Supplementary Table 1. Data collection and refinement statistics of HEW lysozyme

Data collection statistics	
Space group	$P4_32_12$
Cell constants (Å)	$a = b$ = 77.326, c = 37.193
Beamline	SPring-8 BL26B1
Detector	CCD MSC saturnA200
Exposure time (sec /frame)	10
Wavelength (Å)	0.7
Camera distance (mm)	150
Resolution (Å)	50.0 – 1.00 (1.02 - 1.00)
Oscillation angel (deg.)	1.0
σ cut-off	0.0
R_{merge} [a, b]	0.072 (0.358)
No. of measurements	984,794
No. of independent reflections	61,262
Completeness (%)	93.9 (58.1)
Multiplicity	17.1 (2.7)
Mean $<I/\sigma(I)>$	63.8 (1.4)
Refinement statistics	
Resolution (Å)	26.804 - 1.300 (1.347 - 1.300)
No. of reflections used	28,205 (2,764)
Completeness (%)	99.63 (100.0)
R_{work} [c]	0.150 (0.159)
R_{free} [c]	0.186 (0.197)
Number of chains (Average B factor ($Å^2$))	
Protein (chain A)	1 (15.18)
Water (chain S)	231 (23.78)
Na (chain NA)	1 (10.60)
Cl (chain CL)	4 (16.32)
Ethylene glycol (chain E)	1 (21.07)
R.m.s. deviations	
Bond lengths (Å)	0.015
Bond angles (°)	1.596

[a] $R_{merge} = \Sigma\Sigma_i \ ||I(h) - I(h)i|/\Sigma\Sigma_i \ I(h)$, where $I(h)$ is the mean intensity after   rejections.

[b] Values in parentheses are for highest resolution shells.

[c] $R_{work} = \Sigma \ | F_p - F_{pc} | / \Sigma \ | F_p |$; R_{free}, the same as R_{work} but calculated on 5% data excluded from refinement