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# Cluster model study of the mechanism and origins of enantio- and chemoselectivity in non-heme iron enzyme-catalyzed C–H azidation†

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The mechanisms and enantio- and chemoselectivities of non-heme iron enzyme-catalyzed C–H azidation were investigated using density functional theory (DFT) calculations. A detailed active site cluster model comprising 337 atoms was constructed, incorporating essential features of the first- and second-coordination spheres and substrate-binding pockets. The catalytic cycle involves N–F bond activation, hydrogen atom transfer (HAT), and radical rebound steps. DFT calculations suggest that the observed enantioselectivity arises from steric effects between the substrate and key active-site residues. Additionally, in the non-heme Fe(N<sub>3</sub>)F complex, the Fe–N<sub>3</sub> bond, which has a lower diabatic bond dissociation energy, preferentially rebounds to form the azidation product.

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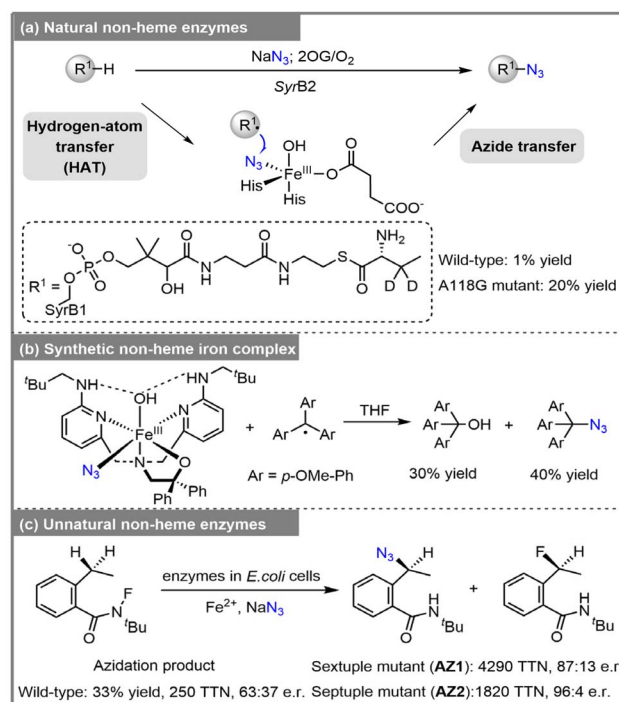
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## 1. Introduction

Organic azides have become widely used as valuable intermediates in organic synthesis due to their versatile reactivity.<sup>1–3</sup> Since the preparation of phenyl azide, the first organic azide, in 1864,<sup>4,5</sup> numerous azidation reactions have been developed, enabling the synthesis of organic azides from various functional groups.<sup>6</sup> One effective method for achieving C–H azidation is through hydrogen atom transfer (HAT) followed by azide transfer.<sup>7–10</sup>

In 2014, Bollinger and colleagues discovered that SyrB2, a non-heme Fe<sup>II</sup>/α-ketoglutarate (αKG)-dependent halogenase, is capable of catalyzing direct C–H azidation.<sup>11</sup> Typically, SyrB2 catalyzes the C–H chlorination of its native substrate, L-threonine, during the biosynthesis of syringomycin E.<sup>12</sup> Researchers discovered that replacing chloride with azide in SyrB2 enabled the formation of azidation products. When L-d<sub>2</sub>-aminobutyrate was used as the substrate, wild-type SyrB2 produced azidation products at a low yield of approximately 1%. The A118G mutation further improved the azidation reactivity, enhancing it by around 13-fold. The reaction proceeds *via* a HAT/azide transfer mechanism, in which the oxoiron(IV) complex abstracts a hydrogen atom from L-d<sub>2</sub>-aminobutyrate, generating an iron(III) intermediate. This intermediate subsequently captures the substrate radical through azide transfer, ultimately leading to the formation of the azidation product (Scheme 1a). Inspired by enzymatic catalysis, several biomimetic models have been developed to emulate the

active sites of αKG-dependent halogenases and hydroxylases.<sup>13–16</sup> However, a mixture of R–OH and R–N<sub>3</sub> products was obtained when using the organocatalysts. Goldberg and co-workers synthesized the Fe<sup>III</sup>(BNPA<sup>Ph2</sup>O)(OH)(N<sub>3</sub>) complex, which reacts with carbon radicals, resulting in a mixture of alcohol (30%) and azide (40%) products (Scheme 1b).<sup>17</sup>



**Scheme 1** (a) Azidation by non-heme enzymes. (b) Azidation by synthetic non-heme iron complex. (c) Unnatural azidation by non-heme enzymes.

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Aside from synthesizing organic catalysts, artificial enzymes constitute another class of catalysts that mimic the functions of natural enzymes.<sup>18–21</sup> By integrating proteins with organo-catalysts, artificial enzymes have emerged as a powerful strategy for developing enzymes capable of driving new-to-nature reactions.<sup>20–22</sup> In 2022, Huang, Garcia-Borràs, Guo and colleagues reported an unnatural C(sp<sup>3</sup>)-H azidation reaction catalyzed by non-heme iron-dependent enzymes, utilizing sodium azide as the external azide source.<sup>23</sup> The wild-type *Sav* HppD (4-hydroxyphenyl)pyruvate dioxygenase from (*Streptomyces avermitilis*) achieved the azidation product with 250 total turnovers (TTN), an enantiomeric ratio (e.r.) of 63:37, and a chemoselectivity of 9:1 favoring azidation over fluorination (Scheme 1c). Through a screening process, two outstanding enzyme variants, **AZ1** (*Sav* HppD V189A/F216A/P243A/N245Q/Q255A/L367I) and **AZ2** (*Sav* HppD V189A/N191A/S230L/P243G/N245F/Q255P/L367I), were identified. Variant **AZ1** displayed higher TTN, while **AZ2** demonstrated enhanced enantioselectivity (the mutation sites involved in **AZ2** are shown in Scheme 2).<sup>23</sup> Additionally, a simplified model—substituting two histidines with imidazole and one glutamate with acetate—was employed to study the reaction mechanism, encompassing N-F bond activation, HAT, and radical rebound steps (Scheme 2). The rate-determining step is N-F bond activation, while the enantioselectivity-determining step is the radical rebound.<sup>23</sup> However, the origins of enantioselectivity and chemoselectivity in this C-H azidation reaction remain unclear.

In this study, we present a computational investigation into the mechanism and, in particular, the origin of selectivity in the azidation reaction, using a large cluster model of over 300 atoms that incorporates both the first- and second-coordination spheres around the iron and substrate. The **AZ2** enzyme variant was selected due to its higher enantioselectivity. In recent years, cluster models have been widely utilized in biocatalysis research.<sup>24–28</sup>

## 2. Computational methods

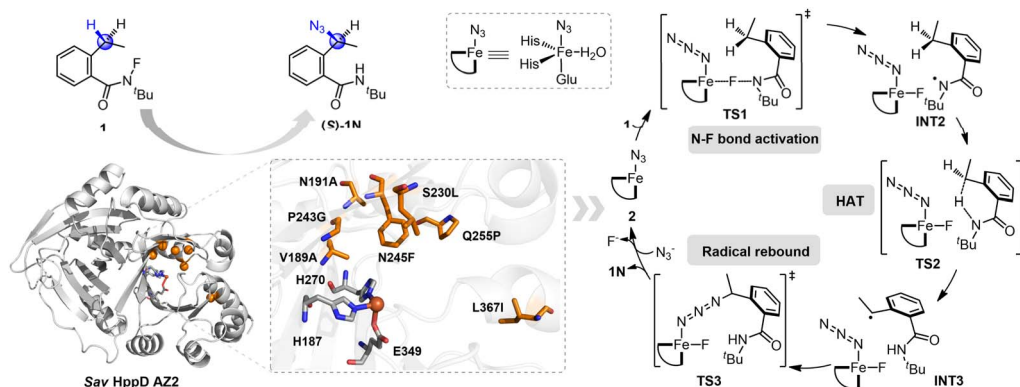
### 2.1 Active site model

The cluster model of the active site used to investigate the reaction mechanism and selectivity was based on the structure

of the variant **AZ2** complex, which was derived from molecular dynamics (MD) simulations (see ESI† for MD simulation details). The model includes the iron, N<sub>3</sub><sup>−</sup>, *N*-fluoroamide substrate **1**, water, and amino acid residues within 4 Å of the substrate, including the side chains of H187, A189, A191, L228, L230, G243, F245, P255, I256, Q269, H270, L293, L323, Q334, F336, F347, E349, F359, G360, K361, N363, F364, I367 (Fig. 1). The C<sup>α</sup> atoms of amino acid residues (H187, A189, A191, L228, L230, F245, L293, L323, Q334, F336, F347, E349, I367) were replaced with hydrogen atoms and fixed to maintain side chain orientations similar to those in the protein structure. The C<sup>β</sup> atoms of these residues included in the cluster model were also fixed during geometry optimization to preserve their positions as in the protein structure. Additionally, the main chain carbonyl or nitrogen atoms of residues (G243, I256, Q269, H270, F359, K361, N363, F364) were replaced with hydrogen atoms and fixed, while the C<sup>α</sup> atoms of these residues were also fixed. In addition, a methyl group was added to the main chain nitrogen atom of P255.<sup>29</sup> The cluster model consists of 337 atoms in total, with an overall charge of 0.

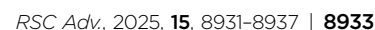
### 2.2 Technical details

All the calculations were carried out with Gaussian 16.<sup>30</sup> Geometry optimizations were performed with (U)B3LYP method.<sup>31,32</sup> We conducted an overlay analysis of the structure optimized by B3LYP method and the MD structure (see ESI† Fig. S2† for details). The SDD basis set<sup>33</sup> with ECP was used for Fe, and the 6-31G(d) basis set<sup>34–36</sup> was used for other atoms. To ensure that the correct unrestricted wavefunctions were obtained, a stability test was carried out with Gaussian keyword stable = opt. Frequency analysis was conducted at the same level of theory to verify that the stationary points are minima or saddle points. Single-point energies were computed at the M06<sup>37</sup>/def2-TZVP level<sup>38</sup> of the theory on gas phase optimized geometries in diethylether (ε = 4.3) with the application of the CPCM solvation model.<sup>23,39</sup> Due to the constraints applied during geometry optimization, the reported values are the computed enthalpies (Δ*H*).<sup>27</sup> The independent gradient model (IGM) analysis<sup>40,41</sup> was conducted with the aid of Multiwfn program,<sup>42,43</sup> and the results were visualized with VMD



Scheme 2 Proposed mechanism for azidation reaction catalyzed by non-heme iron enzymes.





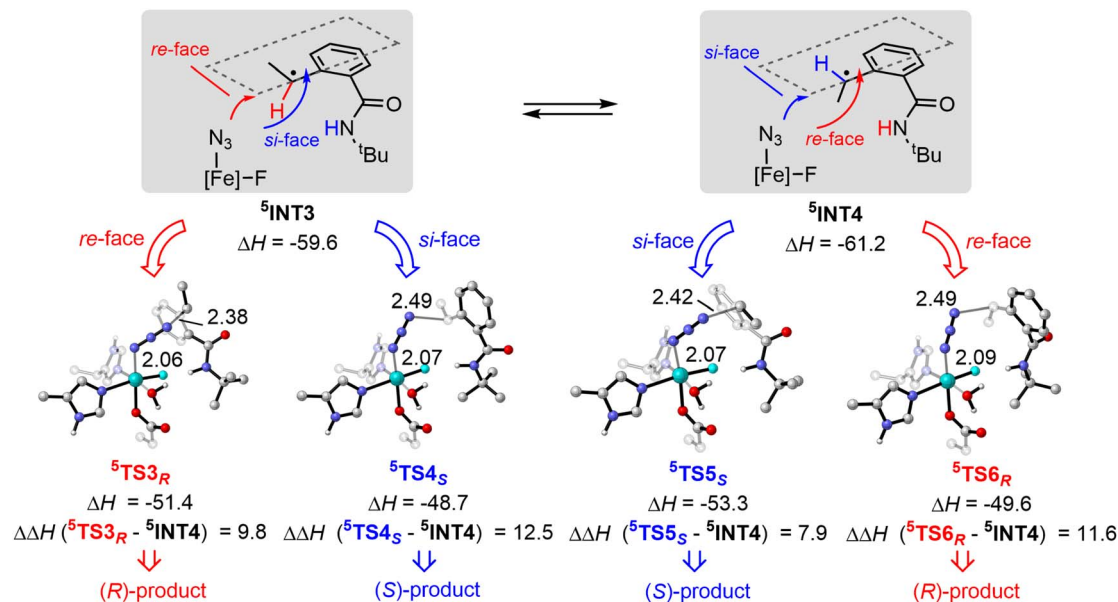


Fig. 3 The energy associated with the radical rebound steps. For clarity, only the reactive center and polar hydrogen atoms are shown. The distances are shown in Å, and the energies are shown in kcal mol<sup>-1</sup>.

energy barrier for the formation of the (S)-product via  $^5\text{TS5}_S$  is 1.9 kcal mol<sup>-1</sup> lower than for the (R)-product via  $^5\text{TS3}_R$ , suggesting that (S)-product formation is more favorable than (R)-product formation. This calculated enantioselectivity aligns with Huang's experimental observations.<sup>23</sup>

### 3.2 Origin of enantioselectivity

The optimized structures of the azide rebound transition states ( $^5\text{TS3}_R$  and  $^5\text{TS5}_S$ ) are shown in Fig. 4. These two transition states differ in activation energy by 1.9 kcal mol<sup>-1</sup>, favoring the (S)-product, which is consistent with experimental observations.<sup>23</sup> To investigate the origin of the stereoselectivity, we performed IGM,<sup>40,41</sup> analysis of the rebound transition state, which selectively visualizes attractive and repulsive intermolecular non-covalent interactions (blue for attractive and stabilizing, red for

repulsive and destabilizing, and green for van der Waals interactions). As shown in Fig. 4, a clear steric repulsion is observed between the substrate's methyl group and L230 in the transition state  $^5\text{TS3}_R$ , which leads to the formation of the (R)-product. In  $^5\text{TS3}_R$ , the distance between a hydrogen atom on the substrate and a hydrogen atom of L230 is 2.20 Å, smaller than the sum of the van der Waals radii of hydrogen (1.2 Å). In contrast, the H...H distance in  $^5\text{TS5}_S$  is 2.56 Å. Therefore, enantioselectivity is primarily governed by steric effects in the rebound transition states, where the mutated amino acid plays S230L a critical role in determining enantioselectivity.

### 3.3 Origin of chemoselectivity

The radical rebound step also serves as the chemoselectivity-determining step, there are three types of radical rebound

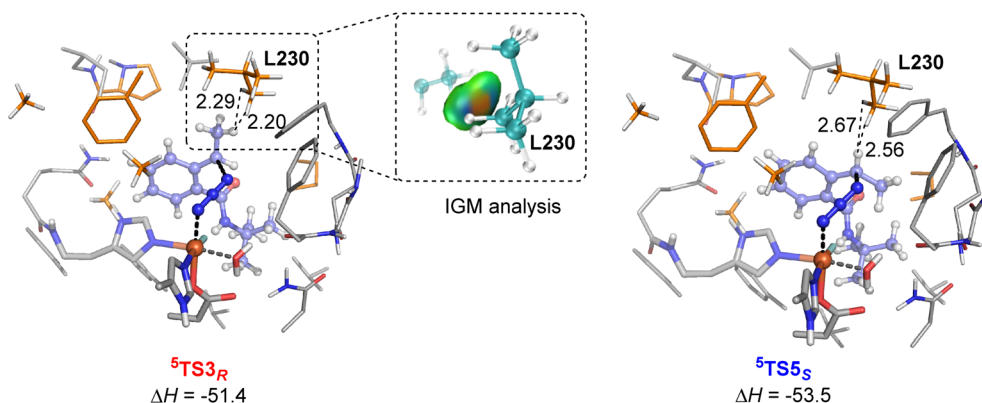


Fig. 4 Optimized structures and IGM analysis of the radical rebound transition state. For IGM analysis, blue, attraction; green, weak interaction; red, steric effect. Isosurface value 0.005. The distances are shown in Å, and the energies are shown in kcal mol<sup>-1</sup>. For clarity, only the polar hydrogen atoms and the hydrogen atoms on the substrates are depicted.





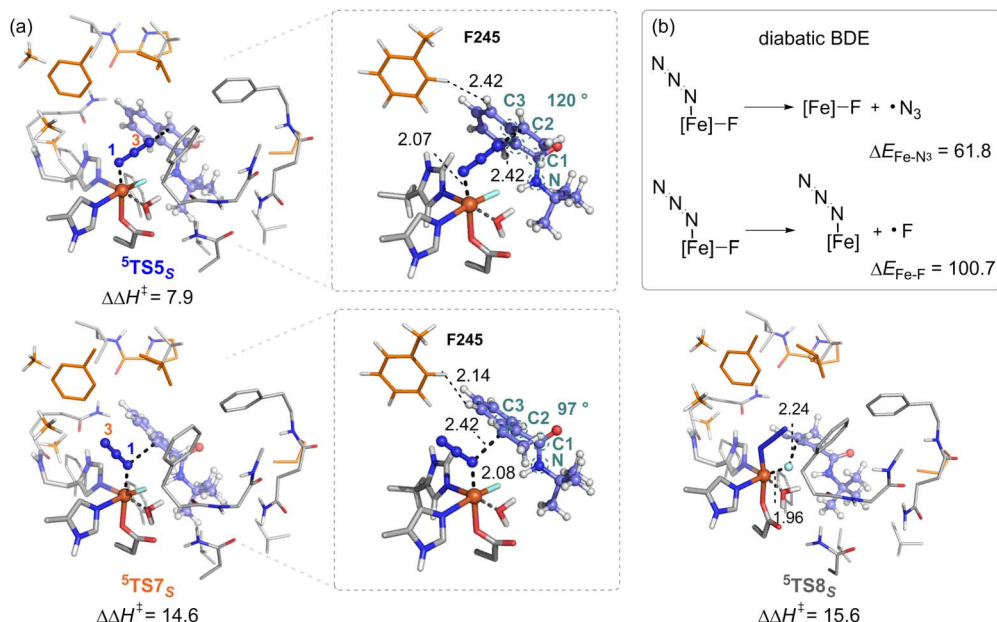


Fig. 5 (a) Optimized transition-state structures of chemoselectivity-determining TSs. (b) The diabatic BDE values for the Fe-N $_3$  and Fe-F bonds of Fe(N $_3$ )F complex. The distances are shown in Å, and the energies are shown in kcal mol $^{-1}$ .

pathways in **INT4**: two pathways involve **TS5** (terminal N3 rebound) or **TS7** (nitrogen N1 rebound) to generate the azidation product, while the third pathway involves **TS8** (fluorine rebound) to produce the fluorine product (Fig. 5a). Both azide rebound pathways—terminal N3 rebound via  $^5\text{TS5}_S$  and nitrogen N1 rebound via  $^5\text{TS7}_S$ —are highly favorable, with energy barriers of 7.9 kcal mol $^{-1}$  and 14.6 kcal mol $^{-1}$ , respectively, relative to  $^5\text{INT4}$ . In contrast, the fluorine rebound transition state ( $^5\text{TS8}_S$ ) requires a higher energy barrier of 15.6 kcal mol $^{-1}$  from  $^5\text{INT4}$ . Thus, azidation is more favorable than fluorination. The calculated enantioselectivity and chemoselectivity align with experimental observations, confirming that the (*S*)-azidation product is the major product.<sup>23</sup>

The diabatic bond dissociation energies (BDEs) of Fe-N $_3$  and Fe-F in the Fe(N $_3$ )F complex were also calculated and are displayed in Fig. 5b. Diabatic BDEs are useful for explaining the selectivity observed in hydroxylation and halogenation reactions involving synthetic non-heme iron complexes.<sup>9,47,48</sup> The results show that the diabatic BDE of the Fe-F bond exceeds that of the Fe-N $_3$  bond by 38.9 kcal mol $^{-1}$ , indicating that azide groups are more likely to rebound, consistent with experimental findings.<sup>23</sup> Additionally, the energy of  $^5\text{TS5}_S$  is 6.7 kcal mol $^{-1}$  lower than that of  $^5\text{TS7}_S$ . A simplified model study of the azide rebound transition state reveals that the dihedral angle of N-C1-C2-C3 in the substrate is approximately 116° (Fig. S4†). In  $^5\text{TS7}_S$ , where N1 rebounds to the carbon radical, the dihedral angle of N-C1-C2-C3 (the four atoms marked with green circles in Fig. 5a) is 97°. This configuration results in significant steric repulsion due to the close proximity between the substrate and the F245 residue in the enzyme environment. The distance between a hydrogen atom on the substrate's benzene ring and a hydrogen atom of F245 is 2.14 Å, which is smaller than the sum of the van der Waals radii of hydrogen (1.2 Å). In contrast,  $^5\text{TS5}_S$  avoids this

steric clash, with a dihedral angle of N-C1-C2-C3 of 120°, and the corresponding H...H distance increases to 2.42 Å.

## 4. Conclusions

In this study, a detailed computational investigation of the C-H azidation catalyzed by a non-heme iron enzyme is presented. A comprehensive active-site model containing over 300 atoms was constructed based on MD simulations. The reaction mechanism involves initial N-F bond activation, followed by hydrogen atom transfer to N-centered radical, resulting in the formation of Fe(N $_3$ )F complex and carbon-centered radical intermediates. The process concludes with the rebound of the azide group to form the final product. In the Fe(N $_3$ )F complex associated with carbon-centered radical, the azide group can approach either the *re*- or *si*-face of the benzyl radical on the substrate, leading to the formation of either the (*R*)- or (*S*)-product. DFT calculations indicate that azide rebound to the opposite face of the hydrogen atom transfer is more favorable. The computed energy difference between the enantioselective azide rebound transition states,  $^5\text{TS3}_R$  and  $^5\text{TS5}_S$ , is 1.9 kcal mol $^{-1}$ , aligning with experimental observations. IGM analysis of the azide rebound transition state reveals that enantioselectivity is primarily governed by steric interactions between the substrate and L230. Moreover, the radical rebound step is identified as the chemoselectivity-determining step in the C-H azidation reaction. Thermochemical analysis of the diabatic BDE of the Fe(N $_3$ )F complex demonstrates that the N $_3$  group, having a lower diabatic BDE, preferentially rebounds to form the azidation product. These findings offer valuable insights into the mechanisms and selectivities of radical-based biocatalytic reactions, providing guidance for the development of novel biocatalytic processes.



## Data availability

The data supporting this article have been included as part of the ESI.† And data for this article, including [XYZ coordinates, topology files, simulation parameters] are available at [Zenodo] at <https://doi.org/10.5281/zenodo.14871340>.

## Author contributions

Hang Liu: calculation, data curation, and writing – original draft. Xiahe Chen: calculation, data curation, and writing – original draft – review & editing. Hongli Wu: calculation. Yuanbin She: conceptualisation, project administration. Yun-Fang Yang: conceptualisation, supervision, writing – review & editing, and funding acquisition. All authors contributed to the analysis and interpretation of the data. All authors have approved the final version of the manuscript.

## Conflicts of interest

There are no conflicts to declare.

## Acknowledgements

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