

**Supplementary Table 2**

Summary of crystallographic analysis of TSH260—K1-70 Fab

<b>X-ray diffraction data</b>	
X-ray source	Rigaku-007HF
Wavelength (Å)	1.54
Detector type	R-Axis IV
Detector distance	160
Temperature (°K)	100
Oscillation range per frame (°)	0.5
Overall rotation (°)	137.5
Resolution range (Å)	30-1.9
Number of observed reflections	286060
Number of unique reflections	56573
Multiplicity	5.1
Completeness (%) (overall and last shell)	94.5 (70.9)
R <sub>merge</sub> (%) (overall and last shell)	8.8 (30.2)
Mean I/sigma (overall and last shell)	11.7 (3.5)
Space group	P2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>
Unit cell parameters (Å), (°)	83.0 89.3 101.3 90.0 90.0 90.0

<b>Refinement</b>	
Refinement program	Refmac5
Resolution range (Å)	30-1.9
Number of reflections (working/test)	53657 (2861)
R <sub>work</sub>	17.7%
R <sub>free</sub>	22.7%
Protein residues modeled	650
Number of protein atoms modeled	5132
Number of water atoms modeled	801
RMSD Bond lengths (Å)	0.011
RMSD Bond angles (°)	1.347
Mean overall B value (Å <sup>2</sup> )	23.2
Mean water B value (Å <sup>2</sup> )	32.8
Ramachandran plot favored (%)	629 (96.8%)
Ramachandran plot allowed (%)	20 (3.1%)
Ramachandran plot outlier region(%)	1 (0.2%)