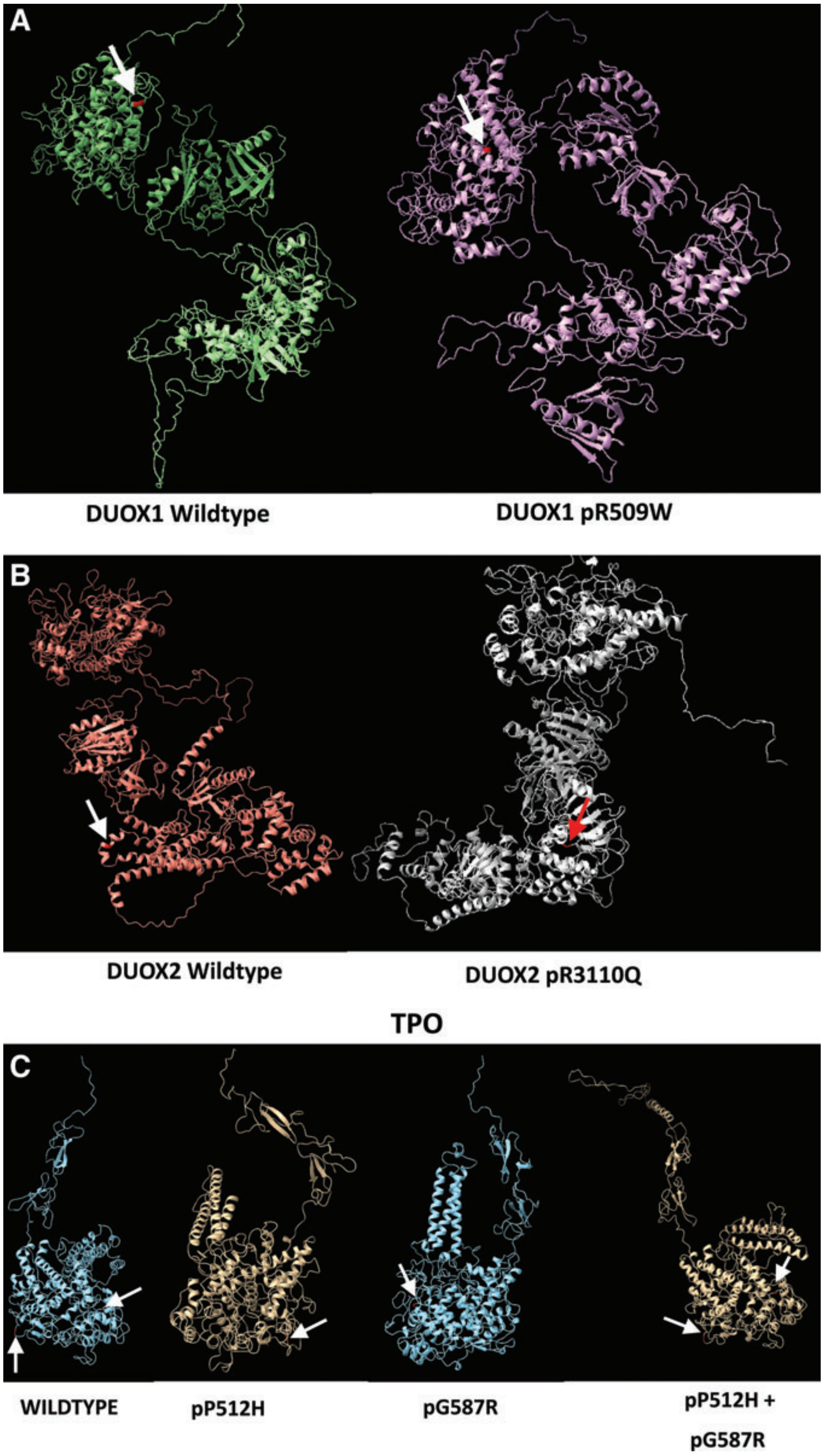
Supplementary Data



SUPPLEMENTARY FIG. S1. Protein modeling *in silico* was performed for each molecule, wild type and mutant: DUOX1 (**A**), DUOX2 (**B**), and TPO (**C**). All reported mutations result in significant protein conformational changes as shown. Methodology for modeling: Kallberg M, Wang H, Wang S, Peng J, Wang Z, Lu H, Xu J 2012 Template-based protein structure modeling using the RaptorX web server. Nat Protoc **7:**1511–1522. Ma J, Peng J, Wang S, Xu J 2012 A conditional neural fields model for protein threading. Bioinformatics **28:**i59–i66. Ma J, Wang S, Zhao F, Xu J 2013 Protein threading using context-specific alignment potential. Bioinformatics **29:**i257–i265.