Supplementary Information, Table S1 Data collection and refinement statistics

	CRY2-KL001
Data collection	
PDB	4MLP
Space group	P1
Cell dimensions	
a, *b*, *c* (Å)	48.1, 93.8, 141.6
α, β, γ (°)	90.1, 90.0, 90.3
Resolution (Å)	50 – 1.94 (1.98 – 1.94) *
R_{sym} or R_{merge}	0.079 (0.601)
$I / \sigma I$	32.2 (3.6)
Completeness (%)	97.1 (95.1)
Redundancy	3.7 (3.8)
Refinement	
Resolution (Å)	1.94
No. reflections	170540
R_{work} / R_{free}	0.180 / 0.217
No. atoms	
Protein	16060
Ligand/ion	112
Water	1557
B-factors	
Protein	32.37
Ligand/ion	32.25
Water	36.97
R.m.s. deviations	
Bond lengths (Å)	0.007
Bond angles (°)	1.087

Each dataset was collected from a single crystal
*Values in parentheses are for highest-resolution shell.