A structural and mechanistic study of π-clamp-mediated cysteine perfluoroarylation

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Natural enzymes use local environments to tune the reactivity of amino acid side chains. In searching for small peptides with similar properties, we discovered a four-residue π-clamp motif (Phe-Cys-Pro-Phe) for regio- and chemoselective arylation of cysteine in ribosomally produced proteins. Here we report mutational, computational, and structural findings directed toward elucidating the molecular factors that drive π-clamp-mediated arylation. We show the significance of a trans conformation prolyl amide bond for the π-clamp reactivity. The π-clamp cysteine arylation reaction enthalpy of activation (ΔH‡) is significantly lower than a non-π-clamp cysteine. Solid-state NMR chemical shifts indicate the prolyl amide bond in the π-clamp motif adopts a 1:1 ratio of the cis and trans conformation, while in the reaction product Pro3 was exclusively in trans. In two structural models of the perfluoroarylated product, distinct interactions at 4.7 Å between Phe1 side chain and perfluoroaryl electrophile moiety are observed. Further, solution 19F NMR and isothermal titration calorimetry measurements suggest interactions between hydrophobic side chains in a π-clamp mutant and the perfluoroaryl probe. These studies led us to design a π-clamp mutant with an 85-fold rate enhancement. These findings will guide us toward the discovery of small reactive peptides to facilitate abiotic chemistry in water.

Chemo- and regioselective modification of proteins is a chemical challenge because polypeptide chains contain numerous similarly reactive functional groups. Often the polymer, fluorophore, or small-molecule drug is rendered electrophilic for conjugation chemistry at nucleophilic protein side-chains. Many undesired side reactions occur and purification often fails. Major advances to overcome these chemistry challenges have been made, including the use of non-natural clickable amino acids within proteins for bio-orthogonal chemistry, engineered enzymatic systems such as sortase A, and non-enzymatic routes that leverage selective chemistry between a matched reaction pair. Recently we reported an enzyme-free, one-step, regio- and chemoselective protein-modification method based on cysteine arylation. We discovered that the π-clamp tetrapeptide (Phe-Cys-Pro-Phe) possessed unique reactivity to achieve self-labeling with a perfluoroaryl (PFA) electrophile (Fig. 1a). The reaction even proceeded selectively in complex glycosylated IgG proteins. Each residue within the π-clamp is important as mutations often diminished the reaction efficiency. Further, the π-clamp-mediated arylation reaction rate is tunable by over four orders of magnitude with different salts. Ammonium sulfate and other structure-stabilizing salts accelerated the reaction, while the addition of a denaturing salt such as guanidinium chloride impeded the reaction. Taken together, these results prompted us to carry out a systematic investigation of the π-clamp-promoted reaction. Here we employ kinetic studies, solution and solid-state NMR, and density functional theory (DFT) calculations to determine the structure-reactivity relationships that underscore this π-clamp mediated reaction. Our findings suggest several structural and chemical features contribute to the unique reactivity of π-clamp including the trans prolyl amide bond, lowered reaction ΔH‡, reduced cysteine pKα, and side chain-perfluoroaryl electrophile interactions.

Results

Trans prolyl amide accelerates π-clamp-mediated arylation reaction. We first investigated if the prolyl amide conformation being either cis or trans in the π-clamp was important. Proline is conformationally unique among amino acids as the backbone phi (φ) torsion angle is restricted by the side chain ring structure.

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The Xaa-Pro amide bond can undergo cis/trans isomerization while other amide bonds are found in the trans conformation for most proteins. Pro is thought to be a key player in the π-clamp, as mutation to D-Pro abrogates the reaction rate. To understand if the conformation of the Cys-Pro amide bond perturbs the reaction we used mutation studies. Proline analogues containing certain functional groups can constrain the Cys-Pro conformation; analogues α-methylproline (αMePro) and 5,5-dimethylproline (5,5-dmP) strongly promote the trans and cis conformations, respectively. Three peptides incorporating proline (the π-clamp, peptide 1A), α-methylproline (peptide 1B) and 5,5-dimethylproline (peptide 1C) at residue 3 were synthesized. The rate constants of their reactions with the PFA probe were measured. We found the α-methylproline mutation (1B) increased the rate constant by a factor of 2.5 relative to π-clamp 1A, whereas the 5,5-dimethylproline mutation (1C) led to a significant loss of reactivity. Computational tools were employed to calculate the Gibbs free energy change (ΔG) of π-clamp-mediated arylation reaction, to further study whether a trans proline analogue provided any energetic advantage. We
previously investigated the reaction energy pathway for cis Pro π-clamp. To calculate ΔG of the arylation reaction between peptide 1B and PFA probe using density functional theory (DFT), we first extracted three snapshots from molecular dynamics (MD) simulations of the trans proline π-clamp and then manually added a methyl group to form αMePro. Similarly, for starting structures of peptide 1C, we extracted four snapshots from MD simulations of the cis proline π-clamp and manually added two methyl groups to form 5,5-dmP. For the product's starting structure, we manually connected the PFA group to the peptide cysteine. After performing geometry optimizations on the starting structures of the peptide and product (Fig. S4), ΔG of the arylation reaction was calculated using DFT (see Section 3 in supporting information for details). We found that trans proline provided a thermodynamic advantage (lower Gibbs free energy of reaction) over cis proline by 11.8 kJ/mol for π-clamp-mediated arylation (Fig. 1c and Table S3). Taken together, both mutation and computational studies show a trans prolyl amide bond is preferred in the π-clamp-mediated arylation reaction.

**Enthalpy of activation is decreased in π-clamp-mediated arylation.** The reactivity of π-clamp cysteine was higher than that of other cysteines, leading to the site-selectivity of π-clamp. Compared to the reaction between PFA probe 2 and the π-clamp double-glycine mutant peptide 3 (GCPG, secondary rate constant k = 0.00065 ± 0.00005 M⁻¹ s⁻¹, Fig. S5), the rate constant for π-clamp peptide 1A (0.63 ± 0.02 M⁻¹ s⁻¹) was enhanced 1000-fold. Ammonium sulfate further accelerated π-clamp-mediated arylation without affecting the regioselectivity.

We investigated whether and how the π-clamp cysteine arylation reaction activation parameters were different from other cysteine using Eyring equation. We chose to compare π-clamp peptide 1A, double glycine mutant 3, π-clamp proline analogue mutants 1B–1C and π-clamp mutants with phenylalanine mutated to leucine (1D), cyclohexylalanine (1E) and pyrrenylalanine (1F). PFA probe 2 was reacted with these peptides and the reaction rate constants (k) were measured at different temperatures (T) (Table S4, Figs S6–S36) to calculate the enthalpy of activation (ΔH‡), the entropy of activation (ΔS‡), and the Gibbs energy of activation (ΔG‡) (see Methods Section for details). As summarized in Table S5, the ΔH‡ for π-clamp and mutants (1A–1F) were lowered by 37–84 kJ/mol compared to that of the double glycine mutant 3, contributing to the significantly enhanced reaction rate. Similarly, to shed light on whether ammonium sulfate changed activation parameters to accelerate the π-clamp-mediated arylation, the rate constant for the reaction between 1A and 2 in the presence of two molar (2 M) ammonium sulfate was measured at different temperatures (Figs S38–S42). We found both ΔH‡ and ΔS‡ were changed by ammonium sulfate (Table 1), but the change of ΔH‡ is more significant and is responsible for the reaction acceleration.

**π-clamp cysteine pKa is reduced even for Phe mutants.** We have shown that the cysteine pKa of π-clamp is lowered by 0.6 pH unit compared to that of the double glycine mutant. To test whether the cysteine pKa values in π-clamp mutants are also perturbed and how important the cysteine pKa value is for enhancing its reactivity, we measured the cysteine pKa in 1D, 1E, 1F and 3.

Several methods have been developed to measure the cysteine pKa in biomolecules. Spectrophotometric titration, where UV absorbance of the cysteine containing molecule is plotted against different pH values, is a convenient method. This method is based on the fact that ionization of cysteine thiol to thiolate results in a large increase in its molar absorption coefficient at 240 nm. To calculate the cysteine pKa of 1D, 1E and 3, we measured the absorbance at 240 nm (A240) of the peptides dissolved in buffers at different pHs. The absorbance of the buffer was used as a blank. Then the pKa was determined (Fig. 2a–c) by fitting the UV absorbance and pH values with the following equation:

\[ y = \frac{A \times 10^{pH} + B \times 10^{pKa}}{10^{pKa} + 10^{pH}} \]

where y is the absorbance of the peptide at 240 nm, A is the upper plateau of absorbance at high pH, and B is the lower plateau at low pH. The cysteine pKa in the double glycine mutant 3 was measured to be 7.95, while the cysteine pKa of both 1D and 1E were 0.6 pH unit lower than that of 3.

The A240 method could not be applied to 1F because of the strong absorbance of the pyrenyl group at 240 nm. Instead we measured pKa based on the reactivity of cysteine at different pHs. The pKa values of cysteine in proteins have been measured by determining their reaction rates with a reagent that is more reactive with thiolate than thiol. Here we used the rate constant of the S-NAr reaction between 1F and 2 to fit for pKa, since thiolate is more reactive than thiol in the perfluoroarylation reaction. The rate constants were plotted against pH and fit with the same equation as in the A240 method, where y is the reaction rate constant, and A and B are the upper and lower plateaus for the reaction rates (Fig. 2d). The cysteine pKa of 1F was determined to be 0.4 pH unit lower than 3. In Fig. 2e, we summarize the cysteine pKa values and the rate constants for the peptides studied. We observed a more than 10-fold rate constant difference between 1D and 1E, even though their pKa values were similar. In

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Table 1. Influence of ammonium sulfate on thermodynamic parameters (310 K) for the arylation reaction between peptide 1A and probe 2.

<table>
<thead>
<tr>
<th>2M (NH₄)₂SO₄</th>
<th>ΔH‡ (kJ·mol⁻¹)</th>
<th>−TΔS‡ (kJ·mol⁻¹)</th>
<th>ΔG‡ (kJ·mol⁻¹)</th>
<th>k (M⁻¹·s⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>−</td>
<td>89 ± 6</td>
<td>−11 ± 6</td>
<td>78 ± 8</td>
<td>0.63</td>
</tr>
<tr>
<td>+</td>
<td>89 ± 3</td>
<td>18 ± 3</td>
<td>67 ± 4</td>
<td>43.3</td>
</tr>
</tbody>
</table>
addition, peptide 1F was more reactive than peptides 1D and 1E, but the cysteine pK\textsubscript{a} of 1F was higher. Although all three π-clamp mutants had a lower cysteine pK\textsubscript{a} compared to that of the double glycine mutant 3 which facilitated ionization of the thiol to the more reactive thiolate, this pK\textsubscript{a} effect was not the only factor to account for the enhanced reactivity of the π-clamp.

ssNMR indicates π-clamp adopts 1:1 cis\textit{trans} Pro3 while the perfluoroarylated product adopts only \textit{trans}. To characterize the backbone conformation of the π-clamp and the S-perfluoroarylated product (PFA-tagged π-clamp), 1D and 2D \textsuperscript{13}C magic-angle-spinning (MAS) NMR spectra were measured on π-clamp peptide 5 (Fig. S43) and π-clamp PFA-tagged product 6 (Fig. S44), in which the π-clamp motif Phe-Cys-Pro-Phe were uniformly \textsuperscript{13}C and \textsuperscript{15}N labeled. The \textsuperscript{13}C cross-polarization (CP) spectrum of peptide 6 (Fig. 3a) shows sharp resonances, but with more peaks than expected for four labeled residues, indicating the presence of multiple resolvable peptide conformations. The Pro3 conformational heterogeneity is manifested as two resolved C\textbeta peaks around 30 ppm, and two partially resolved C\textdelta peaks around 48 ppm. In the carbonyl region, structural polymorphism is also readily observed, especially among the multiple Cys2 CO peaks, ~169 ppm, which are resolved from the carbonyl signals of the other labeled residues. The \textsuperscript{15}N CP spectrum (Fig. 3b) further highlights this conformational polymorphism: the N-terminal Phe1 amino group shows four resolved \textsuperscript{15}N signals at 22–35 ppm, indicating four distinct conformations. Likewise, Pro3 exhibits four resolved \textsuperscript{15}N peaks at 130–135 ppm.

To further resolve and assign the \textsuperscript{13}C and \textsuperscript{15}N chemical shifts, we measured 2D \textsuperscript{13}C-\textsuperscript{13}C correlation spectra (Fig. 4) of peptides 5 and 6, and 2D \textsuperscript{13}N-\textsuperscript{13}C correlation spectra (Fig. S45) of peptide 6. The 2D \textsuperscript{13}C-\textsuperscript{13}C correlation spectrum of peptide 5 (Fig. 4a) shows larger \textsuperscript{13}C line widths than the PFA-tagged peptide 6 (Fig. 4b) due to the
conformational distribution and the dry state of the peptide. Measurement of the dried, unreacted peptide 5 by solid-state NMR was necessary due to the unfavorable dynamics of this very soluble peptide in a hydrated state. The aliphatic linewidths of peptide 5 range from 2.0 ppm to 3.0 ppm, while the PFA-tagged peptide 6 exhibits $^{13}$C linewidths of 0.7–1.4 ppm. Within this linewidth range, peptide 5 shows a single set of chemical shifts for each residue, with the exception of Pro3, which exhibits chemical shifts for both cis and trans isomers (vide infra). The Phe1 and Phe4 chemical shifts are not well resolved: their C$\alpha$–C$\beta$ cross peaks partially overlap, and a single set of C$\beta$ cross peaks with the aromatic side chain carbons are observed (Fig. 4a), indicating that the two Phe residues have similar conformations. Cys2 displays a C$\beta$ chemical shift of ~25 ppm (Fig. 4a and c), which corresponds to the reduced state, confirming that the unreacted peptide 5 does not form disulfide bonds.

Upon reaction of peptide 5 with the PFA probe to form product 6, all $^{13}$C and $^{15}$N peaks sharpen (Figs 4b,d and S45), allowing us to resolve four sets of chemical shifts for each residue. In peptide 6, the inter-residue Cys2-Pro3 cross peaks allow the multiple sets of chemical shifts to be separated into four different molecules. No cross peaks between the different forms are observed at a 13C spin diffusion mixing time of 50 ms. Phe1 and Phe4 exhibit resolved C$\alpha$ and C$\beta$ chemical shifts that differ by ~5 ppm and ~3 ppm respectively (Fig. 4b). Multiple sets of aromatic C$\gamma$, C$\delta$, and C$\varepsilon$ chemical shifts are also resolved for Phe1 and Phe4, indicating that Phe1 and Phe4 experience different chemical environments, likely due to the PFA tag. Cys2 shows a C$\beta$ chemical shift of ~40 ppm, characteristic of oxidized Cys2, as expected for PFA-modified cysteine.

We were especially interested in the prolyl amide bond conformation. Pro3 shows interesting chemical shift differences between the peptide 5 and the PFA-tagged peptide 6. In the unreacted state (peptide 5), two sets of Pro3 C$\beta$ and C$\gamma$ chemical shifts are observed: one set shows a large C$\beta$ and C$\gamma$ chemical shift difference of ~13 ppm while the other set shows a smaller chemical shift difference of ~5 ppm (Fig. 4c). These C$\beta$ and C$\gamma$ chemical shift differences$^{24}$ are characteristic of the cis and trans isomers of Pro, and peak intensities indicate that the two forms have a cis:trans ratio of 1:1 in the unreacted peptide 5. Upon reaction with the PFA probe, the multiple resolved Pro3 chemical shifts all show similar C$\beta$ and C$\gamma$ chemical shift differences of ~5 ppm, indicating that the Pro3 in peptide 6 predominantly shifts to the trans conformer (Fig. 4d).

Overall, these $^{13}$C and $^{15}$N chemical shifts (Tables S6, S7) indicate there is no single well-defined secondary structure for the $\pi$-clamp motif in peptide 5 or 6. The unreacted $\pi$-clamp peptide 5 adopts a broadly distributed
conformation with an approximate 1:1 ratio of the cis and trans Pro3 isomer. Reacting with the PFA probe causes peptide 6 to adopt four distinct conformations, but only the trans isomer at Pro3. Using the compiled 13C and 15N chemical shifts of peptide 6, a TALOSN 25 prediction yielded similar backbone (φ,ψ) torsion angles for the four forms (Fig. S46), with the largest torsion angle difference occurring at Phe4. This difference is likely from prediction uncertainty due to the lack of chemical shift information of the residue C-terminal to Phe4. For the unreacted peptide 5, because of the large spectra linewidths, there is significant uncertainty in predicting these (φ,ψ) torsion angles. However, since all four distinct sets of peptide 6 chemical shifts fall within the broad linewidths of the unreacted peptide 5, the average backbone conformations may not differ dramatically between the two peptides.

A clamp-like claw structure is one of the two reaction products from ssNMR and modeling studies. To generate a structural model for the perfluoroarylated π-clamp product based on the backbone conformation predicted from chemical shifts, 13C-19F distances were measured using 13C-19F REDOR of two partially labeled π-clamp peptides: peptide 7 with uniform 13C, 15N labeling at only Phe1 (Fig. S47) and peptide 8 with uniform 13C, 15N labeling at Pro3 and Phe4 (Fig. S48). By examining these two peptides, we can determine the distance between the PFA and each Phe. Figure 5 shows representative REDOR S0 and S spectra at a mixing time of 4 ms. 13C spins that are close to the 19F spins exhibit larger intensity differences between the S0 and S spectra than 13C spins that are farther from 19F spins. Figure 5d plots the intensity ratio S/S0 as a function of the REDOR mixing time for a few representative peaks; the full set of REDOR curves used for modelling are summarized in Fig. S49. The Phe1 backbone Cα peak has the largest dephasing among all peaks, reaching a value of 0.07 ± 0.02 at 6 ms, while the Phe1 Cζ shows a more moderate dephasing trend. The Pro3 Cβ and Phe4 Cζ show linear decay in contrast to the expected universal two-spin REDOR curve. We attribute these decay trajectories to the multi-spin nature of the system, with 8 19F spins at varying distances from each 13C.

Given the system complexity, we first analyzed these 13C-19F REDOR data semi-quantitatively. In contrast with the Phe1 backbone Cα peak which has the largest degree of dephasing, the Phe4 Cα and Cζ backbone sites show...
minimal dephasing, reaching only S/S₀ values of ~0.8 at 8 ms. This indicates that the PFA tag is closer to Phe1 than Phe4. Among the ¹³C signals from Pro3, Cδ reaches the lowest dephasing at a S/S₀ value of ~0.4 at 8 ms, while Pro3 Cα, Cβ and Cγ each show minimum S/S₀ of ~0.6 at 8 ms, indicating Pro3 Cδ is closer to the PFA tag.

More quantitative distance information was extracted by multi-spin simulations utilizing the SIMPSON program. We compared the experimental data first to 2-spin simulations to obtain the apparent ¹³C-¹⁹F distance, and then to 5-spin system containing one ¹³C and four ¹⁹F spins in model-dependent simulations. In these simulations, the ψ and χ₁ angle of Phe1, χ₁, χ₂ and χ₃ of Cys2 and χ₁ of Phe4 were iteratively set to 180°, 60° or −60°. For each simulated curve, the root-mean-square deviation (RMSD) was calculated between each experimental REDOR data set, and the minimum among all calculated RMSD values corresponds to the best fit. The 2-spin simulations provided reasonable fits for each ¹³C site (Fig. S50). For all sites in Pro3, the distances range from 6.3–7.0 Å. Slightly longer distances for Phe4 CA and CB (7.7 Å and 7.4 Å respectively) are observed, and the distance for Phe4 CZ is 6.0 Å. For Phe1, the fast dephasing CA and CZ fit relatively well to distances of 3.8 Å and 5.2 Å, respectively. The 5-spin model-dependent simulations unfortunately did not simultaneously fit well for all ¹³C sites with any set of dihedral angle combinations. However, taking the best-fit 5-spin REDOR curve for each ¹³C site (Figs 6b, S51), the shortest ¹³C-¹⁹F distance among the four nearest neighbor ¹⁹F agreed well with the best-fit distances determined from the 2-spin simulations.

These distances were taken as a set of REDOR derived, nearest-neighbor ¹³C-¹⁹F distances: 3.6 Å F1α, 4.6 Å F1β, 6.0 Å F1ζ, 6.0 Å F1′α, 6.0 Å F1′β, 4.8 Å F1′ζ, 7.0 Å P3α, 7.5 Å P3β, 7.7 Å P3γ, 6.4 Å P3ζ, 8.1 Å F4α, 7.8 Å F4β, and 6.5 Å F4ζ. Using a smaller interval of 30°, the dihedral angles were rotated iteratively again and the nearest neighbor ¹³C-¹⁹F distance was compared to the above set of distances. In the generated best-fit models, shown in Fig. 6c, model 1 (left) uses F1 CA and Cβ, and model 2 (right, wide clamp-like) uses F1 CA’ and Cβ’ for fitting. The ¹³C-¹⁹F distances from these models were used in 5-spin REDOR simulations, and plotted against the experimental REDOR S/S₀ values (Figs S52, S53) for validation. Model 2 gave decent fits for all ¹³C sites while model 1 has worse fits, even though the shortest ¹³C-¹⁹F distances are similar in the two models. In both models, distinct non-covalent interactions between Phe1 side chain and perfluoroaryl electrophile at around 4.7 Å distance and similar backbone structures were observed (Fig. 6c and d).

**A pyrenylalanine π-clamp mutant non-covalently interacts with the perfluoroaryl electrophile in solution.** We hypothesized the phenyalanine side chains in π-clamp interact non-covalently with the PFA electrophile to facilitate the reaction. ¹⁹F solution NMR and isothermal titration calorimetry experiments were carried out to test this hypothesis. We started with an un-reactive π-clamp mutant (Phe-Ser-Pro-Phe), but were unable to detect interactions by NMR experiments. Prompted by our earlier experiments, we investigated a
pyrenylalanine mutant which may interact with the PFA electrophile more strongly. Peptide 4A (Py-Ser-Pro-Py, where Py is pyrenylalanine) and the control peptide double-glycine mutant 4B (Gly-Ser-Pro-Gly) were prepared. We mixed 4A with 1 equivalent of probe 2 and observed a change in 19F solution NMR chemical shift and peak shape when compared to the mixture of 4B and probe 2, or probe 2 alone (Fig. 7a). In addition, the 19F chemical shift was changed during titration when we added 4A to a fixed amount of 2 (Fig. 7b). In contrast, this effect was not observed for the same titration of peptide 4B (Fig. 7c). These results suggest the pyrenyl side chains are interacting with the PFA electrophile. To corroborate the 19F solution NMR studies, we investigated the interaction...
of 4A and 2 by isothermal titration calorimetry. Probe 2 was added to peptide 4A or 4B to detect non-covalent interaction (Fig. 7d). When compared to the non-pyrenylalanine case 4B as a control, weak binding was observed between 4A and 2. The binding curve (Fig. 7e) did not display simple two state interactions and could not be fit nor could we determine the binding stoichiometry.

Discussion

The π-clamp accelerates abiotic perfluoroarylation chemistry in water. Here we carried out structural and mechanistic studies to understand this transformation. Several structural and chemical features were found to facilitate the reaction. We found that Pro3 played an important role in the π-clamp function. A π-clamp α-methylproline mutant favoring the trans Pro conformation accelerated the rate of arylation by more than 15-fold, compared to the 5,5-dimethylproline mutant that favored a cis Pro conformation. Trans Pro provided a thermodynamic advantage over cis Pro for π-clamp-mediated arylation as shown by DFT calculation. The ΔH‡ for the π-clamp arylation reaction is decreased by 64 kJ/mol when compared to a non-π-clamp cysteine, enabling 1000-fold rate enhancement and regioselective cysteine modification at the π-clamp. Ammonium sulfate salt lowers the ΔH‡ by 40 kJ/mol relative to the reaction without the salt and thus promote the reaction. In addition, the π-clamp cysteine pKa is reduced by 0.4–0.6 pH unit even for Phe mutants.

Structural and biophysical studies indicate certain conformations may promote the reaction, and side-chains in the π-clamp interact non-covalently with the PFA electrophile. Solid-state NMR indicated a mixture of cis-/trans Pro in the unreacted π-clamp was fully converted to the trans conformation upon perfluoroarylation. Two ssNMR structural models of the reaction product highlight the interactions between the Phe1 side chain and perfluoroaryl-electrophile moiety. 19F solution NMR titration experiments and the ITC data support the hypothesis that the π-clamp side chains may interact with the PFA electrophile.

The structural models from our ssNMR study are not fully consistent with the π-clamp α-methylproline mutant product structures used in DFT calculations, although they both have trans Pro. As the comparison shown in Fig. S54, the largest torsion angles differences between the calculated structures and clamp-like NMR structure model 2 occurred at Phe1-psi and Pro3-psi. These two angles contribute to the calculated structures being more compact than the NMR structure. In addition, all of the calculated structures have Phe4 in close proximity to the PFA tag. This would theoretically cause the Phe4 Cα and C3 simulated REDOR curves to decay rapidly, while the experimental data shows a much slower decay (Fig. S54). The inconsistency may come from the fact that we did not directly sample the PFA-labeled π-clamp product in MD simulations, due to a lack of parameters to describe the PFA in the reaction product. In addition, two slightly different molecules have been used in our computation and ssNMR studies. We think that the ssNMR models better describe the structural feature of the PFA labeled π-clamp product. However, our DFT calculations which indicate that trans Pro is thermodynamically favored over cis proline in the π-clamp perfluoroarylation reaction should be valid, considering that for all the geometrically-optimized calculated structures we sampled, larger or similar reaction ΔG were observed for trans Pro compared to the cis Pro structures.

Figure 7. F NMR and ITC indicate interactions between peptide 4A side chain and PFA probe 2. (a) 19F solution NMR spectra for probe 2 (top), 2 mixed with 1 equivalent 4A (middle), and 2 mixed with 1 equivalent 4B (bottom). Conditions: 2 mM peptide or probe, 20 mM phosphate, pH 7, 10% D2O, 90% H2O. (b,c) 19F solution NMR spectra for the titration experiment in which the equivalent of peptide 4A (b) or 4B (c) relative to 2 was increased. Concentration of 2 was fixed at 2 mM. (d) Isothermal titration calorimetry binding curves for 2 interacting with 4A and 4B. 5 mM probe 2 was added into 0.2 mM 4A or 4B in the titration experiment. e) Processed ITC binding curve where the interaction between 2 and 4B was deducted as background from the interaction between 2 and 4A.
Our studies here have led to the discovery of a π-clamp mutant 1G with an 85-fold rate enhancement. A convergent effect was observed when we combined α-methylproline, which promoted the trans Pro conformation, and the large hydrophobic side chain in pyrenylalanine. Taken together, we generated π-clamp mutant 1G with a rate constant of $53.3 \pm 2.3 \times 10^{-1} \text{s}^{-1}$, which is 85-fold higher π-clamp peptide 1A (Figs S55, S56). We anticipate our findings could direct us toward the design and screening of other small reactive peptides to facilitate selective abiotic chemistry enabled by local environment.

**Methods**

**Kinetics Study.** The reactions were carried out with 200 mM phosphate, 20 mM TCEP at 37 °C unless otherwise noted. To measure the second order rate constants, reaction mixture was prepared on ice and divided into several 10-µL aliquots. All aliquots were immediately put in 37 °C water bath unless otherwise noted. For reactions that take more than 1 hour to monitor, all aliquots were heated in a PCR machine set at 37 °C to prevent solvent evaporation. Reactions were quenched by addition of 100 µL 50% water: 50% acetonitrile: 0.5% TFA at different time points and then subjected to LC-MS analysis. The initial concentration of probe and substrate were known. The second-order rate constants were determined by fitting the following kinetics equation:

$$y = \frac{\ln([\text{peptide}]_0/[\text{probe}]_0)}{[\text{probe}]_0 - [\text{peptide}]_0} = k_t t$$

Error of reaction rate constant was obtained from the linear fitting of the kinetics curves for measuring the reaction rate constants.

**Determination of the standard enthalpy/entropy of activation.** The secondary rate constant ($k_t$) for the reaction between π-clamp peptide and probe 2 was experimentally measured at different temperatures (T). Then ln($k_t/T$) was plotted against 1/T. The standard enthalpy of activation ($\Delta H^\ddagger$) and the standard entropy of activation ($\Delta S^\ddagger$) were calculated (Table S5) by fitting ln($k_t/T$) against 1/T with the following Eyring equation:

$$\ln \frac{k}{T} = \frac{-\Delta H^\ddagger}{R} + \frac{\Delta S^\ddagger}{R} - \frac{\Delta G^\ddagger}{RT}$$

where $k_t$ is transmission coefficient ($\kappa = 1$), $k_B$ is Boltzmann constant, $h$ is Planck’s constant, $T$ is absolute temperature and $R$ is gas constant. The errors for $\Delta H^\ddagger$ and $\Delta S^\ddagger$ were obtained from the linear fitting. $\Delta G^\ddagger$ was calculated as $\Delta H^\ddagger - T\Delta S^\ddagger$, and the error for $\Delta G^\ddagger$ was calculated from error propagation. The Eyring plots were summarized in Fig. S37.

**References**


**Acknowledgements**

This work was supported by an MIT Startup fund, the National Institutes of Health (NIH; R01GM110535) and the Sontag Foundation Distinguished Scientist Award (to B.L.P.). C.Z. is a recipient of the George Büchi Research Fellowship, the MIT Koch Graduate Fellowship in Cancer Research, and the Bristol-Myers Squibb Graduate Fellowship in Synthetic Organic Chemistry. The solid-state NMR segment of this work was partially funded by NIH grant GM088204 to M.H. The theory work was funded by a grant from the NSF (CHE-1464804). J.J.S. would like to thank the Royal Commission for the Exhibition of 1851 for a Research Fellowship. The Biophysical Instrumentation Facility for the Study of Complex Macromolecular Systems (NSF-0070319) is gratefully acknowledged.

**Author Contributions**
P.D., C.Z. and B.L.P. conceived the work and designed the experiments. P.D. performed the mechanistic and kinetics studies. J.K.W. and M.H. performed the solid-state NMR studies. M.W., J.J.S., T.Z. and T.V.H. performed the computational studies. P.D., J.K.W. and B.L.P. wrote the manuscript, with input from all other authors.

**Additional Information**

Supplementary information accompanies this paper at doi:10.1038/s41598-017-08402-2

**Competing Interests:** The authors declare that they have no competing interests.

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