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**Supplementary information, Table S1** Data Collection and Refinement Statistics

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	SsTRIC	RsTRIC Native	RsTRIC Se-Met
<b>Data collection</b>			
X-ray source	SPring-8 BL41XU	Swiss Light Source X06SA	SPring-8 BL41XU
Wavelength (Å)	1.0000	1.0000	0.9792
Space group	<i>P</i> 2 <sub>1</sub>	<i>R</i> 3	<i>R</i> 3
Cell dimensions			
<i>a, b, c</i> (Å)	102.7, 171.4, 103.3	156.0, 156.0, 82.4	156.7, 156.7, 82.5
<i>α, β, γ</i> (°)	90.0, 117.9, 90.0	90.0, 90.0, 120.0	90.0, 90.0, 120.0
Resolution (Å)	50.0-2.64 (2.80-2.64)	50.0-3.41 (3.50-3.41)	50.0-3.60 (3.82-3.60)
<i>R</i> <sub>sym</sub>	0.099 (1.130)	0.072 (0.285)	0.129 (0.921)
<i>I</i> / <i>σ</i> ( <i>I</i> )	14.59 (1.63)	15.20 (6.65)	13.62 (3.00)
Completeness (%)	98.2 (97.5)	95.3 (40.6)	99.6 (98.1)
Redundancy	7.02 (6.93)	5.1 (4.8)	10.5 (10.6)
CC <sub>1/2</sub>	1.000 (0.685)	0.996 (0.963)	0.999 (0.917)
<b>Refinement</b>			
Resolution (Å)	50.0-2.64	50.0-3.41	
No. reflections	90876	9730	
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub>	21.1/25.2	24.7/27.3	
No. atoms			
Protein	14438	2794	
Ligand/ion	55	28	
Water	143		
B-factors			
Protein	73.3	42.7	
Ligand/ion	67.0	26.4	
Water	61.7		
R.m.s. deviations			
Bond lengths (Å)	0.011	0.004	
Bond angles (°)	1.350	0.960	
Ramachandran plot (%)			
Favored	97.1	98.0	
Outliers	0.0	0.0	

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