis Avançats (ICREA), Passeig Lluís Companys, 23, 08010 Barcelona, Spain

Supporting Information

ABSTRACT: Biomimicry valuably allows the understanding of the essential chemical components required to recapitulate biological function, yet direct strategies for evaluating the roles of amino acids in proteins can be limited by access to suitable, subtly-altered unnatural variants. Here we describe a strategy for dissecting the role of histidine residues in enzyme active sites using unprecedented, chemical, post-translational side-chain-$\beta,\gamma$ C–N bond formation. Installation of dehydroalanine (as a “tag”) allowed the testing of nitrogen conjugate nucleophiles in “aza-Michael”-1,4-additions (to “modify”). This allowed the creation of a regioisomer of His (iso-His, His$_{iso}$) linked instead through its pros-N$\equiv$C bond formation. Installation of dehydroalanine (as a “tag”) allowed the testing of nitrogen conjugate nucleophiles in “aza-Michael”-1,4-additions (to “modify”). This allowed the creation of a regioisomer of His (iso-His, His$_{iso}$) linked instead through its pros-N$\equiv$C atom rather than naturally linked via C4, as well as an aza-altered variant aza-His$_{iso}$. The site-selective generation of these unnatural amino acids was successfully applied to probe the contributing roles (e.g., size, H-bonding) of His residues toward activity in the model enzymes subtilisin protease from Bacillus lentus and Mycobacterium tuberculosis pantothenate synthetase.

INTRODUCTION

Covalent protein chemistry provides well-appreciated opportunities in protein labeling and the attachment of cargoes. It also has great potential in allowing the creation of subtle changes and in the creation of precise alterations and functional mimics in proteins, beyond the limits of traditional biology, that in turn can allow deeper understanding of protein mechanism. Among one of the most intriguing strategies is a notion of alteration to test recapitulation of (e.g., enzymatic) activity through the replacement of a “lost” functional group with a variant (sometimes known as chemical “rescue”). This has been applied in various ways including, for example, the rescue by a noncovalently associated prosthetic (that may have relevance to more general activation by small molecules); or by the “uncaging” of encoded “caged” unnatural amino acids. As a form of “covalent chemical rescue”, chemical modifications of amino acid residues in enzyme active sites have primarily explored cysteine (Cys) aminoethylation to mimic lysine (Lys) (e.g., ribulosebisphosphate carboxylase/oxygenase, aspartate aminotransferase, leader peptidase, aldolase, topoisomerase, sugar lyase, and pantothenate synthetase); with other, more rare, examples of attempted mimicry of arginine (Arg); glutamate (Glu); and even histidine (His). However, most of these mimics differ in critical parameters such as size, constitution, and/or side-chain length. To our knowledge, no strategies for mimicking amino acids as their direct regioisomers have been possible to date; these would have the potential to act as precisely different isosteres allowing careful dissection of contributing functions. Here, we create and test the effectiveness of the first such regioisomer of His in proteins, using a variant that is linked regioisomerically through its pros-N$\equiv$C atom (iso-His, His$_{iso}$) rather than naturally linked via C4 (Figure 1a) and its aza-analogue (aza-His$_{iso}$).

RESULTS

We chose to explore the effect of chemical mutagenesis on enzyme activity through conversion via cysteine (Cys) to the His-mimic residue iso-histidine (His$_{iso}$, Figure 1). His can be a sensitive catalytic residue in several enzymes and Cys would provide a dramatically different side chain in a logical mutational analysis pathway: e.g., His $\rightarrow$ Cys $\rightarrow$ His$_{iso}$ (Figure 1a). We reasoned that His$_{iso}$ (and variants) could in principle be introduced site-selectively using a “tag-and-modify” approach (Figure 1b) based on the installation of dehydroalanine (Dha) (potentially from cysteine (Cys) followed by conjugate Michael-type addition. Until now, addition of sulfur nucleophiles to Dha (“thio-Michael-type” additions) has been the dominant use of this unnatural amino acid residue in proteins, including use in “chemical rescue”. However, other potential nucleophiles, such as amines, could

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be considered (“aza-Michael-type” additions, Figure 1b), thereby opening the door to this new form of protein modification.\textsuperscript{32} We report here a validation of this approach on intact proteins through the first examples of $\beta_\gamma$-C,N bond formation.\textsuperscript{33–35} Prior examples of aza-Michael additions, attempted only on extended acrylamido/vinylsulfonamido motifs, are rare\textsuperscript{36} and would not allow the precise mutagenesis via $\beta_\gamma$-C,N bond formation intended here. While aza-Michael reactions have typically required essentially protein-incompatible conditions (harsh catalysis\textsuperscript{37} and/or the use of organic solvents\textsuperscript{38,39}), the noted beneficial effect of aqueous media upon rate\textsuperscript{40} and the success of vinylsulfonamides\textsuperscript{41} suggested some potential.

We tested the proposed $\beta_\gamma$-C,N “aza-Michael” addition of imidazole to Dha on intact proteins using the subtilisin from Bacillus lentus\textsuperscript{42} (SBL, EC 3.4.21.62). SBL is a suitably robust model protein for this approach; it has no native Cys allowing the positioning of Dha via the chemical conversion of a Cys residue introduced through mutagenesis. Thus, the single cysteine mutant SBL-S156C (Ser156 $\rightarrow$ Cys156) was used to generate SBL-Dha156 using 2,5-dibromohexanediamide (DBHDA).\textsuperscript{30} Site 156 sits at the base of the S$_1$ (Schechter–Berger nomenclature\textsuperscript{43}) pocket of the active site. Gratifyingly, full conversion to the desired SBL-S156His$_{iso}$ demonstrating the first examples of $\beta_\gamma$-C,N bond formation on proteins, was observed after incubation of SBL-S156Dha with imidazole for 5 h at 37 °C (Figure S1). Importantly, determination of the activity of SBL-His$_{iso}$156 revealed that the conditions of installation were compatible with maintaining protein function. Prior studies have allowed chemical installation of bulky charged groups\textsuperscript{44} or classical mutagenesis to His at this site;\textsuperscript{45} through the determination of kinetic parameters (SBL-His$_{iso}$156, $k_{cat} = 122 \pm 6$ s$^{-1}$; $K_M = 0.71 \pm 0.06$ mM$^{-1}$; SBL-wt, $k_{cat} = 153 \pm 4$ s$^{-1}$; $K_M = 0.73 \pm 0.05$ mM$^{-1}$), it was confirmed that this site, where His$_{iso}$ is essentially isoseric to His without H-bond donation, has a minimal role in activity determination, consistent with an outward facing disposition.\textsuperscript{46}

Next, M. tuberculosis pantothenate synthetase (PanC; EC 6.3.2.1)\textsuperscript{47} was selected as a model protein to probe the proposed His-to-His$_{iso}$ activity “modulation” (Figure 1a). PanC catalyzes the ATP-dependent condensation of $\delta$-pantoate and $\beta$-alanine forming pantothenate (Figure 2a).\textsuperscript{17} Biosynthesis of pantothenate (vitamin B5) is essential for the growth of bacteria, yeast, and plants and, in particular, for virulence of M. tuberculosis; it is thus a potential therapeutic target.\textsuperscript{48} In the catalytic site of PanC, histidines His44 and His47 were identified as having a proposed\textsuperscript{49} critical role in ATP binding (Figure 2b); prior mutation of His $\rightarrow$ Ala in either site led to decrease in activity.\textsuperscript{22} These therefore presented potentially sensitive sites at which to test regioisomeric His$_{iso}$ mutation. Notably, both sites are buried (cf. the more surface-exposed SBL-156 site) and would provide a more stringent test of the His$_{iso}$ formation strategy.

Dha was introduced to position 44 or 47 of PanC protein by site-directed mutagenesis first to Cys44 or Cys47 to give PanC-H44C or PanC-H47C. We then explored chemical conversion to Dha through bis-alkylation/elimination reagent. Wild type PanC-wt has no native cysteine, which, as for SBL, we envisaged would enable full control of the site of Dha formation. Consistent with literature reports,\textsuperscript{22} PanC proved a challenging substrate protein, strikingly susceptible to unfolding and precipitation: this necessitated a novel strategy for Dha generation. Typical Dha-forming reaction with DBHDA\textsuperscript{30} (Figure 3, $R_1 = R_2 = \text{CONH}_2$) or the use of temperatures >25 °C over prolonged periods with any reagents

![](image1.png)

**Figure 1.** (a) Concept of protein activity probing via post-translational mutagenesis to regioisomeric His$_{iso}$ or aza-His$_{iso}$ in a protein (e.g., enzyme active site). (b) Proposed “tag-and-modify” approach to the installation of His$_{iso}$ or aza-His$_{iso}$ based on dehydroalanine (Dha) formation followed by novel $\beta_\gamma$-C,N aza-Michael addition.

![](image2.png)

**Figure 2.** (a) The condensation of $\delta$-pantoate with $\beta$-alanine catalyzed by pantothenate synthetase (PanC). (b) PanC active site image highlighting His47 and His44 and their proposed interaction with the $\alpha$ and $\beta$ phosphates of ATP, respectively, during catalysis [derived from PDB 1N2E (ref 48)].
proved detrimental to PanC (as judged by CD spectroscopy (Figure S5)). It was therefore not possible to directly chemically introduce Dha into this sensitive protein using standard methods.

Methyl 2,5-dibromopentanoate (MDBP)\textsuperscript{50} (Figure 3, R\textsubscript{1} = COOMe, R\textsubscript{2} = H), however, proved both sufficiently reactive with PanC and advantageously soluble in aqueous buffer so as to allow rapid monoalkylation. This allowed us to consider the exploitation of a rate-limiting second alkylation step to enable isolation of intermediates not typically accessible with DBHDA. This, in turn, allowed us to develop a novel, "interrupted" alkylation−elimination method (Figure 3b) as a solution to the problems of accessing Dha: first, rapid monoalkylation (prior to purification away from conditions detrimental to protein stability), followed by, second, simple prolonged incubation to allow sulfonium formation and elimination to Dha. Thus, with only 50 equiv of MDBP complete monoalkylation (step 1, Figure 3b) of PanC-H44C was observed after 45 min at 25 °C (Figure S6). Removal of excess MDBP by gel filtration at this monoalkylated state successfully ablated protein precipitation in later steps and then allowed incubation at 25 °C for 16 h with concomitant full conversion to PanC-H44Dha via intramolecular alkylation−elimination (steps 2 and 3, Figure 3b, and Figure S7). In this way, even these highly sensitive proteins proved tractable substrates. Moreover, an essentially identical "interrupted" approach also allowed the site variant PanC-H47Dha, in which site 47 is part of a helix and thus more buried, to be generated (Figure 3c). Thus, PanC-H47C was fully monoalkylated after 16 h incubation with MDBP (50 equiv), purified, then incubated, and hence, gratifyingly, fully converted after excess reagent removal and incubation (48 h at 25 °C, Figure 3c and Figure S8) to PanC-H47Dha.

Next, the reactivities of these relatively buried sites (Dha\textsubscript{44} and Dha\textsubscript{47}) were tested. First, "thio-Michael-type" addition of β-mercaptoethanol to PanC-H44Dha allowed complete conversion to the desired adduct (Figure S9), thereby confirming both accessibility and electrophilic reactivity of Dha\textsubscript{44} in PanC. Then, β,γ-C,N "aza-Michael" addition of imidazole to PanC-H44Dha and PanC-H47Dha was initially tested at 25 °C due to the noted instability (Figure S5). Pleasingly, initial examples of aza-Michael reaction at pH 9−10 were observed to PanC-H\textsubscript{iso} and PanC-H\textsubscript{iso}, however these required high excesses of imidazole and long reaction times (3 days) and typically resulted in only partial or variable conversions (50 to >95%, Figure S10). Despite instability over long periods, shorter reaction times at 37 °C proved successful (Figure 3a,b). It also proved possible to install an aza-analogue to create PanC-H\textsubscript{iso} and aza-H\textsubscript{iso} in PanC-
H44Hiso, PanC-H44azaHiso, and PanC-H47Hiso (as well as stability to enzymatic digestion) were fully confirmed by peptide mapping using proteolytic digest followed by LC−MS analysis (Figures S11, S12, and S14). Notably, attempted use of a variety of substituted imidazoles under essentially identical reaction conditions (Figure S13) failed, suggesting that only something isosteric to His (such as Hisiso or aza-Hisiso) could be accommodated at either site and highlighting the highly hindered nature of these sites. Interestingly, lower conversions were observed (Figure S15) for unoptimized test reactions with other N-heterocycles, suggesting that electronics (with potential influence upon nucleophilicity and/or basicity) may also play an important role in reactivity in such reactions.

Having successfully installed Hisiso even into these buried sites, we next tested its effect upon the enzyme activity of PanC. Kinetic parameters for PanC variants were determined by coupled spectrophotometric assay (Table 1 and Figure S16−18). Regioisomeric Hisiso, which lacks hydrogen bond donor character, allows examination of hydrogen bonding; His44’s primary role has been suggested as such a hydrogen bond donor. The measurement of these steady state parameters in the Bi-Uni-Uni-Bi Ping-Pong mechanism suggested for PanC22 requires some caution with direct mechanistic interpretation, but $k_{cat}$ reports directly on ADP formation allowing interrogation of the first half-reaction, the reversible formation of adenyl-pantoate-ADP. Mutation of His44 to Cys44 or Dha44 reduced this activity to 1−2%, as judged by $k_{cat}$, to levels consistent with prior analyses for Ala44.23 Through the creation of PanC-H44Hiso, we were able to probe the effect of altered function through this regioisomeric, “chemical mutation.” Thus, while Hisiso is a poor substitute for His in PanC, its insertion gives only the lower levels of activity seen for Ala, Cys, or Dha.

To probe the potential structural implications of the intermediate activity that was observed only for Hisiso further, we conducted a series of molecular dynamics simulations (Figure 4 and Figures S21−25), based on the available X-ray structure.24 Three cases were considered: the wt enzyme and the His44Hisiso and His44Cys mutants (Figure 4). Both neutral and protonated forms were considered for His44Hisiso. Stable Michaelis complexes were readily obtained for each complex after 40 ns; no substantial changes were seen upon increasing the simulation time. The simulations of the wt enzyme show that the side chain of His44 forms a $\text{tele-N−H}\cdots\text{O-ATP}$ hydrogen bond with the $\beta$-phosphate (Figure 4, top left). This interaction is still present in the His44Hisiso mutant if His44 is protonated (Figure 4, top right). However, only a small population of the protonated form would be expected to be present at the working pH, and the predominant form (neutral Hisiso) preferentially adopts a rotated conformation that displays no interaction with the $\beta$-phosphate. In this case Hisiso moves out toward the solvent (Figure 4, bottom right).

Together these observations are consistent with the intermediate $k_{cat}$ of PanC-His44Hisiso;33 the retained 5% activity might be attributed to a small population of protonated Hisiso and/or the facilitation of ADP release caused by the conformational rearrangement that Hisiso undergoes upon deprotonation. This population would be expected to be altered in the aza variant aza-Hisiso, a mutant that showed only lower activity. Mutation of His44 to Cys (Figure 4, bottom left) also suppresses the hydrogen bond, since Cys is further away (almost 8 Å) and prefers to interact with other residues, consistent with the lowest $k_{cat}$. Notably, suppression of the hydrogen bond in all cases changes the orientation of the $\beta$-phosphate of ATP, moving it away from the histidine that aids its activation (Figure S26), suggesting that this conformational change could be a structural determinant in the lower activities of the Hisiso and Cys mutants.

**DISCUSSION**

We demonstrate for the first time the creation of a regioisomeric pros-N-linked imidazole ring in the chemical mutant Hisiso as a mimic histidine for the C4-linked imidazole

### Table 1. Steady-State Kinetic Parameters of Wild-Type and “Chemical Mutants” of M. tuberculosis PanC

<table>
<thead>
<tr>
<th>entry</th>
<th>PanC</th>
<th>$k_{cat}$ [s$^{-1}$]</th>
<th>$K_M$ [mM]</th>
<th>$k_{cat}/K_M$ [s$^{-1}$·M$^{-1}$]</th>
<th>$K_M$ [mM]</th>
<th>$k_{cat}/K_M$ [s$^{-1}$·M$^{-1}$]</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>wild-type</td>
<td>1.6 ± 0.1</td>
<td>1.3 ± 0.1</td>
<td>1219</td>
<td>0.61 ± 0.01</td>
<td>2598</td>
</tr>
<tr>
<td>2</td>
<td>H44C</td>
<td>0.011 ± 0.001</td>
<td>0.5 ± 0.1</td>
<td>22</td>
<td>0.03 ± 0.02</td>
<td>368</td>
</tr>
<tr>
<td>3</td>
<td>H44Hiso</td>
<td>0.020 ± 0.003</td>
<td>1.1 ± 0.3</td>
<td>19</td>
<td>0.106 ± 0.008</td>
<td>193</td>
</tr>
<tr>
<td>4</td>
<td>H44Hiso</td>
<td>0.08 ± 0.01</td>
<td>nd$^b$</td>
<td>nd$^b$</td>
<td>0.16 ± 0.09</td>
<td>500</td>
</tr>
<tr>
<td>5</td>
<td>H44azaHiso</td>
<td>0.0123 ± 0.002</td>
<td>nd$^b$</td>
<td>nd$^b$</td>
<td>0.12 ± 0.01</td>
<td>102</td>
</tr>
</tbody>
</table>

$^25$°C, 100 mM Hepes (pH 7.8), 10 mM MgCl$_2$, 10 mM ATP, [N-pantoate] or [β-alanine] is 0.01−5 mM while the other is saturated and constant at 5 mM. Coupled assay with 1 mM phosphoenolpyruvate, 200 μM NADH, myokinase, pyruvate kinase, and lactate dehydrogenase (18 U/mL each). $^b$nd = not determined due to an inability to determine a $K_M$ using concentration range <5 mM, and the associated β-alanine. $K_M$ is thus a $K_M$app; see Supporting Information.

![Figure 4. Representative structures obtained from molecular dynamics simulations (40 ns) of the wt enzyme (top left) and the mutants of the His44 residue to Cys (bottom left), neutral iso-His (bottom right), and protonated iso-His (top right).](https://example.com/fig4.png)
in His in two enzymes, as well as a corresponding aza variant (aza-Hisiso). This ability to perform aza-Michael-type chemical, post-translational mutation not only allows mechanistic hypothesis testing, as we have shown here, but may have broader utility in exploring other His-mediated modulation of activities such as nucleophilicity, basicity, metal-binding, and even the pH range in which a protein might operate. As such, iso-His highlights the broader value of regioisomeric mutants and might now be considered a new, conservative mutation that may be installed even into active sites in sensitive proteins, as we show here. And such, both this post-translational strategy and the new Hisiso and aza-Hisiso mutations disclosed here complement other methods for exploring the role of histidine in proteins.54,55,56 For example, prior cotranslational biosynthetic methods using residue-specific replacement54 or amber-codon suppression55,56 have allowed incorporation of certain non-cargoes, probes, or labels.32

Michael-type chemistry at Dha may provide a usefully general biosynthetic tolerances. More generally, post-translational, aza-isomeric analogues but all can struggle with other analogues, the new Hisiso and aza-His iso mutations disclosed here may be installed even into active sites in sensitive proteins, as and might now be considered a new, conservative mutation that iso-His highlights the broader value of regioisomeric mutants and more generally, post-translational, aza-Michael-type chemistry at Dha may provide a usefully general mode of protein conjugation for the attachment of other cargoes, probes, or labels.52

ASSOCIATED CONTENT

Supporting Information
The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acscentsci.7b00341.

Figures S1–26 and details of protein expression and purification, LC–MS and MS/MS analyses, enzyme activity assays, chemical mutations, structural analyses, sequences, and computational methods (PDF)

AUTHOR INFORMATION

Corresponding Author
*E-mail: Ben.Davis@chem.ox.ac.uk.

ORCID

Gonçalo J. L. Bernardes: 0000-0001-6594-8917
Justin M. Chalker: 0000-0002-7504-5508
Carme Rovira: 0000-0003-1477-5010
Benjamin G. Davis: 0000-0002-5056-407X

Present Address
‡G.J.L.B.: Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge CB2 1EW, U.K., and Instituto de Medicina Molecular, Faculdade de Medicina da Universidade de Lisboa, Av. Prof. Egas Moniz, 1649-028 Lisboa, Portugal.
J.M.C.: School of Chemical and Physical Sciences, Flinders University, Sturt Road, Bedford Park, South Australia, 5042, Australia.

Notes
The authors declare no competing financial interest.

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(51) We thank a referee for this excellent suggestion.


(53) Molecular mechanics revealed too that, as might be expected, any d-isomer (Figure S21) formed from the aza-Michael addition would face directly away from ATP. It may therefore be that any measurement of $k_{\text{cat}}$ determined here is an underestimate from a population of l-isomer PanC-Hisiso in a mixture with much less active d-isomer PanC-Hisiso.

