

1 **Supplementary materials**

2 **Crystal Structure of Escherichia coli originated MCR-1, a phosphoethanolamine**
3 **transferase for Colistin Resistance**

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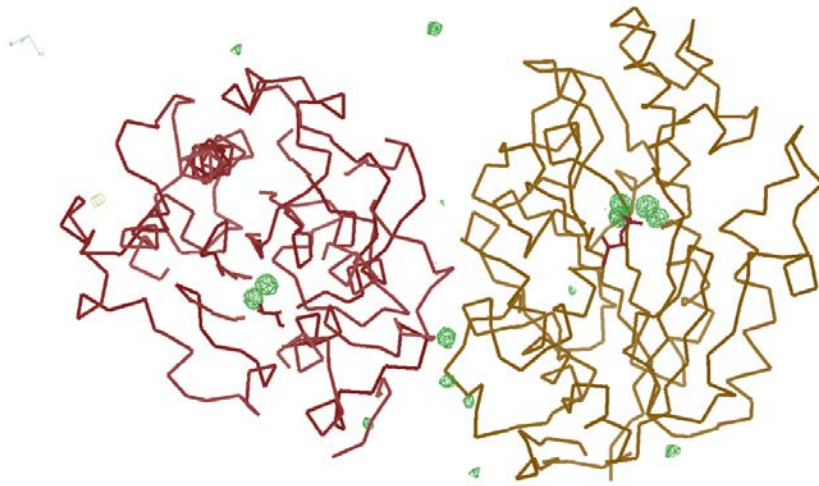
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21 **Supplementary Table 1. Crystallographic Data and Refinement Statistics**

Data Collection	
	MCR-1-ED
Cell dimensions a, b, c (Å) α, β, γ (°)	54.4, 55.8, 219.4 90, 90, 90
Space group	P2 ₁ 2 ₁ 2 ₁
Wavelength (Å)	0.9790
Resolution (Å) ^a	50.00-2.33 (2.37- 2.33)
Unique reflections	29251 (1160)
Redundancy	11.5 (9.8)
$\langle I / \sigma I \rangle$	22.27 (2.84)
R _{sym}	0.104(0.582)
Completeness (%)	97.5 (77.6)
Refinement	
R _{work}	0.186
R _{free}	0.236
RMSD from ideal Bond lengths (Å) Bond angles (°)	0.009 1.184
Average B-factors (Å ²)	35.5
Ramachandran plot (%): favored/allowed/outliers	96.22/3.46/0.31
^a Values in parentheses are from the highest-resolution shell.	

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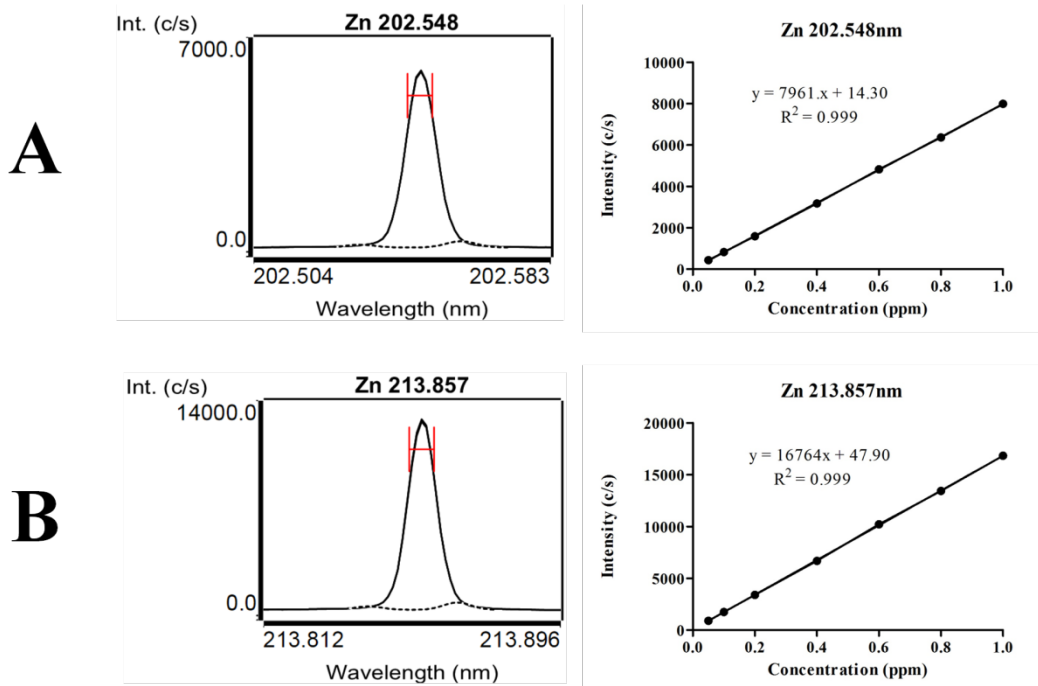
38 **Supplementary Figure 1. Phased anomalous difference map (5.0 r.m.s.d.)**

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46 **Supplementary Figure 2. Metal content determination in MCR-1 protein.** The Zn
 47 content measurement at the wavelength of 202.548nm (A) and 213.857nm (B). The
 48 left panels show the Zn content in the MCR-1 protein sample, and the right panels
 49 depict the corresponding Zn standard curves compiled for determining the Zn
 50 concentration in the MCR-1 protein sample.

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66 **Supplementary Figure 3.** Sequence alignment between MCR-1 (full length) and LptA (PDB code: 4KAY).
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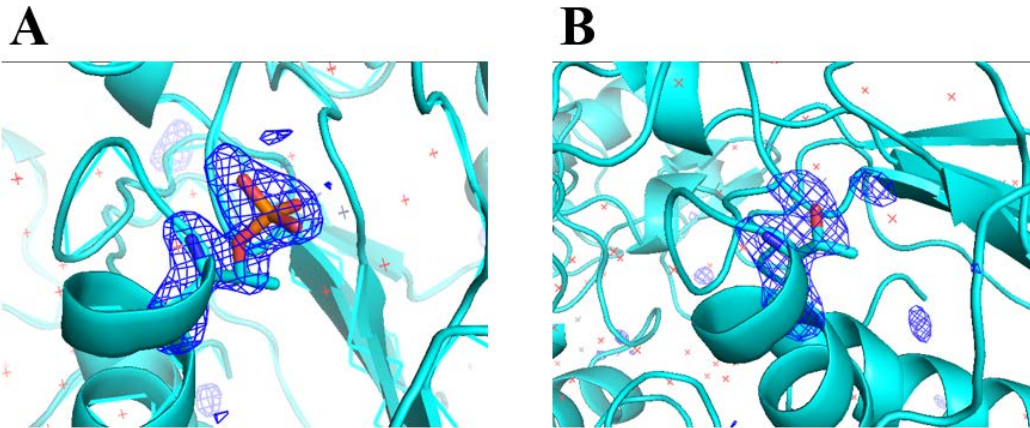
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82 **Supplementary Figure 4.** The Omit-map density of the phosphorylation site at
83 T285 of both chain A and B. (A) Phosphorylated T285 on chain A; (B) Non-
84 phosphorylated T285 on chain B.

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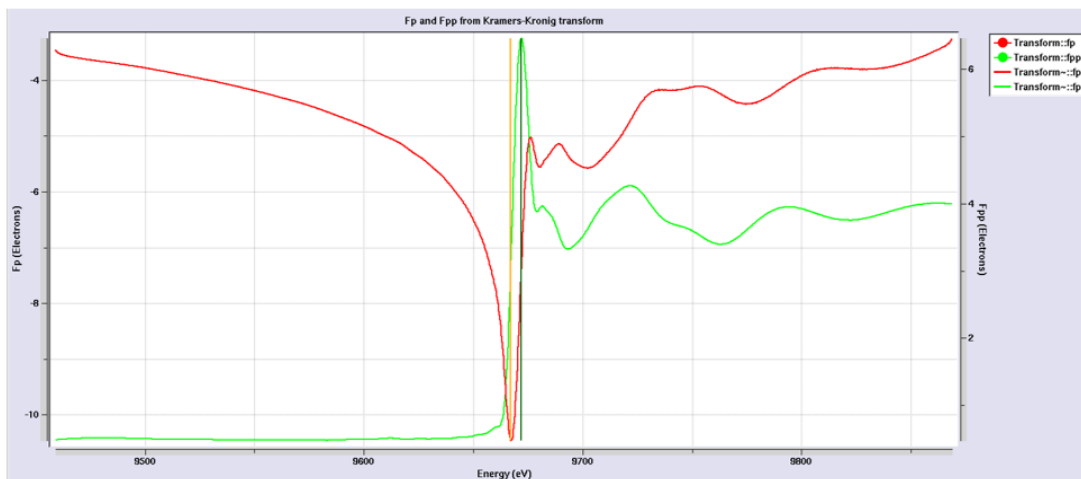
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115 **Supplementary Figure 5.** Florescence scan of Zinc ions in crystals.

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