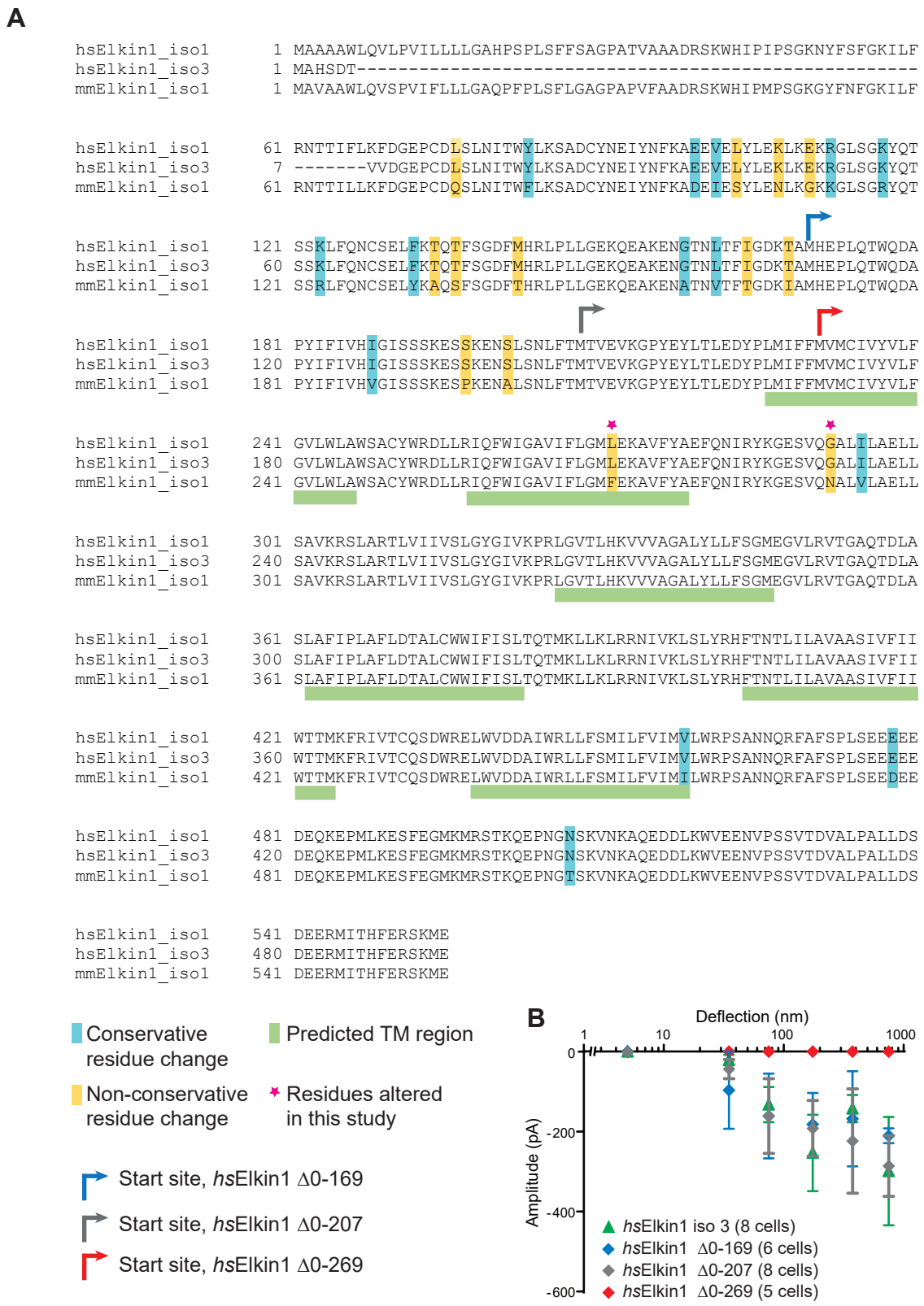

Figure 4- figure supplement 1: Sequence alignment of human and mouse Elkin1 protein and the effect of N-terminal deletions on *hs*Elkin1 function

(**A**) Sequence alignment of the human (*hs*) Elkin1-iso1 and -iso3 against the mouse (*mm*) Elkin1 protein. The predicted transmembrane regions are marked with green, conservative residue variations in teal and non-conservative residue variations in yellow. The two residues that have been studied here are marked with a magenta star. Arrows indicate the start site for cloned truncation proteins. (**B**) Stimulus-response curve analysis of *hs*Elkin1-iso3 versus *hs*Elkin1 truncation mutants. Note that function is only lost once the first predicted TM domain is disrupted.