Supplementary Table 1 Crystallographic statistics.

Parameters	α-LA+Zn^{2+}	β-LG+Zn^{2+}
Data collection	7WQG	7WQL
Wavelength (Å)	0.987	0.987
Space group	P3	C2
Unit cell		
a, b, c (Å)	92.84 92.84 66.17	132.14 42.46 70.04
α, β, γ (°)	90 90 120	90 104 90
[a]Resolution (Å)	34.36-2.50 (2.59-2.50)	33.97-2.00 (2.07-2.00)
[a]Completeness (%)	99.77 (99.82)	98.39 (97.62)
Mean I/sigma(I)	27.2 (2.20)	8.5 (1.81)
[b]$CC_{1/2}$ of the highest resolution shell	0.992 (0.979)	0.994 (0.869)
Refinement		
Unique reflections	22053 (2227)	25383(2461)
Reflections used in refinement	22053 (2227)	25367(2459)
Reflections used for R-free	1180 (147)	1997(193)
Non-hydrogen Atoms	5890	2601
Protein residues	725	314
Wilson B-factor ($Å^2$)	37.40	30.77
[c]R_{work} (%)	0.1440 (0.2216)	0.2071(0.2614)
[d]R_{free} (%)	0.2216 (0.2234)	0.2614(0.3012)
macromolecules	5829	2481
ligands	7	6
RMS(bonds)	0.012	0.018
RMS(angles)	1.08	1.51
Ramachandran favored (%)	90.04	92.90

Ramachandran allowed (%)	9.68	6.45
Ramachandran outliers (%)	0.28	0.65

[a]Highest resolution shell is shown in parentheses.

[b]CC1/2 is the correlation coefficient of the half datasets.

[c]Rwork = ∑hkl | |Fobs| – |Fcalc| | / ∑hkl |Fobs|, where Fobs and Fcalc is the observed and the calculated structure factor, respectively.

[d]Rfree is the cross-validation R factor for the test set of reflections (5% of the total) omitted in model refinement.