

**Supplementary information, Table S1** Data collection, and refinement statistics

	Se YTH-YTHDF2	YTH-YTHDF2	YTH-YTHDF2:m <sup>6</sup> A
Wavelength(Å)	0.979	0.979	0.979
Space group	<i>P</i> 6 <sub>5</sub>	<i>P</i> 6 <sub>5</sub>	<i>P</i> 6 <sub>5</sub>
Cell parameters			
a, b, c (Å)	139.28 139.28 113.22	139.28 139.28 112.95	80.73 80.73 113.48
$\alpha$ , $\beta$ , $\gamma$ (°)	90, 90, 120	90, 90, 120	90, 90, 120
Resolution(Å)	37.89-2.20(2.32-2.20) <sup>a</sup>	43.86-2.15(2.27-2.15)	38.03-2.10(2.21-2.10)
<i>R</i> <sub>merge</sub> (%)	12.1(68.8)	10.0(54.2)	12.2(53.5)
I/ $\sigma$ I	9.3(2.9)	10.3(3.0)	12.0(3.7)
Completeness (%)	90.8(92.9)	97.0(98.4)	100.0(100.0)
Average redundancy	5.1(5.0)	4.5(4.5)	8.2(8.4)
<b>Refinement(F&gt;0)</b>			
No. reflections (overall)		62258	23209
No. reflections (test set)		3329	1247
<i>R</i> <sub>work</sub> / <i>R</i> <sub>free</sub> (%)		21.27/27.02	21.71/26.91
No. non-H atoms			
Protein		7090	2465
m <sup>6</sup> A nucleotide			40
Water		422	234
B factors (Å <sup>2</sup> )			
Protein		33.9	27.6
m <sup>6</sup> A nucleotide			21.4
Water		35.0	32.4
R.m.s. deviations			
Bond lengths (Å)		0.0087	0.0061
Bond angles (°)		1.2557	1.1220
Rampage plot % residues			
Favored		97.3	97.3
Allowed		2.7	2.7
Outliers		0	0

<sup>a</sup> Values in parentheses are for highest-resolution shell.