

CORRECTION

# Correction: Disease-relevant mutations alter amino acid co-evolution networks in the second nucleotide binding domain of CFTR

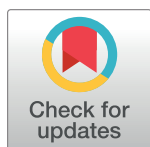
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There is an error in the caption for [Fig 1](#). The correct number of sequences should be 5,032 as listed in the manuscript. Please see the complete, correct [Fig 1](#) legend here.

There is an error in the caption for [S1 Fig](#). Panel A should be labeled “Ser<sup>1251</sup>”. Please see the complete, correct [S1 Fig](#) caption below.

There are a number of errors in the [S2 File](#) caption. Please see the complete, correct [S2 File](#) caption below.

There are a number of errors in the [S2 Table](#) caption. Please see the complete, correct, [S2 Table](#) caption below.



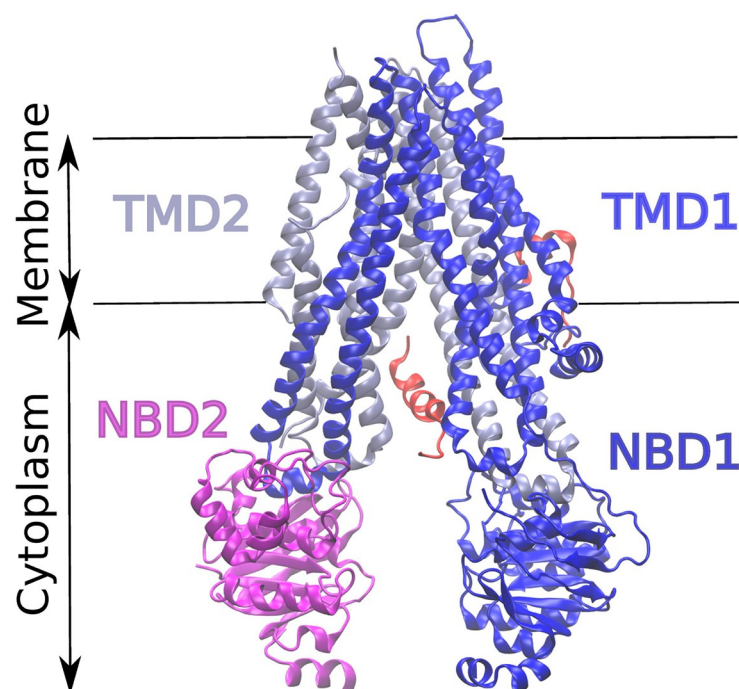
## OPEN ACCESS

**Citation:** Ivey G, Youker RT (2020) Correction: Disease-relevant mutations alter amino acid co-evolution networks in the second nucleotide binding domain of CFTR. PLoS ONE 15(2): e0229986. <https://doi.org/10.1371/journal.pone.0229986>

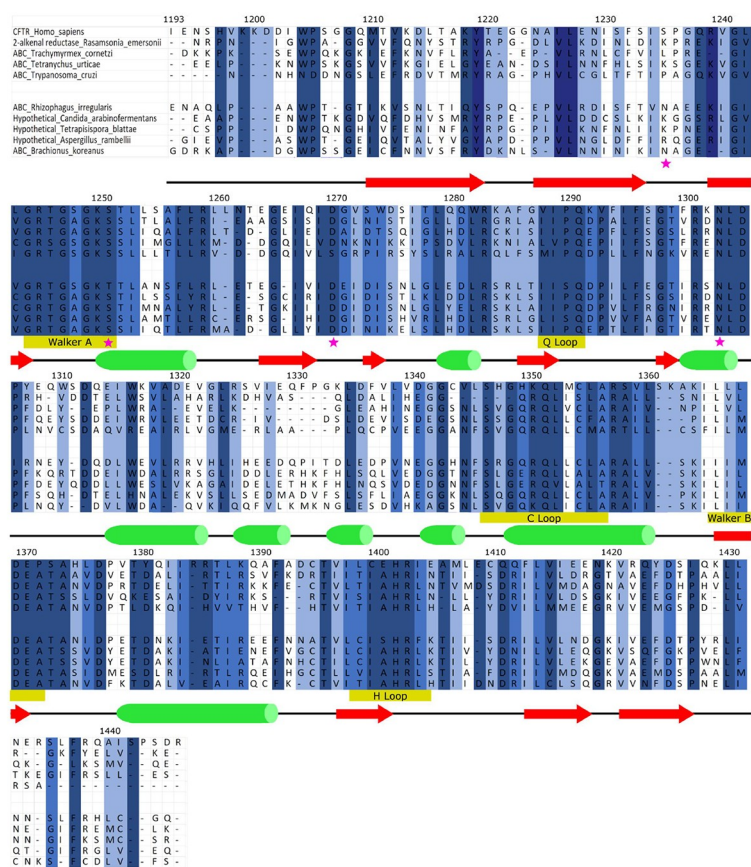
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A



B



**Fig 1. Structure of CFTR protein and multiple sequence alignment of NBD2.** (A) The domain structure of the Cystic Fibrosis Transmembrane Conductance Regulator (CFTR) is shown (PDB:5UAK). Transmembrane Domain 1 (TMD1) is ice blue, Transmembrane Domain 2 (TMD2) is dark blue, Nucleotide Binding Domain 1 (NBD1) is dark blue, Nucleotide Binding Domain 2 (NBD2) is magenta, and the Regulatory (R)-domain is red. Important note—the local resolution varies from 2.4 to 6 angstroms (3.9 angstroms overall) and significant portions of the protein were not resolved including residues 1–14, 645–843, 1173–1206 (N-terminus of NBD2), 1437–1480, and the majority of the R-domain [49]. (B) Multiple sequence alignment of conserved regions in NBD2 of CFTR. For visual simplicity, ten sequences out of 5,032 of the alignment are shown. For the whole MSA, residues shaded in dark blue are > 80% conserved. Residues shaded medium blue >60% conserved and residues shaded in light blue are ~ >40% conserved. Secondary structure is depicted below the alignment with green cylinder represent alpha-helix and red arrow represent beta-sheet. Pink star denotes amino acid position identified as mutated in CF patients and investigated by covariance algorithms in this paper. Selected sequences shown are *Homo sapiens*, *Rasamsonia emersonii*, *Trachymyrmex cornetzi*, *Tetranychus urticae*, *Trypanosoma cruzi*, *Rhizophagus irregularis*, *Candida arabinofermentans*, *Tetrapisispora blattae*, *Aspergillus rambellii*, and *Brachionus koreanus*.

<https://doi.org/10.1371/journal.pone.0229986.g001>

## Supporting information

**S1 Fig. NBD2 coupling matrices for SCA.** Heat maps represent coupled positions identified by the Statistical Coupling Analysis for perturbations (A) Ser<sup>1251</sup>, (B) Ser<sup>1235</sup>, (C) Asn<sup>1303</sup>, and (D) for the wildtype (Full MSA). High scores are represented by warm colors (red), and cool colors depict low scores. Coupled positions at or below the scrambled score for that MSA were colored dark blue.

(PNG)

**S2 File. Raw covariance scores for S1251T perturbation analyses.**

(XLSX)

**S2 Table. Select coupled residue distances for wildtype, S1251T, and S1235R for ATP-free and ATP-bound NBD2 structures.**

(XLSX)

## Reference

1. Ivey G, Youker RT (2020) Disease-relevant mutations alter amino acid co-evolution networks in the second nucleotide binding domain of CFTR. PLoS ONE 15(1): e0227668. <https://doi.org/10.1371/journal.pone.0227668> PMID: 31978131