Table S1. Data collection and refinement statistics.

Data collection	Native	Phasing $UO_2(C_2H_3O_2)_2$	Native	SeMet
Number of crystals	1	1	1	1
Space group	$P2_12_12_1$	$P2_12_12_1$	$P4_122$	$P4_122$
Wavelength (Å)	0.9551	0.9551	0.9551	0.9786
Cell dimensions, *a*, *b*, *c* (Å)	63.1, 116.0, 123.0	63.2, 116.8, 123.4	77.4, 77.4, 108.6	76.1, 76.1, 110.7
α, β, γ (°)	90, 90, 90	90, 90, 90	90, 90, 90	90, 90, 90
Resolution range (Å) [a]	25-2.50(2.59-2.50)	44-3.10(3.21-3.10)	25-3.05(3.16-3.05)	40-4.20(4.35-4.20)
Unique reflections [a]	31805	17206	6699	4552
Degrees of data (°)	286	471	286	309
Completeness (%) [a]	99.1 (97.4)	99.9 (99.4)	99.3(98.0)	99.8 (100.0)
R_{sym} (%) [a]	6.1 (66.2)	16.5	8.4 (49.1)	8.7 (29.9)
Mn (I / σI) [a]	16.3 (2.0)	14.6 (1.9)	19.3 (2.7)	22.4 (8.4)
Redundancy [a]	7.3 (5.1)	16.3 (12.6)	13.7 (9.6)	12.8 (12.7)
Wilson plot *B*-factor (Å^2)	68	89	109	139
Phasing power (acentrics)				
Isomorphous		0.83		
Anomalous		0.18		
Figure of Merit (centrics) (to 4.02Å)		0.22 (0.37)		
Figure of Merit (acentrics) (to 4.02Å)		0.14 (0.30)		
Refinement				
Resolution range (Å) [a]	25-2.50(2.56-2.50)		25-3.05(3.12-3.05)	
R_{factor} (%) [a]	22.9 (30.2)		27.8 (34.9)	
Free R_{factor} (%) [a]	28.8 (40.1)		29.3 (41.5)	
Residue range built	A:15-212 B: 1-210 C:10-210 D: 8-210		14-210	
Free *R* reflections (%)	5.1		4.9	
Free *R* reflections, no. [a]	1600 (101)		316 (30)	
No. non-hydrogen protein atoms	6655		1630	
No. water molecules	70		0	
Model quality				
RMSD bond lengths (Å)	0.008		0.006	
RMSD bond angles (°)	1.106		0.881	
Mean *B*-factors				
Overall (Å^2)	79.3		146.5	
Protein atoms, (Å^2)	79.5		146.5	
Protein atoms NTD,(N-69) (Å^2)	58.7		132.9	
Protein atoms αE-EF linker (70-97) (A^2)	80.0		148.5	
Protein atoms FAT,(98-C) (Å^2)	90.1		152.5	
Water (Å^2)	63.2		-	
Ramachandran plot (%) favored / allowed / disallowed	92.5 / 7.5 / 0		90.4 / 9.5 / 0	

[a]Parentheses indicate the highest-resolution shell.