Extended Data Table 1 | Data collection and structure refinement statistics

Data Collection*	
Space group	*P21 21 21*
Cell dimensions	
a, *b*, *c* (Å)	60.1, 108.8, 216.3
α, β, γ (°)	90, 90, 90
Resolution (Å)	50.0-3.00 (3.11-3.00)†
R_{pim} (%)	5.2 (76.4)
$I / \sigma I$	21.6 (0.6)
Completeness (%)	97.8 (86.4)
Redundancy	10.1 (5.3)
Refinement	
Resolution (Å)	50.0-3.00
No. reflections	27,458
R_{work} / R_{free} (%)	23.2 / 26.1
No. atoms	
Protein	4,328
Peptide	236
Lipids/others	146
B-factors (Å^2)	
GCGR	119.7
T4L	155.8
Peptide	111.0
Lipids/others	168.0
R.m.s. deviations	
Bond lengths (Å)	0.009
Bond angles (°)	1.05

*Diffraction data from ten crystals were used to solve the structure.
†Values in parentheses are for the highest-resolution shell.