Supplementary information, Table S1

Table S1 Data collection and refinement statistics (molecular replacement)

	dTale2 (148-610)
Data collection	
Space group	P3221
Cell dimensions	
a, *b*, *c* (Å)	a=b=101.28, c=95.59
α, β, γ (°)	α=β=90, γ=120
Wavelength (Å)	0.9791
Unique reflections	29024 (1435)
Resolution (Å)	15.00-2.20 (2.24-2.20)
R_{sym} or R_{merge}	6.9 (31.0)
I / sigma	37.6 (5.8)
Completeness (%)	100.0 (100.0)
Redundancy	10.9 (11.1)
Refinement	
Resolution (Å)	2.2
No. reflections	28963
R_{work} / R_{free} (%)	20.60/24.28
No. atoms	
Protein	3191
Water	160
B-factors	
Protein	42.13
Water	42.71
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.184
Ramachandran plot statistics (%)	
Most favorable	94.9
Additionally allowed	5.1
Generously allowed	0
Disallowed	0

Values in parentheses are for the highest resolution shell. $R_{merge} = \Sigma|I_i - Im|/\Sigma I_i$, where I_i is the intensity of the measured reflection, and I_m is the mean intensity of all the symmetry-related reflections. $R_{work} = \Sigma|F_o - Fc|/\Sigma F_o$, where F_o and F_c are the observed and calculated structure factor amplitudes, respectively. R_{free} is calculated with 5% reflections not used in refinement.