Supplementary information, Table S1B Crystallographic data and structure refinement statistics of YHT^{YTHDF2}

Data collection and refinement statistics	
Data collection	
Wavelength (Å)	0.97915
Resolution range (Å)	50.0-2.12(2.2-2.12) [a]
Space group	$P6_5$
Unit cell	a=76.69, b=76.69, c=131.24 α=90°, β=90°, γ=120°
Total reflections	259897
Unique reflections	24637
R-merge	0.119 (0.893)
I/sigma(I)	12.81（3.27)
Completeness (%)	99.54（99.47）
Redundancy	10.5(9.5)
Refinement	
R-work	0.1860
R-free [b]	0.2214
Deviation from identity	
rmsd (bonds, Å)	0.008
rmsd (angles,°)	1.043
Average B-factor (Å^2)	47.10
Ramachandran plot	
Most favored regions (%)	88.1
Allowed regions (%)	11.9
Generously allowed regions (%)	0

[a] The values for the data in the highest resolution shell are shown in parentheses.
[b] R-free = $\sum$ Test||Fobs|–|Fcalc||/ $\sum$ Test |Fobs|, where "Test" is a test set of about 5% of the total reflections randomly chosen and set aside prior to refinement for the complex.