

**Supplementary information, Table S1. Data collection and model statistics.**

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<b>Model</b>	<b>NAIP5-FliC_D0<sub>L</sub></b>	
<b>Data collection</b>		
Electron microscope	FEI Titan Krios	
Voltage (kV)	300	
Electron Detector	Gatan K2 camera	
Pixel size (Å)	1.30654	
Electron dose(e-/ Å)	50 (32 frames)	
Defocus range(μm)	1.5~3.0	
<b>3D Reconstruction</b>		
Software	Relion-1.4	
Class	class5	class6
Particles for final refinement	245,315	381,293
Symmetry	C1	
Resolution (motioncor1, Å)	6.53	7.90
Resolution (motioncor2, Å)	4.93	4.58
Resolution (motioncor2+mask, Å)	4.42	4.51
Resolution (motioncor2+mask,,merge Å)	4.28	
Map sharpening B-factor (Å <sup>2</sup> )	-250	
<b>Model building</b>		
Software	COOT	
<b>Refinement</b>		
Software	PHENIX, VMD	
Resolution (Å)	4.28	
CC	0.740	
<b>Model composition</b>		
Protein residues	1313	
ATP	1	
<b>Validation</b>		

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**R.m.s deviations**

Bonds length (Å) 0.008

Bonds Angle (°) 1.175

**Ramachandran plot statistics (%)**

Preferred (%) 89.98%

Allowed (%) 9.56%

Outlier (%) 0.46%

**Completeness of model**

Amino acid residues defined by electron density Chain A: S<sup>404</sup>-E<sup>1403</sup> Chain B: A<sup>10</sup>-V<sup>247</sup>

Chain C: A<sup>421</sup>-R<sup>495</sup>

Except for amino acid residues<sup>1</sup>

H<sup>248</sup>-L<sup>403</sup>

Except for side chains<sup>2</sup>

Chain C: A<sup>421</sup>-A<sup>423</sup>

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<sup>1</sup> Residues not included in the model

<sup>2</sup> Occupancy set to 0.00 in the model