

## SUPPORTING INFORMATION

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# Supporting Information

## Characterizing Y224 conformational flexibility in FtmOx1-catalysis using $^{19}\text{F}$ NMR spectroscopy

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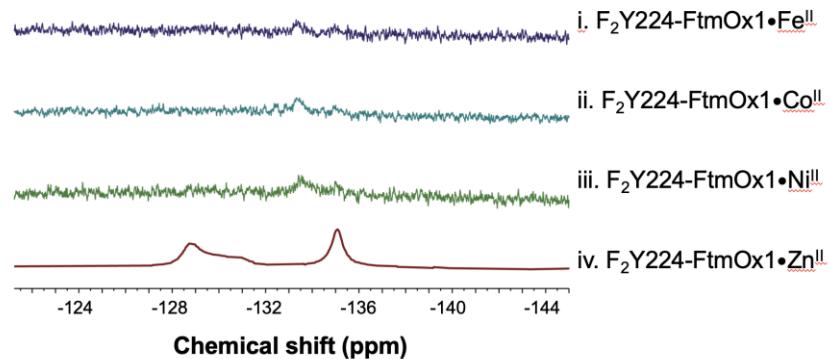
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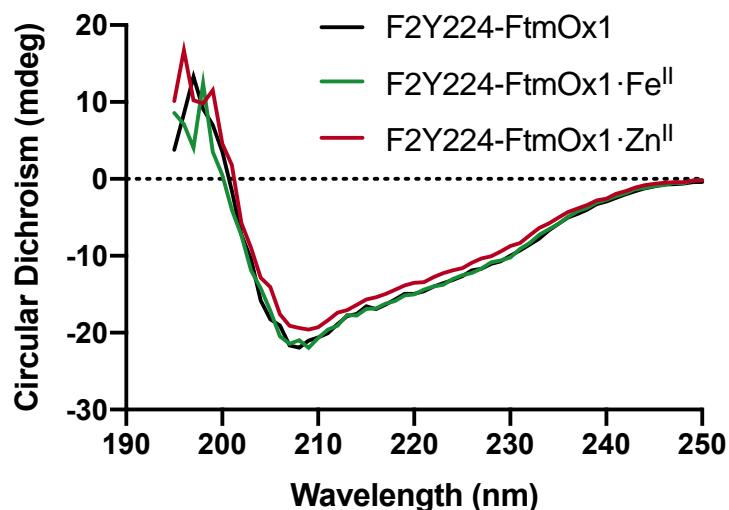
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## Supplementary Figures



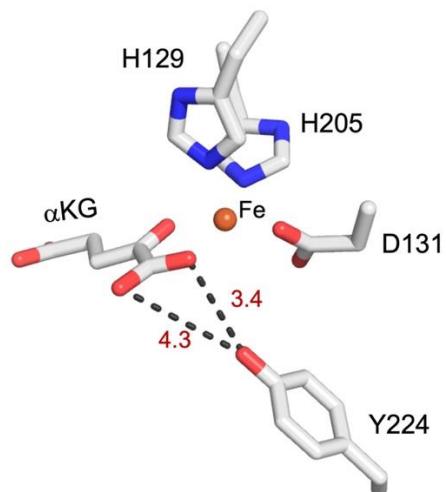
**Figure S1.**  $^{19}\text{F}$  NMR studies on  $\text{F}_2\text{Y224-FtmOx1}$  complexed with different metal ions.



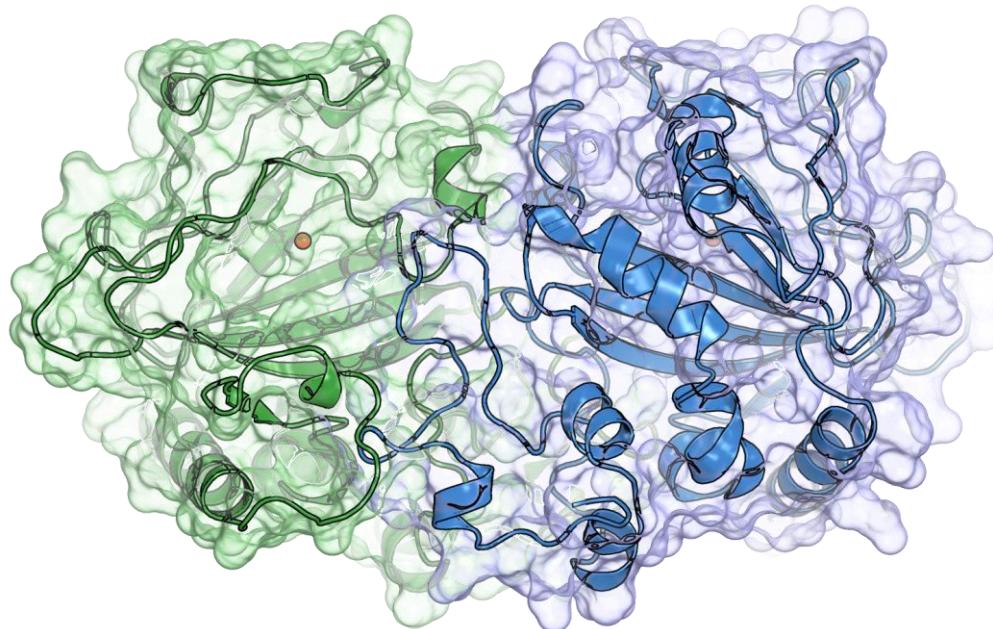
**Figure S2.** CD spectrum of  $\text{F2Y224-FtmOx1}$  apo protein (black),  $\text{F2Y224-FtmOx1}\cdot\text{Fe}(\text{II})$  (red), and  $\text{F2Y224-FtmOx1}\cdot\text{Zn}(\text{II})$  (green).

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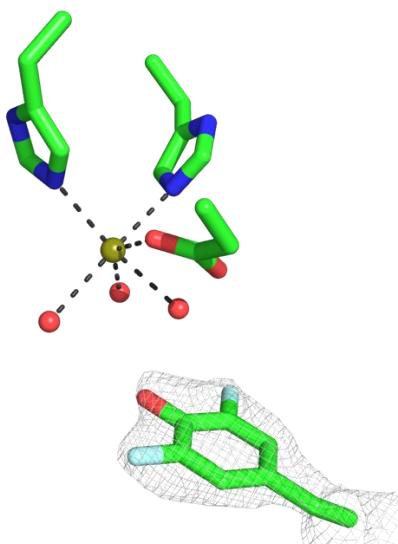
**Figure S3.** Binary structure of FtmOx1•Fe<sup>II</sup>•αKG (pdb entry 4Y5S) complex. The distances between Y224 and two oxygen atoms of 1-carboxyl group of αKG are presented on the black dashed lines.



**Figure S4.** Overall architecture of F<sub>2</sub>Y224-FtmOx1•Fe<sup>II</sup> (pdb entry 9J1I) shown as a functional dimer with one monomer color-coded based on secondary and surface structures (shown as stereo images). The iron centers are labelled as deep olive spheres.

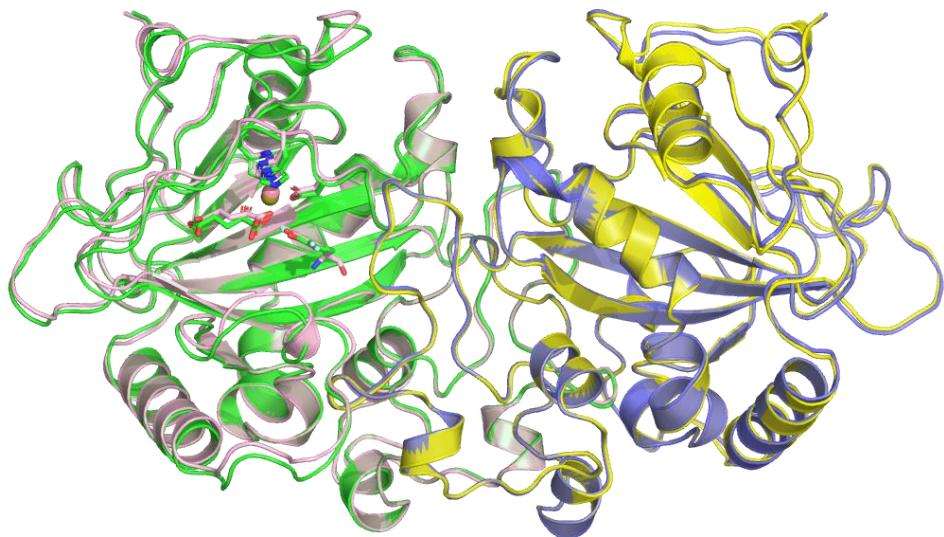
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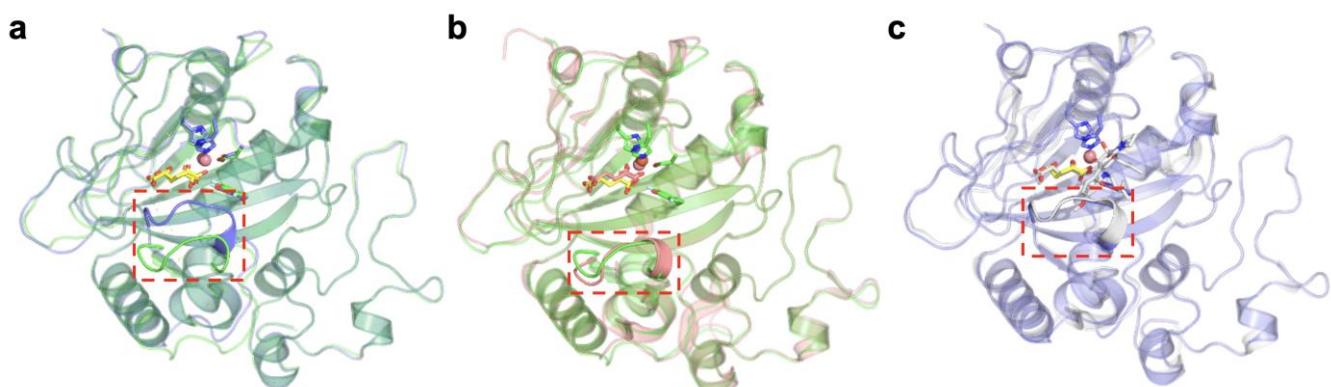
**Figure S5.** The composite omit map of F<sub>2</sub>Y224-FtmOx1•Fe<sup>II</sup> metallo-center (pdb entry 9J1I) (2mF<sub>o</sub> – DF<sub>c</sub>) at 1 $\sigma$  contour. The electron density around F2Y224 is shown in grey mesh.

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**Figure S6.** Superimposition of F<sub>2</sub>Y224-FtmOx1•Co<sup>II</sup>•αKG (pdb entry 9J1H) complex with F<sub>2</sub>Y224-FtmOx1•Fe<sup>II</sup>•αKG (pdb entry 4Y5S) complex.

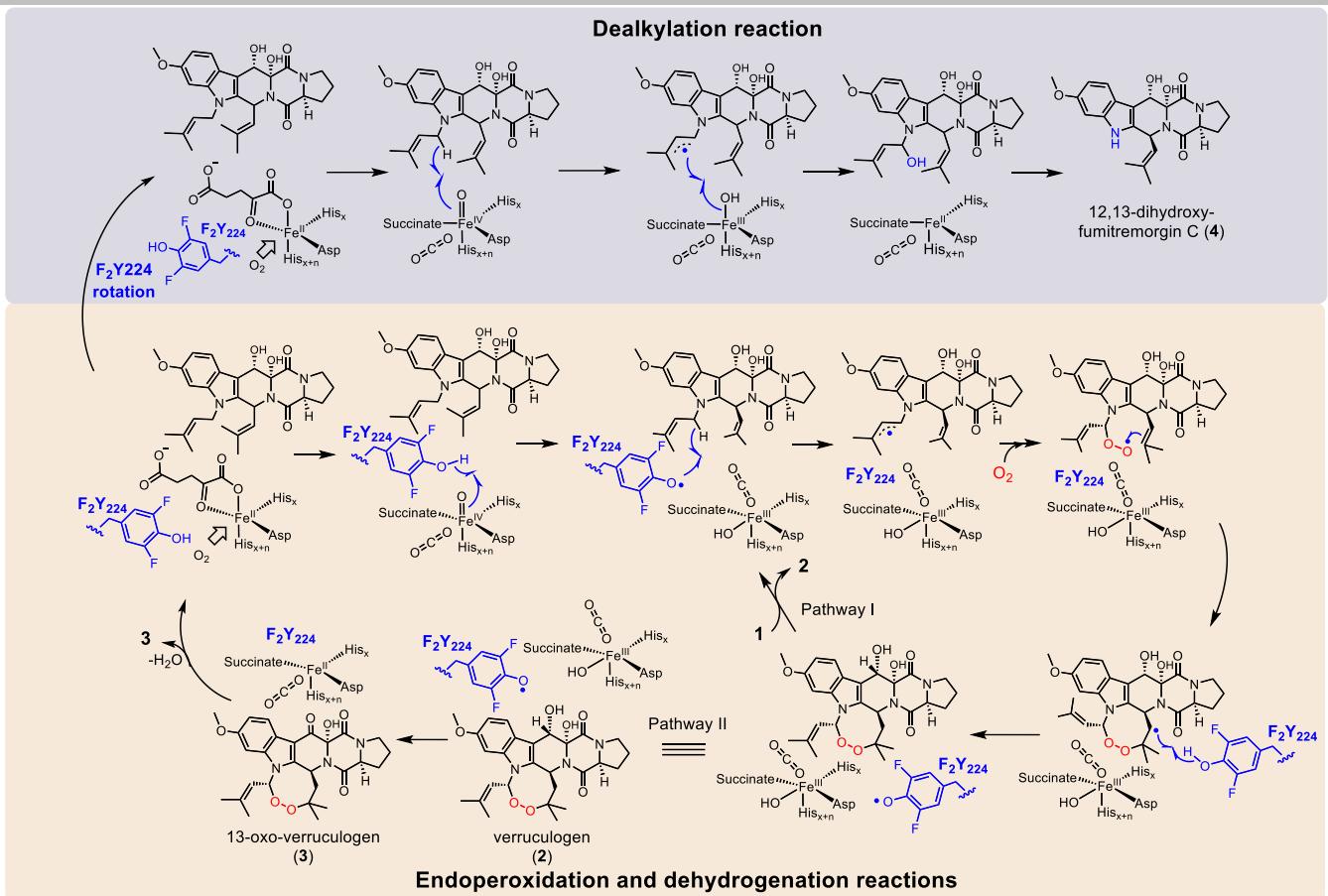
The F<sub>2</sub>Y224-FtmOx1•Co<sup>II</sup>•αKG overall architecture and metallo-center are shown in green and purple cartoon and green sticks, respectively. The F<sub>2</sub>Y224-FtmOx1•Fe<sup>II</sup>•αKG overall architecture and metallo-center are shown in pink and yellow cartoon and sticks, respectively.



**Figure S7.** Structural comparions of the loops (65ADKYPPHF72) in different FtmOx1 crystal structures.

(a) Superimposition of chain A (green) onto chain B (purple) of F<sub>2</sub>Y224-FtmOx1•Co<sup>II</sup>•αKG (pdb entry 9J1H) complex. (b) Superimposition of chain A (green) of F<sub>2</sub>Y224-FtmOx1•Co<sup>II</sup>•αKG with FtmOx1•Fe<sup>II</sup>•αKG (pdb entry 4Y5S) complex. (c) Superimposition of chain B (purple) of F<sub>2</sub>Y224-FtmOx1•Co<sup>II</sup>•αKG with FtmOx1•Co<sup>II</sup>•αKG•13-oxo-fumitremorgin B (**6**) (pdb entry 7WSB) complex. The structures were shown in cartoon mode with 75% transparency while structurally different loops (65ADKYPPHF72) are highlighted by red-dotted squares with no transparency.

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**Figure S8.** The proposed mechanistic models for F<sub>2</sub>Y224-FtmOx1- catalysis.

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### Supplementary Tables

**Table S1.** Crystallographic data collection and refinement statistics for the FtmOx1•Fe<sup>II</sup> structure.

Data Collection	
Wavelength (Å)	0.9785
Resolution range (Å)	36.08 - 2.11 (2.19 – 2.11)
Space group	P 1 2 <sub>1</sub> 1
Unit cell a, b, c (Å) $\alpha, \beta, \gamma$ (°)	60.44 45.61 105.15 90 100.02 90
Unique reflections	32539 (3155)
Multiplicity	3.2 (2.6)
Completeness (%)	99.16 (97.23)
Mean I/sigma(I)	11.18 (1.79)
CC <sub>1/2</sub>	0.997 (0.686)
R <sub>sym</sub>	0.069 (0.536)
Refinement	
R <sub>work</sub>	0.1746 (0.2312)
R <sub>free</sub>	0.2146 (0.2739)
Number of non-hydrogen atoms	4726
macromolecules	4501
ligands	3
water	222
Protein residues	569
RMS bonds (Å)	0.008
RMS angles (°)	0.88
Ramachandran favored (%)	98.39
Ramachandran outliers (%)	0
Average B-factor (Å <sup>2</sup> )	41.12
macromolecules	41.17
ligands	39.80
solvent	40.28

<sup>1</sup>Statistics for the highest-resolution shell are shown in parentheses.

<sup>2</sup> R<sub>free</sub> is calculated with 5% of the data randomly omitted from refinement.

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**Table S2.** Crystallographic data collection and refinement statistics for the FtmOx1•Co<sup>II</sup>•αKG binary complex.

Data Collection	
Wavelength (Å)	0.9785
Resolution range (Å)	47.93 - 2.00 (2.07 – 2.00)
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>
Unit cell a, b, c (Å) α, β, γ (°)	62.032 62.077 151.02 90 90 90
Unique reflections	39836 (3641)
Multiplicity	5.9 (3.7)
Completeness (%)	99.04 (91.92)
Mean I/sigma(I)	9.28 (1.99)
CC <sub>1/2</sub>	0.992 (0.846)
R <sub>sym</sub>	0.118 (0.470)
Refinement	
R <sub>work</sub>	0.1726 (0.2505)
R <sub>free</sub>	0.1939 (0.2932)
Number of non-hydrogen atoms	4919
macromolecules	4466
ligands	33
water	420
Protein residues	565
RMS bonds (Å)	0.007
RMS angles (°)	0.98
Ramachandran favored (%)	95.66
Ramachandran outliers (%)	0.36
Average B-factor (Å <sup>2</sup> )	31.68
macromolecules	31.53
ligands	31.71
solvent	33.24

<sup>1</sup>Statistics for the highest-resolution shell are shown in parentheses.

<sup>2</sup> R<sub>free</sub> is calculated with 5% of the data randomly omitted from refinement.