# SUPPLEMENTARY DATA

## Supplementary Text and References

Based on the model-structure and conservation, we provide molecular-level interpretation of additional clinical mutants for which experimental data is available.

*H1069Q*. The most frequent mutation in Caucasian and African American population. The mutation was shown to decrease protein stability[1, 2] and cause mislocalization in mammalian cells[2, 3]. Biochemical studies determined that H1069Q substitution decreases affinity for ATP[4, 5] and markedly diminishes catalytic phosphorylation[6]. However, the transport activity is not lost entirely, since this mutant can complement yeast strain lacking endogenous copper ATPase[7]. The previous study showed that the effect of mutation on folding is likely due to inherent instability of the nucleotide-binding domain of ATP7B in the absence of ATP[8], and the positioning of His1069 in the N-domain was resolved in an NMR study of the isolated domain [5]. In our analysis, His1069 is indeed highly conserved, and situated in the functional patch detected by PatchFinder. The model-structure provides the context of this position relative the rest of the structure, situating His1069 in the interface of the N-domain with the P-domain (Fig. S8A, Table S1). As part of the functional site, His1069 could thus be critical for interaction with ATP, with the N-terminal domains or with other proteins.

*D765N*. Asp765 is highly conserved, located in the model at the extracellular end of TM4. Equivalent to LCopA Glu189, Asp765 probably is important for the copper exit site as well, as suggested by Gourdon et al. for LCopA[9]. This ascribes Asp765 a role in the copper transport mechanism, and suggests that the negative charge can only be partly compensated by

the Asn polar side-chain (Fig. 5D, Table S1). The study of Huster et al. supported this role, revealing partial transport activity of the D765N mutant as well as decreased expression[10].

*G710S and G712D of the mouse ATP7B, matching human Gly711*. The G710S mutant was recently characterized, exhibiting complete loss of activity in copper uptake[10]. The mouse equivalent to Gly711, Gly712, was also examined upon mutation to Asp. The mutation is associated with copper accumulation in the liver and liver disease as well as slight increase of copper in the brain[11]. Our analysis suggested a deleterious effect to a substitution in Gly711, since it is highly conserved, while we could not determine the sensitivity to mutation of mediocrely conserved Gly710 based on accessibility and conservation alone. Further examining the structural location of these positions, we observed that the model places Gly710 and Gly711 in the kinked region in TM2, strongly suggests a role in conformational changes during transport cycle (Fig. S8B, Table S1).

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## SUPPLEMENTARY FIGURES

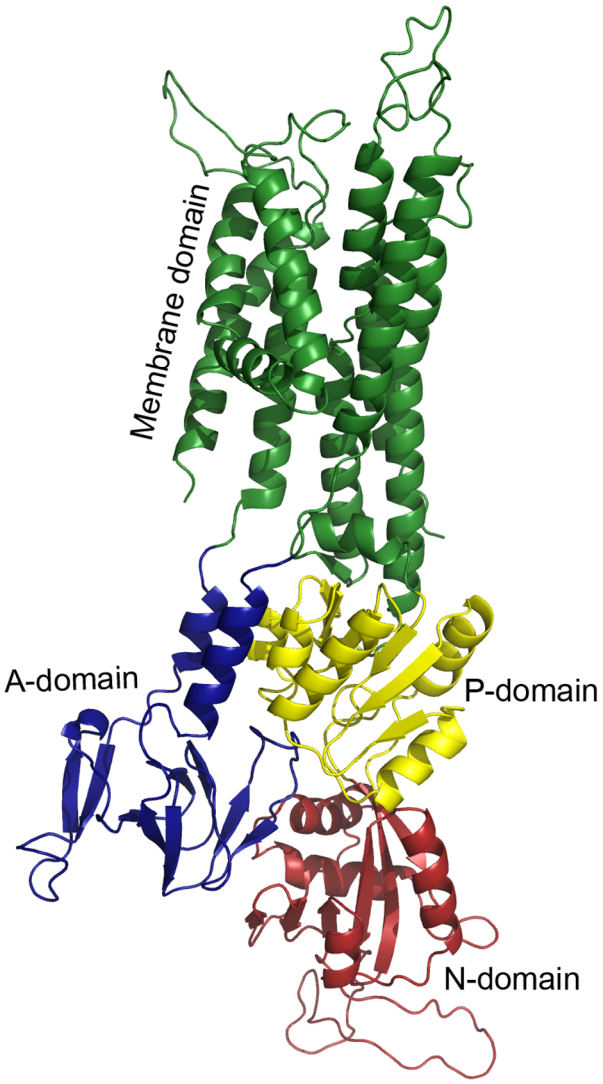


**Figure S1. Overall architecture of the ATP7B model-structure.** The ATP7B model, consisting of positions 643-1377 of the 1465 amino acid sequence, is shown as cartoon and viewed from the side, with the cytoplasm below. The membrane helices, and the A-, N- and P-domains are colored green, blue, red and yellow, respectively.

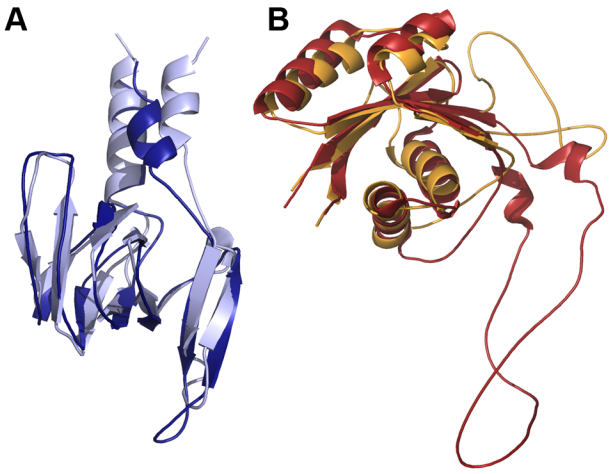


**Figure S2. Comparison to NMR data. A.** The NMR structure of the A-domain from ATP7A (PDB ID 2KIJ, light blue) was aligned to the corresponding domain from the ATP7B model (dark blue) using PyMol (http://www.pymol.org/) **B.** The NMR structure of the unbound form of the N-domain, solved for ATP7A (PDB ID 2KMV, orange) aligned to the N-domain in the ATP7B model (red). Excluding the flexible loop regions, it is apparent that both NMR structures show excellent agreement with the domains conformation from the model of the entire core structure.

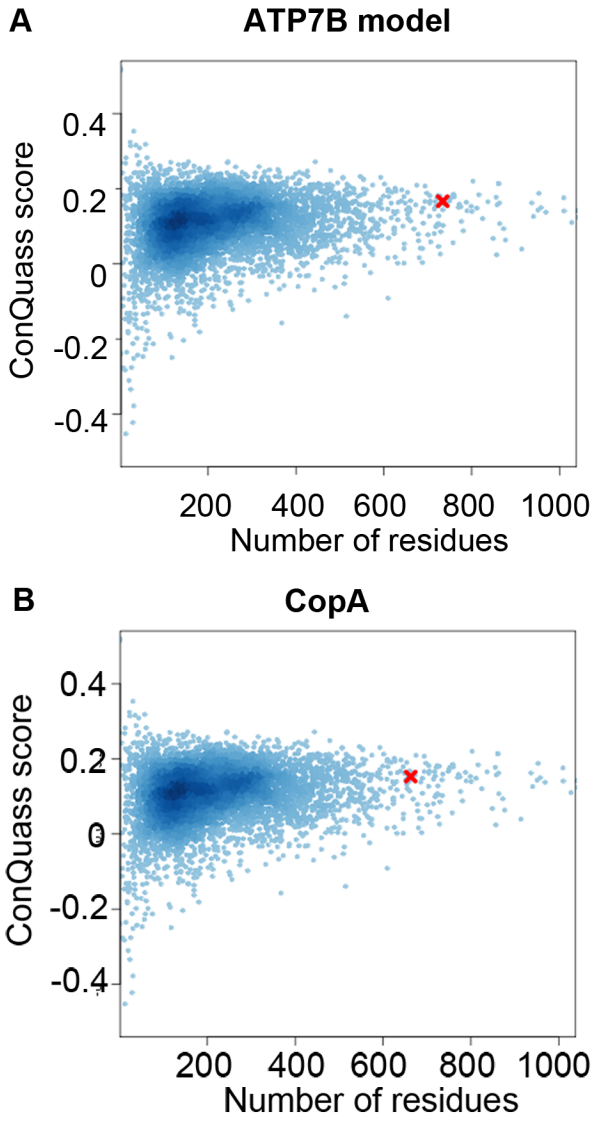


**Figure S3. ConQuass scores [12] of the ATP7B model and LCopA structure.** In both panels, the ConQuass scores of all the structures in the Protein Data Bank (PDB) are shown as blue dots, and displayed as a function of the number of residues in the structures. The ConQuass scores of the ATP7B model (panel A) and LCopA structure [9] (panel B) are marked in red. It is evident that both receive high probability scores, with that of ATP7B model slightly exceeding that of the LCopA crystal structure.

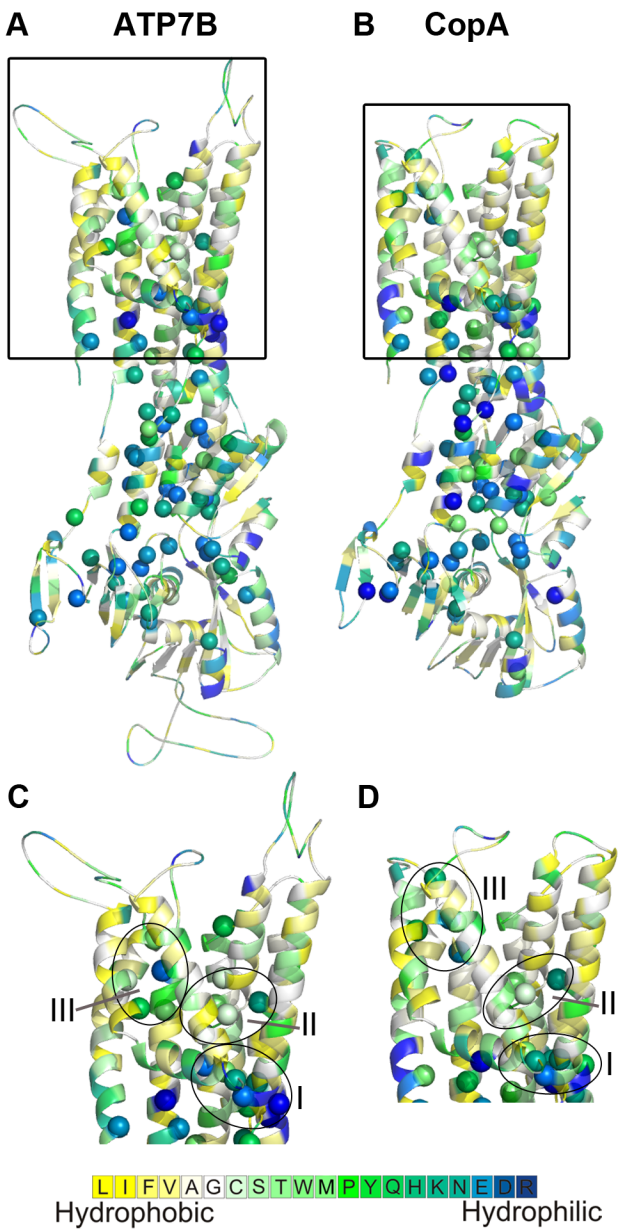


**Figure S4. Hydrophobicity analysis of ATP7B and LCopA- three highly conserved and hydrophilic sites in the membrane domain.** In panels **A** and **B,** the ATP7B model and LCopA structure are displayed in cartoon representation, and displayed from the side with the cytoplasm below. Cα atoms of highly hydrophilic positions, as well as of potential $Cu^{+}$ binding Met and Cys, which are also highly conserved (with ConSurf grades of 7-9), are shown as spheres. Panels **C** (ATP7B) and **D** (LCopA) show a zoom-in of the membrane domains, emphasized in squares in the matching panels **A** and **B**. The three membrane regions containing highly conserved polar residues are marked with squares and numbered. Roman letters I, II and III correspond to the potential entry, membrane site and exit, respectively.

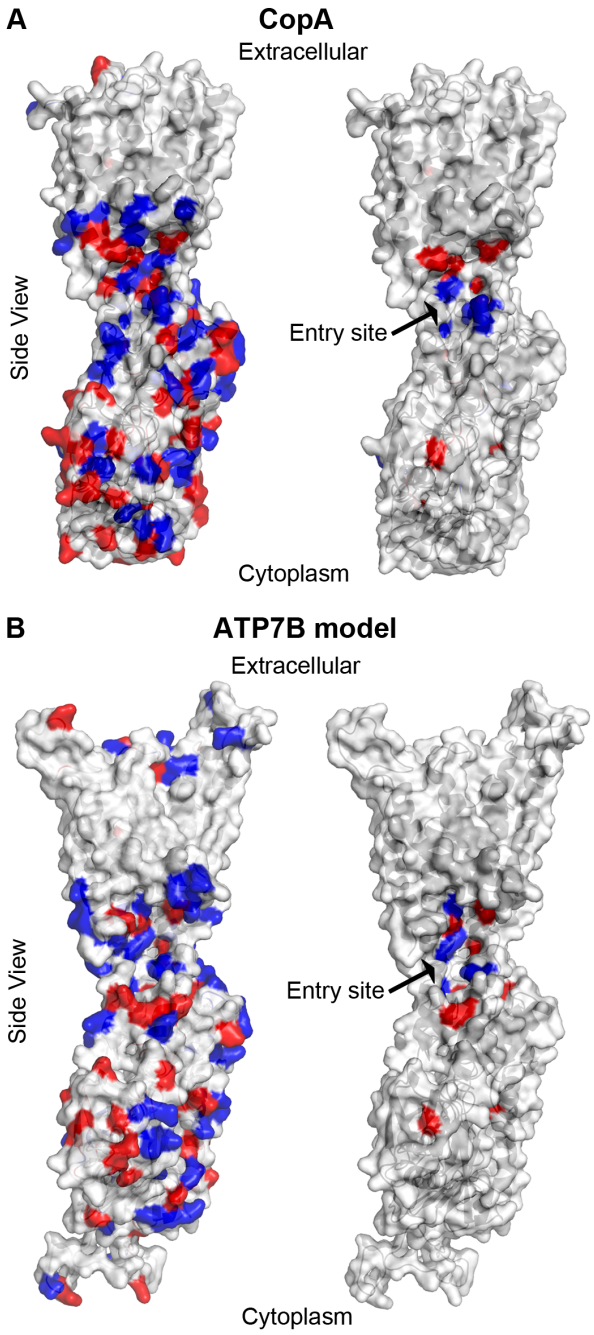


**Figure S5. Mapping of charged residues on the LCopA structure and ATP7B model.** Side view of the LCop structure (**A**) and ATP7B model (**B**), colored white and shown in partly transparent surface representation. On the structures shown on left hand side, all the negatively and positively charged residues are colored red and blue, respectively. On the right hand side, only charged residues that are highly conserved (ConSurf grades of 8 and 9) are colored. It is apparent that most of the charged residues are not highly conserved, and are mapped to the cytoplasmic domains. A single cluster of highly conserved residues is evident in both structures, which is mapped to the copper membrane entry site (marked).

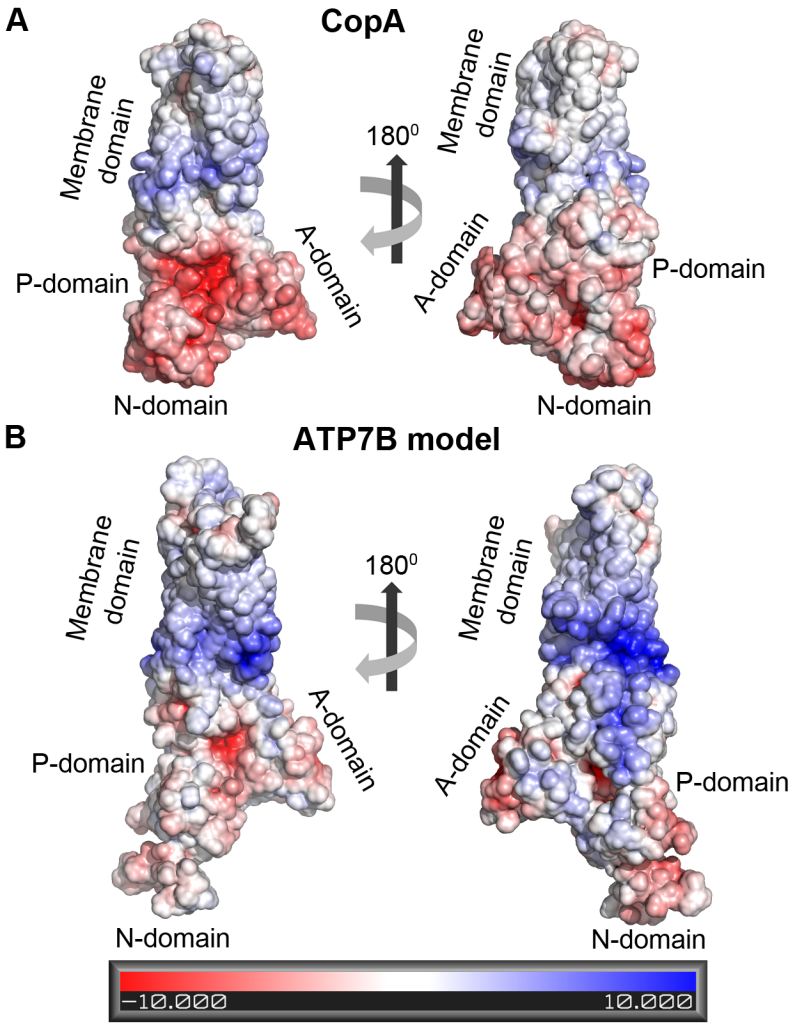


**Figure S6. Mapping of electrostatic potential on the surface LCopA structure and ATP7B model.** Two-side view of the LCop structure (A) and ATP7B model (B) with the cytoplasm below. The structures are shown in surface representation and colored by electrostatic potential according to the legend below, as computed by solving the non-linearized version of the Adaptive Poisson Boltzman Solver (APBS) software (reference below). It is apparent that both structures contain a negatively charged patch at the interface between the soluble domains (left hand side), which is more emphasized at the LcopA structure. The ATP7B model, on the other hand, shows a more prominent positively charged region, situated around the presumed membrane boundaries at the cytoplasmic side.

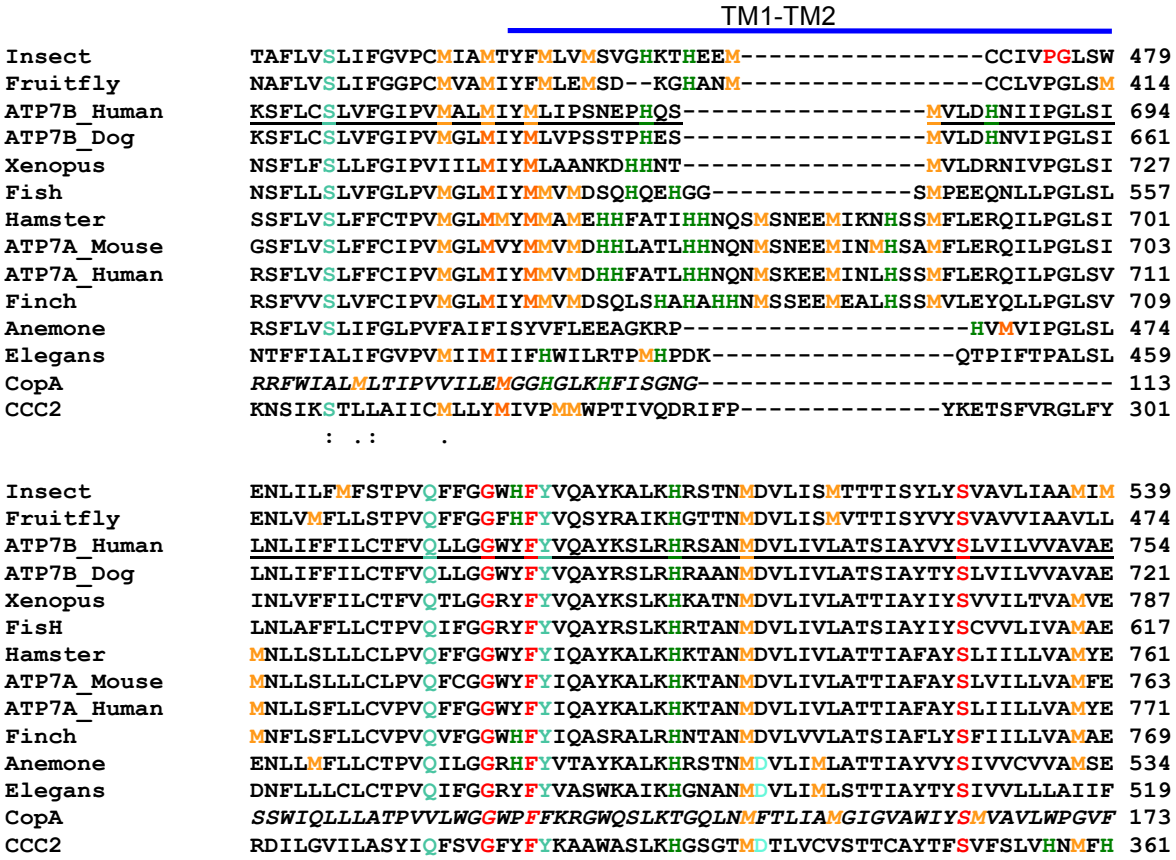


**Figure S7. Sequence alignment of eukaryotic Cu-ATPases in the region of TM1-TM2 transmembrane segment.** Sequences were aligned using ClustalW [13]. Conserved positions and copper preferred ligators His, Met and Cys, are highlighted in colors. The TM1-TM2 loop is marked by a blue line. ATP7B sequence is underlined; and bacterial sequence (CopA) is in italic. It is apparent that TM1,2 loop is longer in eukaryotic pumps and that the entire TM1,2 region is more hydrophilic and enriched in Met and His residues

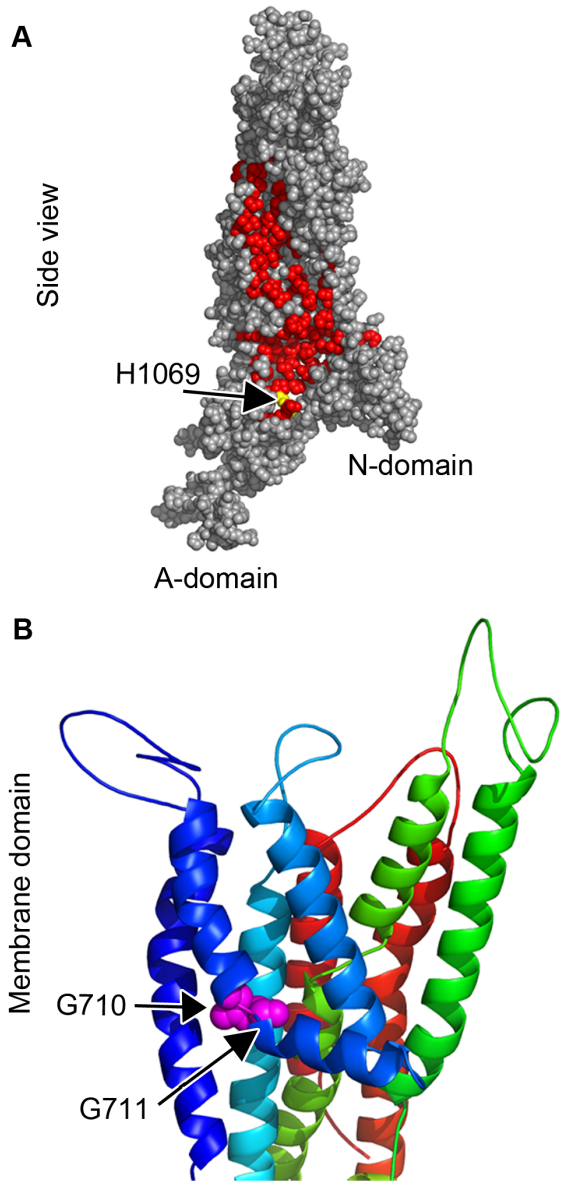


**Figure S8. Structural interpretation of His1069, Gly710 and Gly711.** Side view of the ATP7B model with the cytoplasm below**. A.** The model is shown as gray spheres with the PatchFinder functional site in red. His1069, colored yellow and marked, is situated on the A-domain, interfacing the N-domain, and is part of the predicted functional site. **B.** Zoom into the membrane domain, with model colored by rainbow. Gly710 and Gly711 (magenta) are situated at the kinked segment of TM2, thus can contribute to the flexibility and conformation of the helix.

**Table S1. Clinical mutations evaluated experimentally.** The columns show the position, clinical substitutions [14], ConSurf conservation grade ([15], with 1-9 indicating variable-to-conserved), relative solvent accessibility inclusion in the PatchFinder functional site and experimental results, from left to right. In addition, the suggested sensitivity was ascribed using an approach based on conservation and accessibility. Positions proposed as sensitive if conserved (grades 8 or 9) and buried (SASA <10%), or part of the functional PatchFinder site. On the other hand, variable (grades 1-2) and exposed (SASA >10%) positions were suggested as not sensitive to mutation. For all other positions, not falling under these distinct categories, the sensitivity of the position was not suggested. Green shade marks suggestions that agreed with the experimental result, red marks the suggestion that contradicted the experiments, whereas yellow mark positions for which we could not suggest the position's sensitivity. We excluded from this analysis positions such as Lys832, for which the experimental effect of mutation was only partial (<50% decreased activity), as such experiments cannot clearly indicate whether the positions in question are indeed sensitive or non-sensitive to substitutions.

| Position | Mut. | Con. | SASA (%) | Patch-Finder | Location | Exp. effect | Suggested sensitivity | Ref. |
|---|---|---|---|---|---|---|---|---|
| M645 | R | 1 | 98.4 | NO | TM1 | Normal copper transport | Not sensitive | 10 |
| G710 | R, S, A, V | 5 | 0 | NO | TM2 | Low copper transport | - | 10 |
| G711 | R, W, E | 9 | 7.8 | NO | TM2 | Copper accumulation in the liver, liver disease, slight increase in the brain | Sensitive | 11 |
| P760 | L | 4 | 5.2 | NO | Loop 3-4 | Low copper transport | - | 10 |
| D765 | N, G | 8 | 3.9 | NO | TM4 | Low transport activity, decreased expression | Sensitive | 10 |
| R778 | G, W, Q, L | 8 | 17.8 | NO | TM4 | Lower stability and abnromal localization | - | 1, 2 |
| P840 | L | 9 | 8.3 | NO | A-domain | Very low copper transport | Sensitive | 10 |
| I857 | T | 7 | 17.6 | NO | A-domain | Decreased transport but does not significantly inhibit catalytic dephopshorylation. | - | 10 |
| A874 | V | 8 | 11.5 | NO | A-domain | Misfolded and mistargeted (located in the ER), no activity | - | 10 and current study |
| G875 | R | 8 | 17.2 | NO | A-domain | Destabilizes the A-domain, decreases affinity for ATP, | - | 16 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | normal transport and trafficking | | |
| I929 | V | 6 | 58.2 | NO | TM5 | Full complementation in yeast | - | [17] |
| G943 | S, C, D | 6 | 18.2 | NO | TM5 | Affects folding | - | [1, 4, 18] |
| P992 | L, H | 9 | 8.3 | NO | TM6 | Inactivation in yeast complementation assay, affects folding, Very low copper transport | Sensitive | [1, 4, 18, 10] |
| V995 | A | 9 | 15.9 | NO | TM6 | Normal variant (based on studies in yeast) | - | [18] |
| D1027 | A | 9 | 6.3 | YES | P-domain | No copper transport | Sensitive | [10] |
| T1031 | S, A | 9 | 6 | NO | P-domain | Significantly decreased but measurable transport activity | Sensitive | [10] |
| R1041 | W, P | 6 | 67.5 | NO | N-domain | Full complementation in yeast | - | [19] |
| P1052 | L | 2 | 59.1 | NO | P-domain | Very low copper uptake | Not sensitive | [10] |
| E1064 | K, A | 9 | 10.1 | YES | N-domain | Inactivation in yeast complementation assay, No copper transport | Sensitive | [4, 8, 10, 19] |
| H1069 | Q | 9 | 30.2 | YES | N-domain | Decrease protein stability and cause mislocalization in mammalian cells. Decreases affinity for ATP and markedly diminished catalytic phosphorylation, Low copper transport | Sensitive | [1-6, 10] |
| C1104 | F, Y | 6 | 5.9 | NO | N-domain | Affects folding | - | [1, 4, 18] |
| V1106 | I, D | 6 | 3.3 | NO | N-domain | Inactivation in yeast complementation assay | - | [19] |
| A1140 | V | 1 | 35.7 | NO | N-domain | Full complementation in yeast | Not sensitive | [19] |
| R1151 | C, H | 2 | 74.3 | NO | N-domain | Small effect on folding of the N-domain | Not sensitive | [4] |
| A1183 | T, G | 7 | 0 | NO | N-domain | Full complementation in yeast | - | [19] |
| G1186 | S, C | 2 | 75.7 | NO | N-domain | Full complementation in yeast | Not sensitive | [19] |

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|---|---|---|---|---|---|---|---|---|
| G1213 | V | 8 | 93.3 | NO | P-domain | Complete loss of transport | - | [10] |
| D1222 | N,Y,V | 9 | 35.4 | YES | P-domain | D1222V- Very low copper transport | Sensitive | [10] |
| V1262 | F | 9 | 1.1 | NO | P-domain | Affects folding | Sensitive | [1, 4, 18] |
| G1266 | R,K,V | 9 | 0 | NO | P-domain | G1266R- Very low copper uptake | Sensitive | [10] |
| N1270 | T, S | 9 | 1.9 | YES | P-domain | Inactivation in yeast complementation, Low copper uptake | Sensitive | [7, 10] |
| P1273 | S,L,Q | 9 | 0 | NO | TM8 | Very low copper uptake | Sensitive | [10] |
| M1359 | I | 9 | 16.5 | YES | TM8 | Copper accumulation and liver disease in mice, lacked a measurable transport activity in copper uptake assay | Sensitive | [20, 21] |
| S1363 | F | 9 | 29.4 | YES | TM8 | Affects folding | Sensitive | [1, 4, 18] |

**Table S2. Suggested sensitivity to mutation.** The 197 positions in which clinical mutations were detected[14] ENREF 14 and are included in the ATP7B model-structure. The detected substitution, ConSurf evolutionary conservation (grades 1-9 for variable-to-conserved) and relative surface accessibility are shown under Mut., Con., and SASA, respectively. The PatchFinder column indicates whether the position was detected as a part of the functional site derived from this analysis. Last, the suggested sensitivity is based on the criteria described in the main text and in Table S1, incorporating conservation and accessibility to suggest the outcome of mutation only for positions for concurring with our criteria.

| Position | Mut. | Con. | SASA (%) | PatchFinder | Suggested sensitivity |
|---|---|---|---|---|---|
| L1043 | P | 1 | 9.8 | NO | - |
| G1089 | E,V | 1 | 19.2 | NO | Not sensitive |
| A1168 | S,P | 1 | 22.8 | NO | Not sensitive |
| A1140 | V | 1 | 35.7 | NO | Not sensitive |
| G1111 | D | 1 | 62.6 | NO | Not sensitive |
| N676 | I | 1 | 65.1 | NO | Not sensitive |
| R1228 | T | 1 | 68.2 | NO | Not sensitive |
| H1207 | R | 1 | 72.5 | NO | Not sensitive |
| Q1142 | H | 1 | 79.6 | NO | Not sensitive |
| K952 | R | 1 | 87.2 | NO | Not sensitive |
| M645 | R | 1 | 98.4 | NO | Not sensitive |
| V949 | G | 1 | 107 | NO | Not sensitive |
| D1047 | V | 1 | 119.9 | NO | Not sensitive |
| I1184 | T | 2 | 6.7 | NO | - |
| T1143 | N | 2 | 34 | NO | Not sensitive |
| A756 | G,V | 2 | 45.7 | NO | Not sensitive |
| L1305 | P | 2 | 46.7 | NO | Not sensitive |
| R1156 | H | 2 | 48.8 | NO | Not sensitive |
| T933 | P | 2 | 57.2 | NO | Not sensitive |
| P1052 | L | 2 | 59.1 | NO | Not sensitive |
| R919 | G,W | 2 | 60.1 | NO | Not sensitive |
| A1065 | P | 2 | 63.3 | NO | Not sensitive |
| D1164 | N | 2 | 67.7 | NO | Not sensitive |
| R1038 | K | 2 | 69.1 | NO | Not sensitive |
| Q1095 | P | 2 | 69.9 | NO | Not sensitive |
| R1151 | C,H | 2 | 74.3 | NO | Not sensitive |
| R758 | M | 2 | 75.2 | NO | Not sensitive |
| D1215 | Y | 2 | 75.7 | NO | Not sensitive |
| G1186 | S,C | 2 | 75.7 | NO | Not sensitive |
| C1375 | S | 2 | 80.4 | NO | Not sensitive |
| T1232 | P | 2 | 85.3 | NO | Not sensitive |

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|---|---|---|---|---|---|
| Q1200 | P | 2 | 106.7 | NO | Not sensitive |
| K832 | R | 3 | 39.5 | NO | - |
| C1091 | Y | 3 | 74.3 | NO | - |
| P690 | L | 3 | 85.9 | NO | - |
| P760 | L | 4 | 5.2 | NO | - |
| M1169 | V,T | 4 | 14.9 | NO | - |
| R969 | W,Q | 4 | 25 | NO | - |
| I967 | F | 4 | 36.8 | NO | - |
| V1109 | M | 4 | 38.1 | NO | - |
| L708 | P | 4 | 55.3 | NO | - |
| P1098 | R | 4 | 55.8 | NO | - |
| V1036 | I | 4 | 68.2 | NO | - |
| L1368 | P | 4 | 70.1 | NO | - |
| V1334 | D | 4 | 74.5 | NO | - |
| R827 | P | 4 | 85.2 | NO | - |
| G710 | R,S,A,V | 5 | 0 | NO | - |
| I747 | F | 5 | 0.7 | NO | - |
| V1146 | M | 5 | 3.1 | NO | - |
| Y713 | C | 5 | 42.1 | NO | - |
| M665 | I | 5 | 60.4 | NO | - |
| S693 | P,C,Y | 5 | 63.7 | NO | - |
| L1083 | F | 5 | 78.9 | NO | - |
| T974 | M | 6 | 2.7 | NO | - |
| I1148 | T | 6 | 2.9 | NO | - |
| V1106 | I,D | 6 | 3.3 | NO | - |
| W1153 | R,C | 6 | 5.4 | NO | - |
| C1104 | F,Y | 6 | 5.9 | NO | - |
| S653 | Y | 6 | 8 | NO | - |
| Y741 | C | 6 | 10.8 | NO | - |
| A1063 | V | 6 | 13.9 | NO | - |
| G943 | S,C,D | 6 | 18.2 | NO | - |
| S975 | Y | 6 | 21.3 | NO | - |
| G691 | R | 6 | 38 | NO | - |
| I929 | V | 6 | 58.2 | NO | - |
| R1041 | W,P | 6 | 67.5 | NO | - |
| Q1004 | P | 6 | 80.6 | NO | - |
| A1183 | T,G | 7 | 0 | NO | - |
| C703 | Y | 7 | 0 | NO | - |
| M1025 | R | 7 | 0.1 | NO | - |
| V1252 | I | 7 | 0.7 | NO | - |
| S721 | P | 7 | 2.2 | NO | - |

| | | | | | |
|---|---|---|---|---|---|
| A1193 | P | 7 | 2.4 | NO | - |
| P768 | H,L | 7 | 2.5 | NO | - |
| V1024 | A | 7 | 4.4 | NO | - |
| V1297 | I,D | 7 | 4.9 | NO | - |
| A1018 | V | 7 | 5.8 | NO | - |
| I1102 | T | 7 | 10.7 | NO | - |
| I857 | T | 7 | 17.6 | NO | - |
| Y715 | H | 7 | 20.3 | NO | - |
| L1255 | I | 7 | 23.2 | NO | - |
| M769 | V,R,I,L | 7 | 29.4 | NO | - |
| L776 | P,V | 7 | 31.5 | NO | - |
| T888 | P | 7 | 34.4 | NO | - |
| E1173 | K,G | 7 | 43.3 | NO | - |
| R1322 | P | 7 | 53 | NO | - |
| W1353 | R | 7 | 79.3 | NO | - |
| G869 | V,R | 7 | 134.4 | NO | - |
| G1341 | S,R,D,V | 8 | 0 | NO | Sensitive |
| G1061 | E | 8 | 0.4 | NO | Sensitive |
| A971 | V | 8 | 1.1 | NO | Sensitive |
| F763 | Y | 8 | 3.5 | NO | Sensitive |
| T977 | M | 8 | 3.7 | NO | Sensitive |
| D765 | N,G | 8 | 3.9 | NO | Sensitive |
| V1216 | M | 8 | 4.2 | NO | Sensitive |
| G1176 | R,E | 8 | 4.5 | NO | Sensitive |
| R1320 | S | 8 | 5.2 | NO | Sensitive |
| S921 | N | 8 | 5.3 | NO | Sensitive |
| S657 | R | 8 | 5.4 | NO | Sensitive |
| T935 | M | 8 | 8.4 | NO | Sensitive |
| V825 | L | 8 | 9.9 | NO | Sensitive |
| L979 | Q | 8 | 10.3 | NO | - |
| T766 | P,M,R | 8 | 10.3 | NO | - |
| A874 | V | 8 | 11.5 | NO | - |
| I1230 | V | 8 | 13.8 | NO | - |
| G875 | R | 8 | 17.2 | NO | - |
| R778 | G,W,Q,L | 8 | 17.8 | NO | - |
| D1279 | Y,G | 8 | 21.2 | NO | - |
| V890 | M | 8 | 22.9 | NO | - |
| L1327 | V | 8 | 23.5 | NO | - |
| D1296 | N | 8 | 24.5 | NO | - |
| V1239 | G | 8 | 26.1 | NO | - |
| A727 | V,D | 8 | 26.7 | NO | - |

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|---|---|---|---|---|---|
| G1012 | R,V | 8 | 30.8 | NO | - |
| Q1256 | R | 8 | 36.1 | NO | - |
| V864 | I | 8 | 50.5 | NO | - |
| Q898 | R | 8 | 63.5 | NO | - |
| F1094 | L | 8 | 71.6 | NO | - |
| G1213 | V | 8 | 93.3 | NO | - |
| D1271 | N,E | 9 | 0 | NO | Sensitive |
| G1266 | R,K,V | 9 | 0 | NO | Sensitive |
| G843 | R | 9 | 0 | NO | Sensitive |
| G998 | D | 9 | 0 | NO | Sensitive |
| P1273 | S,L,Q | 9 | 0 | NO | Sensitive |
| S744 | P | 9 | 0 | NO | Sensitive |
| A1328 | T | 9 | 0.2 | NO | Sensitive |
| C985 | Y | 9 | 0.2 | NO | Sensitive |
| G1281 | C,D | 9 | 0.4 | YES | Sensitive |
| I1336 | T | 9 | 0.4 | NO | Sensitive |
| A982 | V | 9 | 0.6 | NO | Sensitive |
| K1248 | N | 9 | 0.9 | NO | Sensitive |
| T1220 | M | 9 | 0.9 | NO | Sensitive |
| A1241 | V | 9 | 1 | YES | Sensitive |
| V1262 | F | 9 | 1.1 | NO | Sensitive |
| A1278 | V | 9 | 1.2 | YES | Sensitive |
| T1033 | A,S | 9 | 1.3 | YES | Sensitive |
| N1270 | T,S | 9 | 1.9 | YES | Sensitive |
| I1236 | T | 9 | 2.9 | NO | Sensitive |
| D842 | N | 9 | 3.2 | YES | Sensitive |
| C980 | Y | 9 | 4 | NO | Sensitive |
| L1373 | P,R | 9 | 4.4 | YES | Sensitive |
| A803 | T | 9 | 4.6 | NO | Sensitive |
| G1221 | E | 9 | 4.8 | YES | Sensitive |
| G1149 | A | 9 | 5.3 | NO | Sensitive |
| T737 | R | 9 | 5.5 | NO | Sensitive |
| L1299 | F | 9 | 5.6 | NO | Sensitive |
| T1031 | S,A | 9 | 6 | NO | Sensitive |
| N878 | K | 9 | 6.1 | NO | Sensitive |
| D1027 | A | 9 | 6.3 | YES | Sensitive |
| N1332 | D,K | 9 | 6.7 | NO | Sensitive |
| P1245 | S,T | 9 | 6.8 | YES | Sensitive |
| G711 | R,W,E | 9 | 7.8 | NO | Sensitive |
| P840 | L | 9 | 8.3 | NO | Sensitive |
| P992 | L,H | 9 | 8.3 | NO | Sensitive |

| | | | | | |
|---|---|---|---|---|---|
| G988 | R,V | 9 | 8.6 | NO | Sensitive |
| W939 | C | 9 | 9.9 | NO | Sensitive |
| I899 | F | 9 | 10 | YES | Sensitive |
| E1064 | K,A | 9 | 10.1 | YES | Sensitive |
| T1029 | A,I | 9 | 10.3 | YES | Sensitive |
| M729 | V | 9 | 11.6 | YES | Sensitive |
| A1358 | S | 9 | 12.1 | YES | Sensitive |
| S1310 | R | 9 | 12.1 | NO | - |
| V731 | E | 9 | 12.3 | NO | - |
| S876 | F | 9 | 13.1 | YES | Sensitive |
| V1243 | M | 9 | 14.5 | NO | - |
| D1267 | A,V | 9 | 14.6 | YES | Sensitive |
| T991 | M,T | 9 | 15 | NO | - |
| S1369 | L | 9 | 15.3 | YES | Sensitive |
| T993 | M | 9 | 15.3 | YES | Sensitive |
| V995 | A | 9 | 15.9 | NO | - |
| M1359 | I | 9 | 16.5 | YES | Sensitive |
| N728 | D | 9 | 18 | YES | Sensitive |
| G1355 | S | 9 | 21.4 | NO | - |
| P1352 | S,L,R | 9 | 21.5 | NO | - |
| T858 | A | 9 | 23.5 | YES | Sensitive |
| S1363 | F | 9 | 29.4 | YES | Sensitive |
| H1069 | Q | 9 | 30.2 | YES | Sensitive |
| D1222 | N,Y,V | 9 | 35.4 | YES | Sensitive |
| G1268 | R | 9 | 36 | YES | Sensitive |
| M996 | T | 9 | 37.9 | YES | Sensitive |
| G1101 | R | 9 | 41.1 | NO | - |
| D918 | N,A,E | 9 | 41.3 | YES | Sensitive |
| Y1331 | S | 9 | 41.6 | YES | Sensitive |
| A1003 | T,V | 9 | 46.7 | YES | Sensitive |
| A861 | T | 9 | 48.1 | YES | Sensitive |
| K1010 | R,T | 9 | 53.9 | YES | Sensitive |
| L795 | F,R | 9 | 55.1 | YES | Sensitive |
| T1178 | A | 9 | 60.4 | NO | - |
| L1371 | P | 9 | 71.1 | YES | Sensitive |
| T1288 | R,M | 9 | 73 | YES | Sensitive |
| G1035 | V | 9 | 74.3 | YES | Sensitive |
| G1099 | S | 9 | 85.6 | NO | - |
| G1000 | R | 9 | 90 | YES | Sensitive |
| T788 | I | 9 | 94.9 | YES | Sensitive |
| E1068 | G | 9 | 100 | YES | Sensitive |

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|---|---|---|---|---|---|
| G891 | D,V | 9 | 100.8 | YES | Sensitive |
| G1287 | S | 9 | 104.6 | YES | Sensitive |