Supplementary Table 1 Data-collection and phasing statistics. Values in parentheses are for the outermost shell.

Proteins	Lysozyme	70028
No. of residues	129	265
No. of Met	2	7
No. of Cys	8	1
Mount tool	Crystal Catcher	Crystal Catcher
Space group	$P4_32_12$	$P4_12_12$
Unit-cell parameter		
a (Å)	78.93	104.30
b (Å)	78.93	104.30
c (Å)	36.96	139.08
Wavelength (Å)	1.54	1.54
Resolution range (Å)	20-1.45 (1.50–1.45)	20–2.3 (2.38–2.30)
No. of unique reflections	21149 (2025)	34724 (3417)
Redundancy	12.6 (10.8)	19.0 (18.9)
Completeness (%)	99.2 (97.4)	100 (100)
R_{merge}[†] (%)	3.4 (24.6)	4.2 (13.0)
$<I/\sigma(I)>$	18.6 (9.4)	18.4 (13.1)
Mosaicity (°)	0.28	0.34
SAD Phasing	Success	Success
Figure of merit (before solvent flattening)	0.443	0.218
No. of molecules in ASU	1	2
Residues built with side chain (%)	96.1	94.9

[†] $R_{\mathrm{merge}} = \sum_{hkl} \sum_i |I_i(hkl) - <I(hkl)>| / \sum_{hkl} \sum_i I_i(hkl)$, where $I_i(hkl)$ is the ith observation of reflection hkl and $<I(hkl)>$ is the weighted average intensity for all observations i of reflection hkl.