Supporting Information

Allosteric Effects of ATP Binding on the Nucleotide-binding Domain of a Heterodimeric ATP-Binding Cassette Transporter

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Table S1. Hydrogen bond network at NBD1-NBD2 interface in the dATP/apo state.

acceptor	donor	distance (Å)	angle (°)	occupancy (%)
NBD1-Walker A-Glu367 (CD)	NBD2-D-loop-Thr524 (OG1-HG1)	3.42	157.05	85.30
NBD1-Walker A-Gly366 (O)	NBD2-D-loop-Asn521 (ND2-HD21)	2.93	157.28	72.07
NBD1-Walker A-Glu367 (OE1)	NBD2-D-loop-Thr524 (OG1-HG1)	2.93	154.54	71.13
NBD1-Walker A-Glu367 (OE2)	NBD2-D-loop-Thr524 (OG1-HG1)	2.94	152.99	68.77
NBD2-D-loop-Val522 (O)	NBD1-Walker A-Glu367 (CA-HA)	3.49	136.61	55.07
NBD1-Switch-Qln526 (CB)	NBD2-D-loop-Asn521 (CA-HA)	3.22	133.56	54.43
NBD1-D-loop-Asp501 (CB)	NBD2-Walker A-Thr390 (N-H)	3.20	148.34	53.97
NBD1-Switch-Qln526 (O)	NBD2-D-loop-Asn521 (CA-HA)	3.51	149.29	51.50

Table S2. Hydrogen bond network at NBD1-NBD2 interface in the apo/apo state.

acceptor	donor	distance (Å)	angle (°)	occupancy (%)
NBD2-D-loop-Val522 (O)	NBD1-Walker A-Thr368 (N-H)	2.96	154.87	95.03
NBD2-D-loop-Asn521 (OD1)	NBD1-Switch-Qln526 (NE2-HE22)	2.99	159.71	89.60
NBD2-D-loop-Asp523 (CA)	NBD1-Walker A-Glu367 (CB-HB2)	3.39	156.66	83.73
NBD2-D-loop-Asn521 (O)	NBD1-Switch-Qln526 (CG-HG2)	3.10	149.19	79.87

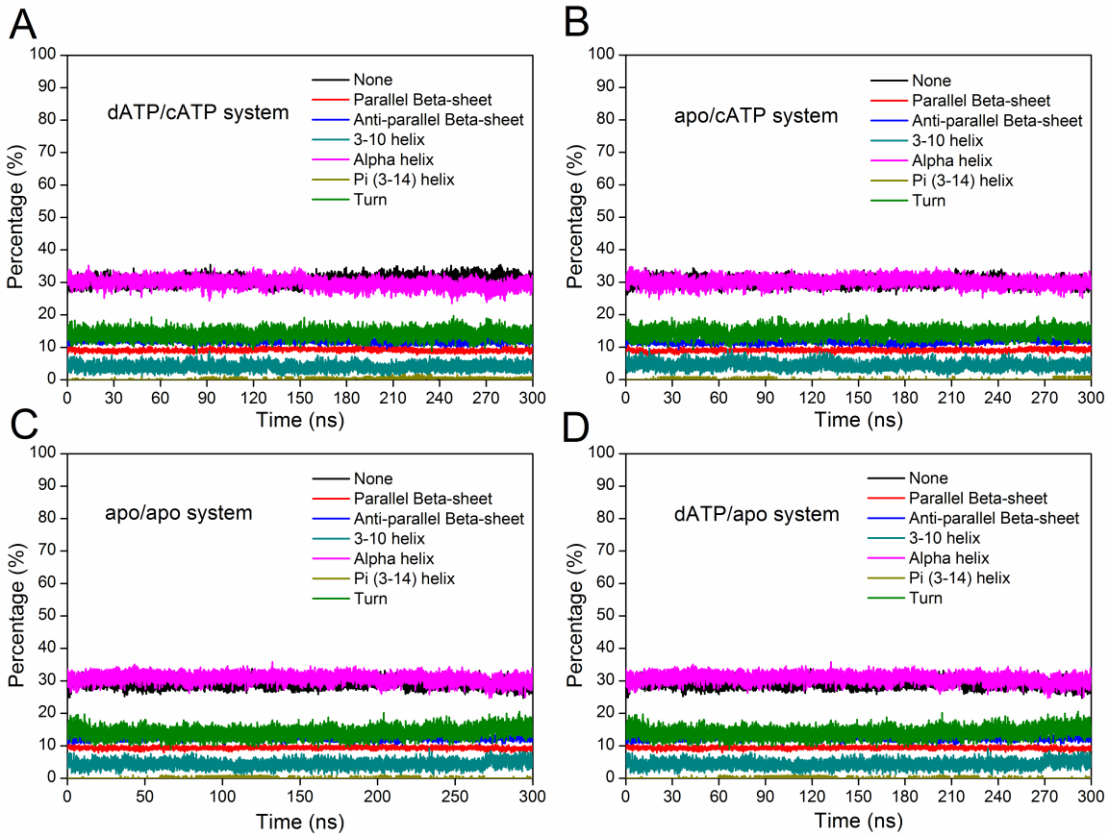

Fig. S1. Secondary structure components of the NBDs over time.

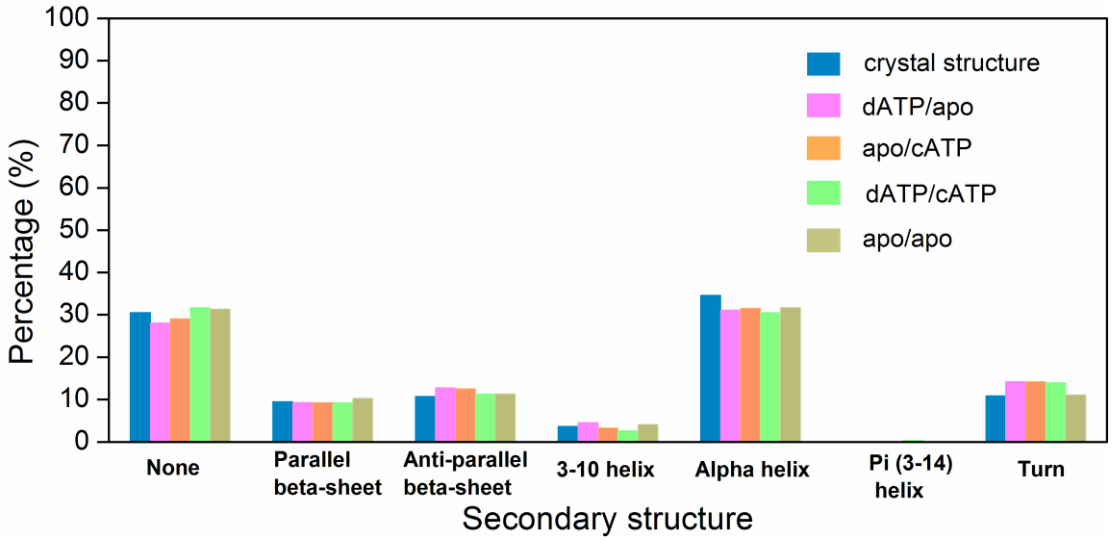

Fig. S2. Secondary structural components of the X-ray (PDB: 3QF4) and average structures obtained over all 3 replicas of each system.

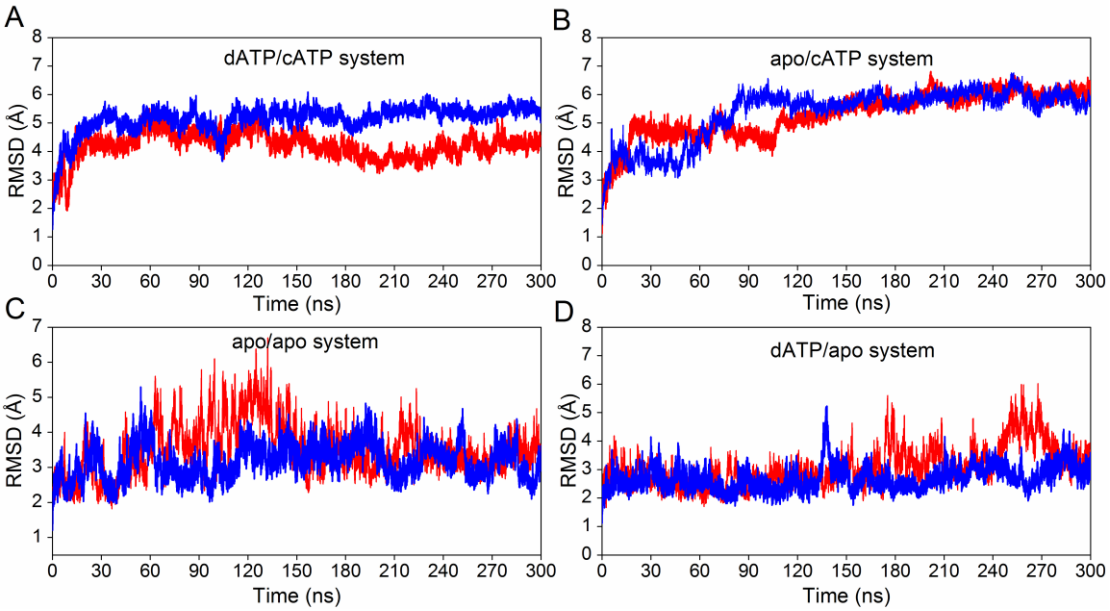

Fig. S3. Time evolution of root-mean-square deviation (RMSD) of protein Cα for the other two MD simulations of each system.

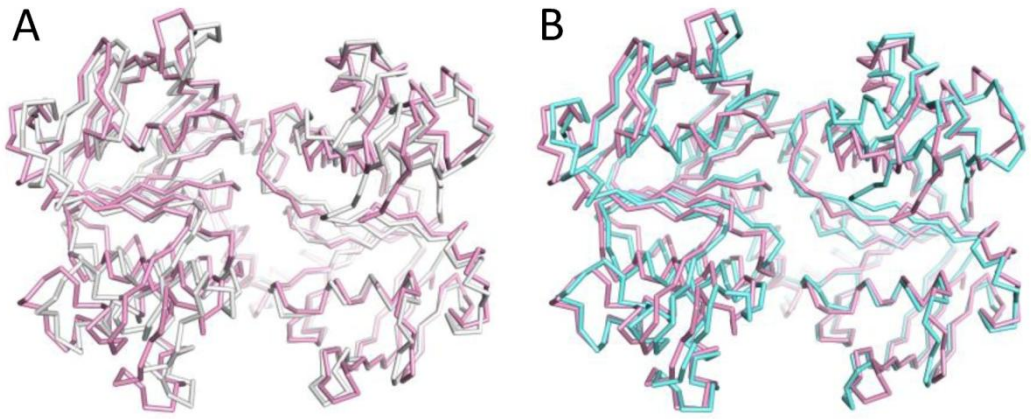

Fig. S4. Structural alignments of the average structure of dATP/apo system (pink) with (A) the crystal structure (3QF4, white), and (B) the average structure of apo/apo system (cyan). The average structures are calculated from the last 60 ns trajectory of each system. All structures are shown as ribbons.

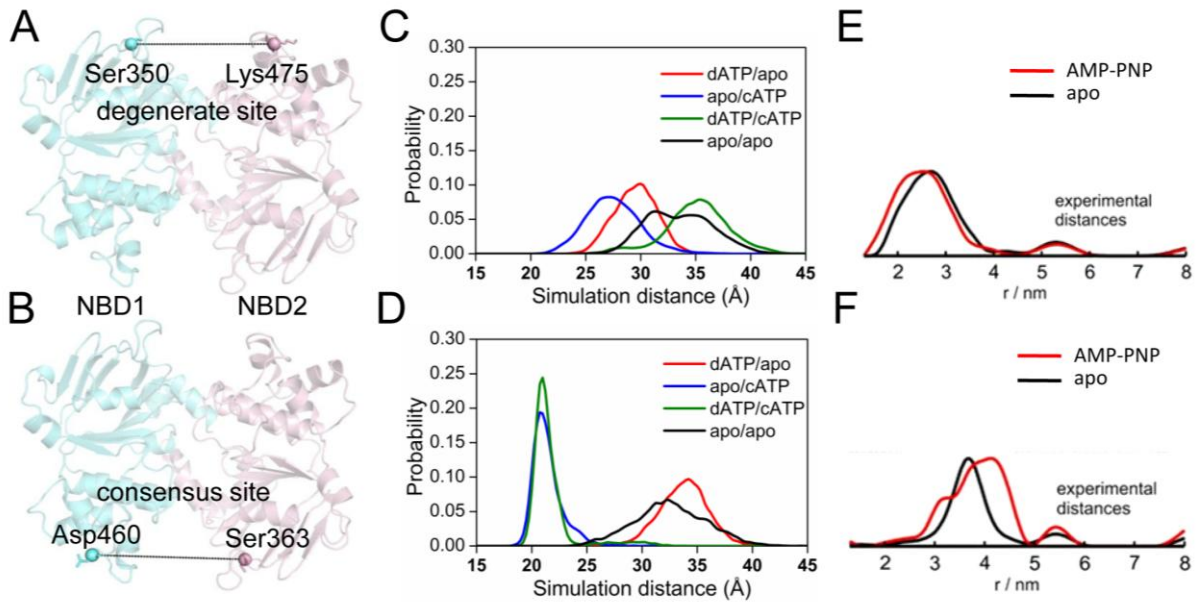

Fig. S5. Structural differences of the ATPase sites in different ATP-bound states. (A and B) Schematic representations of two distances used in DEER measurements. (C and D) Distance distributions between Cα atoms for spin-label pairs obtained all 3 replicas of each system. (E and F) Distance distributions of structurally equivalent pairs obtained by DEER measurements (Hohl et al., *Proc. Natl. Acad. Sci. U. S. A.*, 2014).

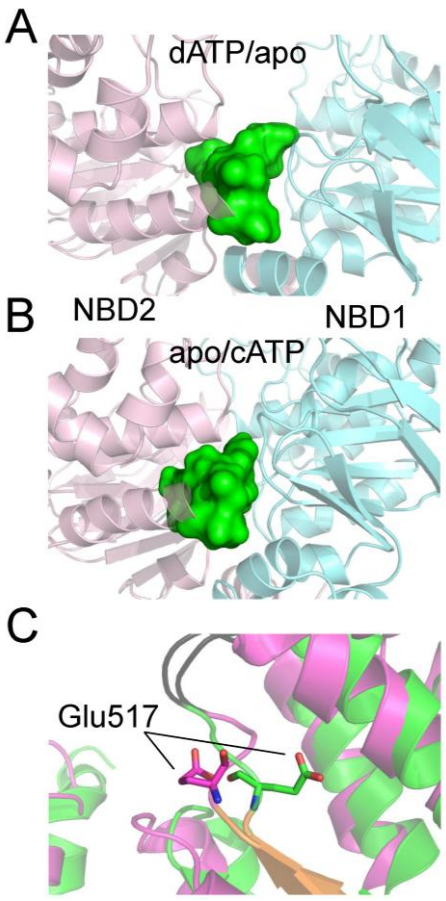

Fig. S6. Flexibility of the noncanonical D-loop in the degenerate site. (A-B) Surface representation of the D-loop (green) of NBD2 (shown as cartoons) in dATP/apo state and apo/cATP state. NBD1 and NBD2 are colored in cyan and pink, respectively. (C) Closeup of the conformational transition of the catalytical residue Glu517 (shown as sticks) and the following region in the apo/cATP (purple) and the dATP/apo states (green). The D-loop and the Walker B motif of NBD2 are highlighted in black and orange, respectively. All the average structures are aligned by the D-loop and Walker B motif.

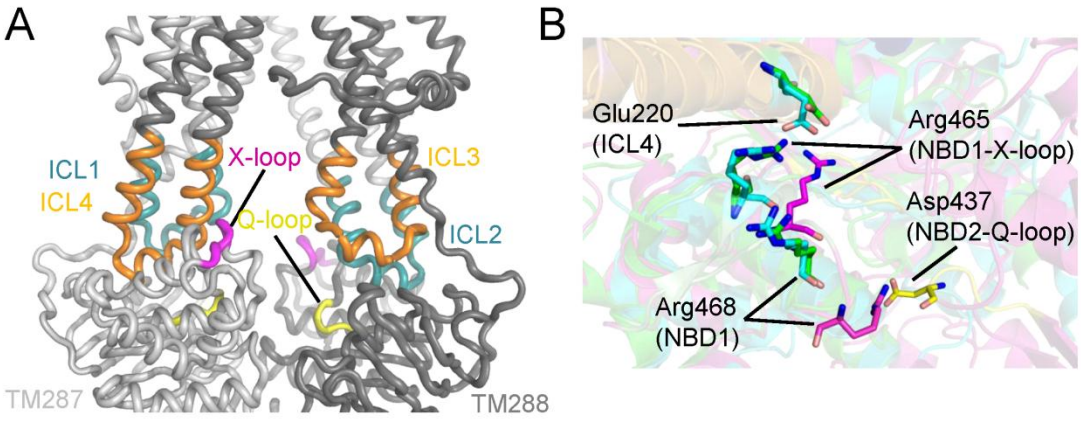

Fig. S7. Potential molecular communication in the NBD-TMD interface of AMP-PNP–bound TM287/288. (A) Overview of the transmission interface between NBDs and TMDs. The intracellular loops (ICL1−4) in TMDs, Q- and X-loops in NBDs are highlighted by different colors. TM287 is colored light gray and TM288 dark gray. (B) The potential signal pathway between NBDs and TMDs in the apo/cATP state. The apo (cyan) and AMP-PNP–bound (green) structures of full-length TM287/288 (shown as transparent cartoons) show the interaction between Glu220 of ICL4 and Arg465 of X-loop in NBD1. The last snapshot of apo/cATP simulation (shown as cartoons, purple) shows the interaction between Arg468 adjacent to the X-loop and Asp437 of the Q-loop in NBD2. All residues are shown as sticks.