Supplementary Table 1 | Data collection and refinement statistics for BT2261-2264

	BT2261-64 Native 1	BT2261-64 Native 2	BT2261-64 SeMet
Data Collection			
Space group	P1	$P2_12_12_1$	$P2_1$
Cell dimensions (a,b,c)	92,123,123	124, 180, 246	222, 92, 261
angles (α,β,γ)	111, 98, 99	90, 90, 90	90, 98.2, 90
Molecules/AU	2 tetramers	2 tetramers	4 tetramers
Resolution (Å)	67-2.75	49-3.4	49-2.8
$I/\sigma I$	5.8 (1.7)[#]	10.3 (2.0)	8.9 (2.1)
Completeness	100 (100)	100 (100)	99.6 (99.1)
Redundancy	3.8 (3.6)	7.6 (7.6)	9.3 (9.2)
Rpim (%)	12.6 (46)	6.9 (43)	7.5 (48)
CC (1/2)	0.96 (0.54)	1.00 (0.68)	1.00 (0.90)
Refinement			
Resolution (Å)	53-2.75	48-3.4	49-2.8
No. reflections	125658	76084	255319
R_{work}/R_{free} (%)	21.0/25.9	20.0/25.5	19.8/25.5
No. atoms			
protein/water/	26165/932	25810/-	49114/-
ligand/detergent	78/35	82/-	164/-
B factors (Å$_2$)			
protein/water	42/21	89/-	68/-
ligand/detergent	41/31	75/-	65/-
R.m.s deviations			
bond lengths (Å)	0.014	0.013	0.008
bond angles (°)	0.95	1.18	1.07
Molprobity clashscore	10.2	13.3	12.3

[#] Values in parentheses are for the highest resolution shell

Supplementary Table 2 | Data collection and refinement statistics for soluble proteins

	BT2263	BT2262	BT1762
Data Collection			
Space group	$P2_1$	$P4_12_12$	$C222_1$
Cell dimensions (a,b,c)	55, 80, 121	167, 167, 100	108, 129, 87
angles (α,β,γ)	90, 100.2, 90	90, 90, 90	90, 90, 90
Molecules/AU	2	4	1
Resolution (Å)	46-1.83	49-3.1	45.7-1.76
I/σI	9.7 (1.5)	15.3 (2.5)	11.2 (1.9)
Completeness	99.3 (100)	100 (100)	98.9 (94.6)
Redundancy	3.6 (3.6)	14.7 (14.8)	4 (3.6)
Rpim (%)	5.8 (55)	5.1 (46)	5.4 (37.4)
CC (1/2)	0.99 (0.58)	0.99 (0.78)	0.99 (0.59)
Refinement			
Resolution (Å)	47.5-1.9	48.7-3.1	45.7-1.76
No. reflections	80356	26387	59338
R_{work}/R_{free} (%)	15.8/19.9	19.9/26.0	15.6/18.8
No. atoms			
protein/water/	7190/876	6180/-	4325/331
ligand/detergent	-/-	-/-	-/-
B factors (Å$_2$)			
protein/water	30/38	86/-	17/21
ligand/detergent	-/-	-/-	-/-
R.m.s deviations			
bond lengths (Å)	0.007	0.010	0.015
bond angles (°)	0.80	1.37	1.57
Molprobity clashscore	2.6	16.2	0.83

Supplementary Table 3 | Data collection and refinement statistics for BT1762-63

Data Collection	BT1762-63 (Native 1)	BT1762-63 (Native 2)
Space group	$P2_12_12$	$P2_12_12_1$
Cell dimensions (a,b,c)	152, 117, 120	111, 152, 253
angles (α,β,γ)	90, 90, 90	90, 90, 90
Molecules/AU	1	2
Resolution (Å)	84-3.10	152-3.10
I/σI	4.8 (1.6)	10.7 (1.5)
Completeness	100.0 (100.0)	100.0 (100.0)
Redundancy	7.2 (7.0)	5.7 (5.7)
Rpim (%)	14.2 (63.4)	4.6 (53.0)
CC (1/2)	0.97 (0.72)	0.98 (0.70)
Refinement		
Resolution (Å)	76-3.10	130-3.10
No. reflections	39461	77436
R_{work}/R_{free} (%)	19.7/25.9	19.8/26.9
No. atoms		
protein/water/	10857/-	21722/-
ligand/detergent	3/-	5/-
B factors (Å$_2$)		
protein/water	75/-	72/-
ligand/detergent	57/-	56/-
R.m.s deviations		
bond lengths (Å)	0.010	0.010
bond angles (°)	1.27	1.25
Molprobity clashscore	13.6	13.0