

Table S1. Data collection and refinement statistics for lysine-methylated selenomethionine EhG α 1.

EhG α 1·GDP	
PDB accession code	4FID
Data collection	
Space group	P2 ₁ 2 ₁ 2 ₁
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	56.3, 56.9, 229.8
α , β , γ (°)	90, 90, 90
	<i>Peak</i>
Wavelength (Å)	0.97954
Resolution (Å)	45.9 - 2.60 (2.62 - 2.60)*
No. unique reflections	43,503
<i>R</i> _{merge} (%)	7.7 (98.2)**
<i>I</i> / σ <i>I</i>	30.7 (2.6)
Completeness (%)	99.3 (94.0)
Redundancy	13.3 (13.3)
Refinement	
Resolution (Å)	45.9 - 2.6 (2.7 - 2.6)
No. reflections	43503 (4336)
<i>R</i> _{work} / <i>R</i> _{free} (%)	18.9 / 25.8 (25.8 / 36.4)
No. atoms	5013
Protein	4905
Ligand/ion	56
Water	39
<i>B</i> -factors (Å ²)	
Protein	58.1
Ligand/ion	57.4
Water	44.8
R.m.s deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.205

*Values in parentheses are for highest-resolution shell.

**All data were collected from a single crystal.