Table S1. Data collection statistics

				Data collection				
	"As-purified"	Derivative (Os)			Derivative (Au)	DecylUQ	AurachinC	6.5 keV
Space group	P2,2,2	P2 ₁ 2 ₁ 2 ₁			P2,2,2	P2,2,2,1	P2,2,2,	P2,2,2,
Unit cell dimension (Å)	a = 112.85	a = 112.30			a = 112.10	a = 110.78	a = 111.18	a = 110.78
	b = 154.92	b = 155.86			b = 154.30	b = 154.01	b = 154.23	b = 154.01
	c = 178.04	c = 178.26			c = 176.70	c = 175.55	c = 176.53	c = 175.55
77		Peak	Inflection	Remote	Peak			
Wavelength (Å)	0.91984	1.14000	1.14050	1.13010	1.03864	1.00150	1.00148	1.907445
Resolution (Å)	50.0 - 2.3 (2.4 - 2.3)	50.0 - 3.5 (3.6 - 3.5)	50.0 - 3.5 (3.6 - 3.5)	50.0 - 4.0 (4.1 - 4.0)	50.0 - 4.2 (4.3 - 4.2)	50.0 - 2.0 (2.1 - 2.0)	50.0 - 2.9 (3.0 - 2.9)	50.0 - 2.3 (2.4 - 2.3)
R _{merge} (%)	8.3 (34.4)	12.3 (38.2)	12.8 (42.4)	8.2 (19.2)	6.2 (8.9)	10.5 (76.5)	8.3 (39.6)	12.4 (58.6)
Ι / σ(I)	14.87 (3.44)	12.69 (4.30)	12.26 (3.96)	15.77 (8.41)	15.38 (12.38)	13.17 (1.86)	16.74 (4.05)	9.97 (2.40)
Completeness (%)	97.9 (87.9)	98.9 (98.9)	98.9 (99.1)	98.7 (99.2)	99.7 (99.9)	96.2 (76.7)	98.8 (95.7)	91.1 (75.9)
Redundancy	3.47 (2.47)	3.36 (3.34)	3.37 (3.42)	3.33 (3.42)	3.83 (3.87)	4.74 (1.86)	3.72 (3.41)	2.54 (1.63)
	Г	1		Refinement				
Resolution (Å)	2.30			and the second se		2.00	2.90	2.30
Total reflections	471,639		10000		10000	921,962	249,689	596,959
R _{work} / R _{free} (%)	19.2 / 23.5		Constant State	and the second	1000	20.0 / 23.7	19.4 / 24.1	20.3 / 24.7
RMSD	11 1000		All the all and and and and all and	and the second		or start	100.000	
bond length (Å)	0.010	I A STATISTICS			and the second	0.008	0.006	0.009
bond angles (°)	1.420		and the second		and the second second	1.179	0.989	1.308
Number of atoms	and an a start of a store	XIN	the top top		and the same			
protein	20136		and the second		. and the second	20029	20094	20029
cofactor (FAD)	318	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				318	318	318
detergent (DDM)	210					210	210	210
water	571		and the second		A Marine State	1142	194	546
ions (SO ₄ ²)	120			and the state		120	120	120
ligand	-	Contraction of Contra	1.000			138	168	138
sulfur	54	Statement in succession				50	59	50
buffer (MES)	72						-	-

Five percent of the reflections were used for calculation of the R_{free} . Values in parenthesis are for the highest-resolution shell. In the *Inset* are one crystallization drop with the hexagonal and the needle crystal forms grown together and a typical diffraction pattern of the needle crystals used for solving the structure.