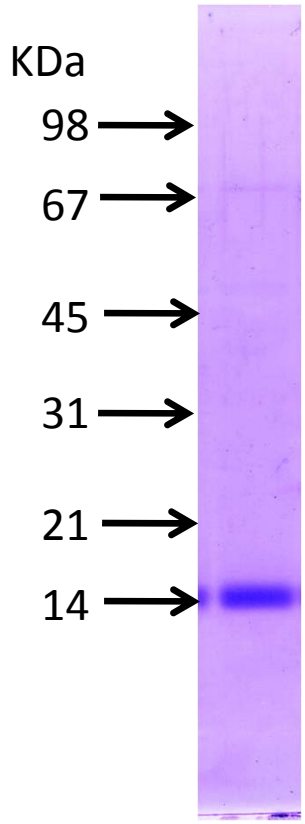
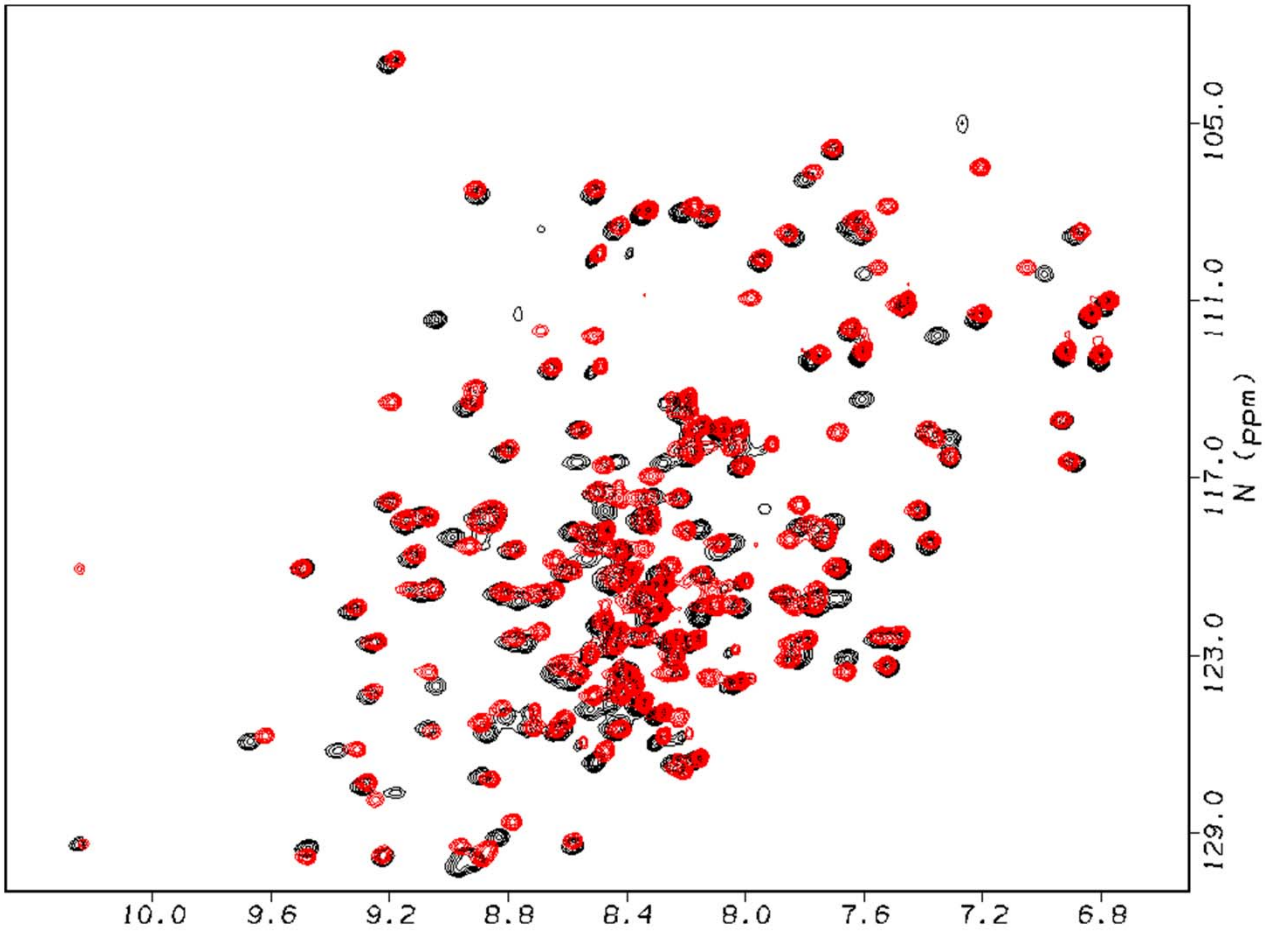
Supplementary Fig 1



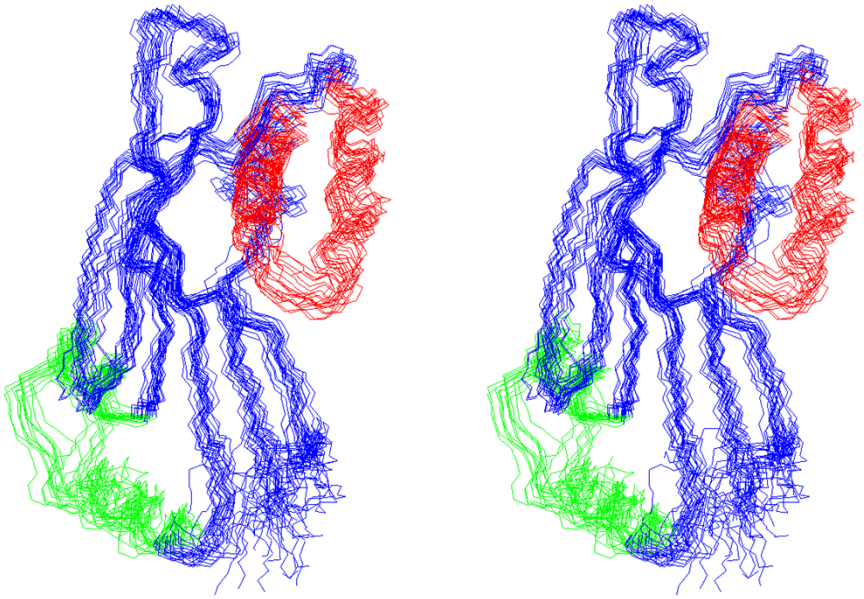
SDS-PAGE of the purified E1064-WND-Δ used for NMR structure determination.
Positions of the molecular weight markers and their mass in Kda are shown on the left.

Supplementary Fig 2



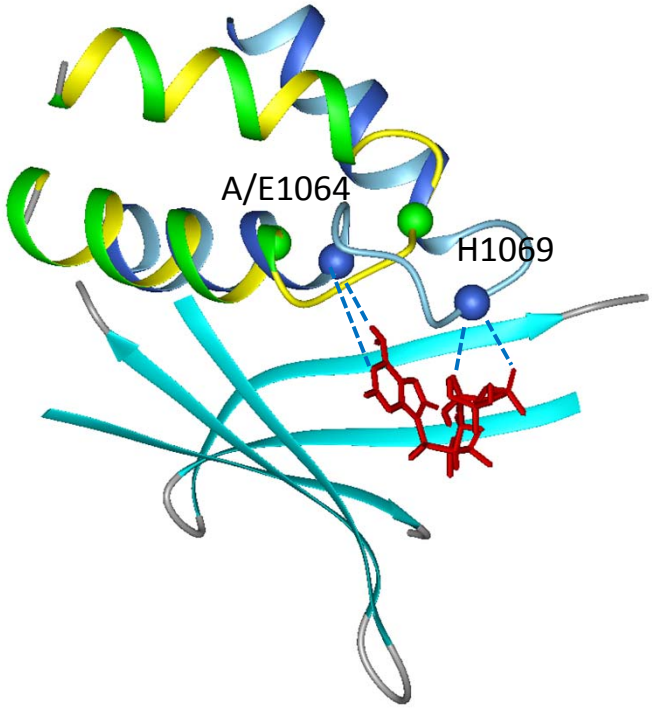
Overlay of the $^{1}H,^{15}N$-HSQC spectra of the wild type *(red)* and E1064A *(black)* N-domains

Supplementary Fig 3



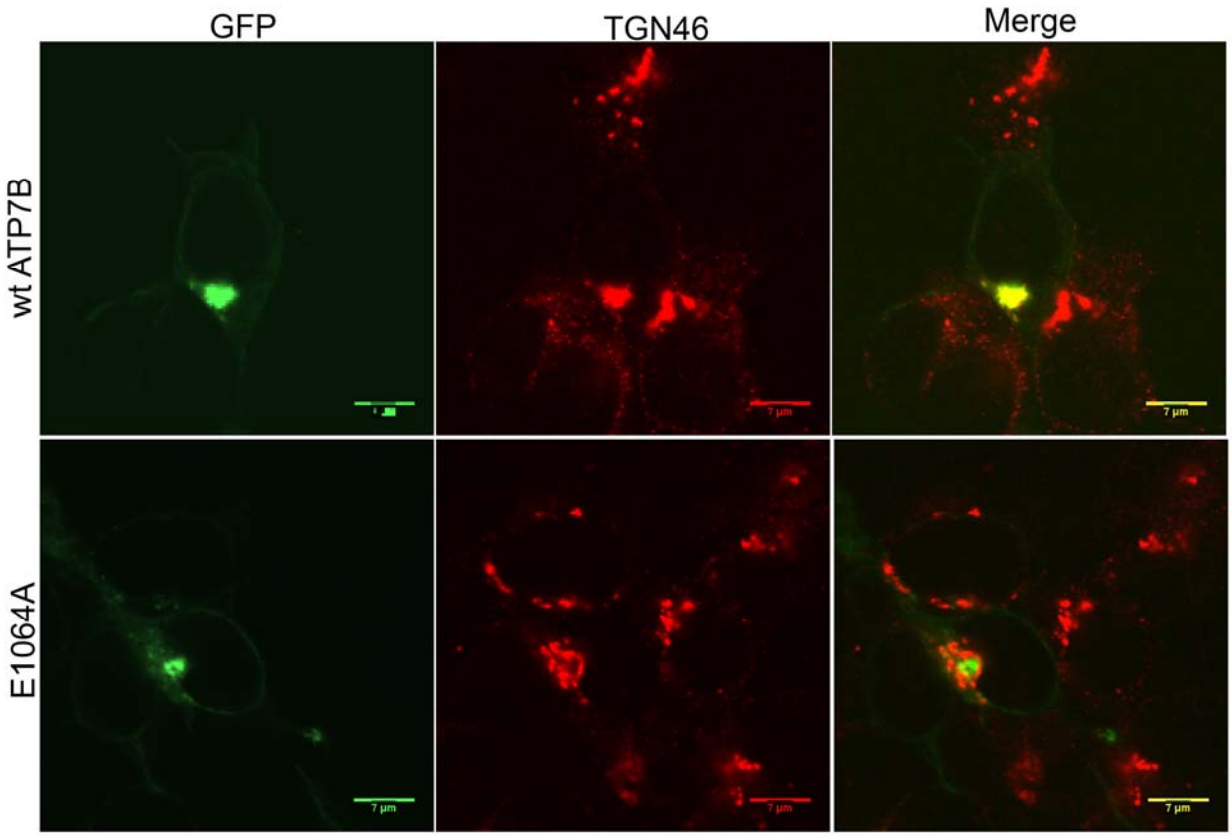
Stereoview of the ensemble of the 20 lowest energy structures of E1064A-WND-Δ. The α1-α2 helical hairpin (residues 1053-1083) is shown in *red*, the α3-α4 helical hairpin (residues 1151-1173) in *green*, and the core β-sheet and the connecting loops in *blue*.

Supplementary Fig 4



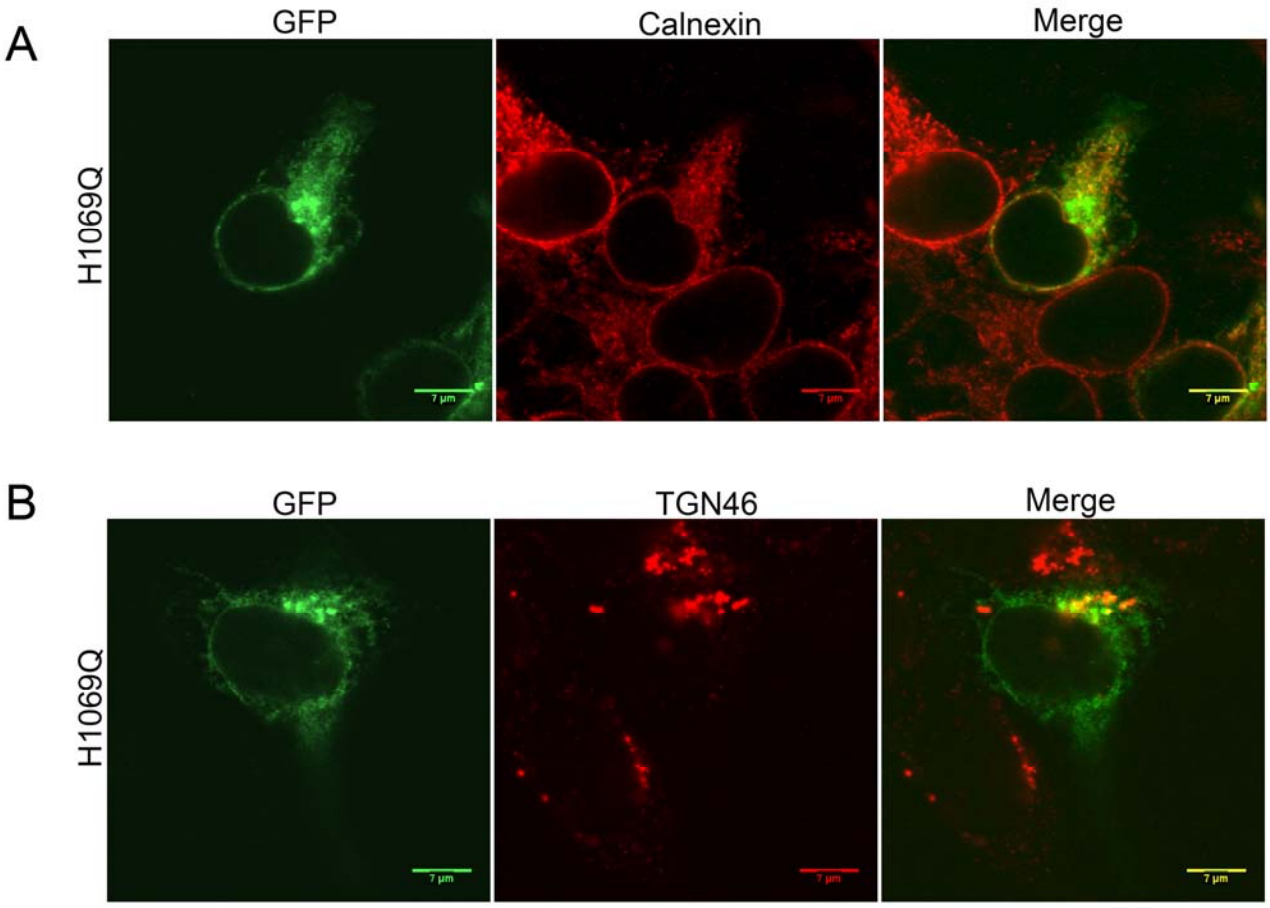
ATP molecule modeled into the structure of the wild type N-domain (2ARF, *blue*) based on the structure of the CopA ATP-binding domain with AMPPCP (3A1C). The position of the α1-α2 helical hairpin in the E1064-WND$\Delta_{1115–1138}$ when the core β-sheets in both structures are aligned to minimize r.m.s.d. is shown in *green*.

Supplementary Fig 5



Subcellular localization of E1064A mutant HEK293TRex cells were transfected with the plasmids expressing a GFP- tagged wt ATP7B (upper panel), or the E1064A mutant (lower panel). Following protein expression at 37^{o}C , cells were immunostained with the anti-TGN46 antibody (red) to visualize TGN and compare with the ATP7B pattern (green). In transfected cells both GFP-tagged wt and mutant were co-localized with the TGN marker (yellow). Scale bar is 7 µm

Supplementary Fig 6



Co-localization of H1069Q mutant with the organelle markers. HEK293TRex cells were transfected with the plasmid expressing the GFP tagged H1069Q mutant (green) and following protein expression at 37^{o}C cells were immunostained with the organelle markers (red) to determine the co-localization of H1069Q with the markers (yellow). (A) Immunostaining with the antibody against the ER marker calnexin. (B) Staining with the with anti-TGN46 antibody. Scale bar is 7 μm

Supplementary Table 1

STATISCTICS FOR STRUCTURE CALCULATION OF E1064A-WND	
Number of NOE-derived distance restraints	
Total	1379
Intra-residue	272
Sequential (|i-j| = 1)	533
Medium-range (1<|i-j| < 5)	228
Long-range (|i-j| > 4)	346
Hydrogen bond restraints	68
RMS violations per distance restraint (Å):	0.0194±0.0028
RMS violations per dihedral angle constraint (°):	0.43±0.11
Average number of violations per conformer:	
Distance restraints	5±2
Dihedral angle constraints	1±1
Van der Waals	1±1
Mean NOE violations larger than 0.25 Å	0
Maximum NOE violation (Å)	0.35
Average RMSD to the mean (Å)[a]	
backbone	1.35±0.23
all heavy atoms	1.77±0.21
residual CYANA Target Function ($Å^2$)[b]	2.38±0.48
Ramachandran plot quality[c]	
% of residues in most favorable regions	82.5
% of residues in allowed regions	17.1
% of residues in generously allowed regions	0.4
% of residues in disallowed regions	0.0
Close contacts	0
RMS deviations from ideal geometry	
Bond lengths (Å)	0.001
Bond angles (^{O})	0.2
MolProbity Clashscore[d]	-2.33

[a] RMSD values calculated for residues 7-140 corresponding to residues 1038-1114,1139-1195 in the full length ATP7B

[b] Structure calculations were performed with CYANA 2.1. A total of 1000 random conformers were subjected to 20000 steps of a simulated annealing process. Twenty lowest energy structures were selected for deposition.

[c] As reported by PROCHECK for residues 7-140

[d] As reported by PSVS for residues 7-140