

Supplementary Table 1 Data collection and refinement statistics (molecular replacement)

	human LC3BΔG120
Data collection	
Space group	P1
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	41.64, 56.48, 67.04
α , β , γ (°)	99.27, 97.45, 109.94
Resolution (Å)	27.62-1.90 (1.97-1.90)*
<i>R</i> _{merge}	0.093 (0.562)
<i>I</i> / σI	19.0 (1.9)
Completeness (%)	93.5 (94.4)
Redundancy	3.60 (3.60)
Refinement	
Resolution (Å)	1.90
No. reflections	40763
<i>R</i> _{work} / <i>R</i> _{free}	0.2094/0.2620
No. atoms	
Protein	474
Ligand/ion	10
Water	247
<i>B</i> -factors (Å ²)	
Protein	32.97
Ligand/ion	32.53
Water	38.43
R.m.s. deviations	
Bond lengths (Å)	39.84
Bond angles (°)	0.41
	0.54

There is 1 crystal for this structure.

*Values in parentheses are for highest-resolution shell.