

Supplementary Table 17. Data collection and refinement statistics (molecular replacement) for *PfFIKK13*^{149-561_D379N} + Nb2G9 + Nb9F10+ ATP_γS.

	<i>PfFIKK13</i> ^{149-561_D379N} + Nb2G9 + Nb9F10+ ATP _γ S
Data collection	
Space group	P 2 ₁
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	82.40, 121.66, 151.06
α, β, γ (°)	90, 90.02, 90
Resolution (Å)	64.17–2.81(2.86–2.81)
<i>R</i> _{merge}	0.196(2.123)
<i>R</i> _{pim}	0.079(0.844)
<i>I</i> / σ <i>I</i>	6.8 (0.4)
Completeness (%)	99.7% (96.1%)
Multiplicity	7.03 (7.28)
CC _{1/2}	0.995 (0.615)
Refinement	
Resolution (Å)	2.81
No. reflections	72237
<i>R</i> _{work} / <i>R</i> _{free}	24.5% / 29.2%
No. atoms	19165
Protein	18999
Ligand/ion	124 AGS / 24 PE4
Water	18
<i>B</i> -factors	
Protein	73.1
Ligand/ion	75.3 AGS / 132 PE4
Water	55.3
R.m.s. deviations	
Bond lengths (Å)	0.0061
Bond angles (°)	1.4940

Values in parentheses are for highest-resolution shell.