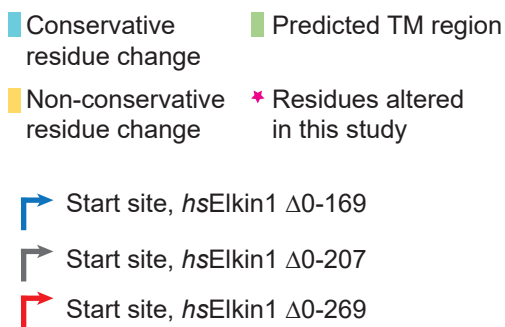
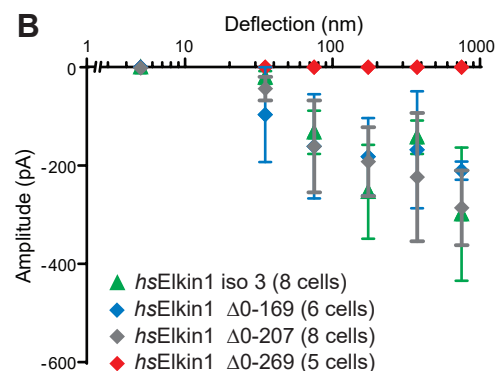


**A**

hsElkin1_iso1	1	MAAAAWLQVLPVILLLLGAHPSPLSFFSAGPATVAAADRSKWHIPIPSGKNYFSFGKILF
hsElkin1_iso3	1	MAHSDT-----
mmElkin1_iso1	1	MAVAAWLQVSPVIFLLLGAQFPPLSFLGAGPAPVFAADRSKWHIPMPSGKGYFNFGKILF
hsElkin1_iso1	61	RNTTIFLKFDGEPCLSLNITWYLSKADCYNEIYNFKAEVELYLEKLEKRLSGSKYQT
hsElkin1_iso3	7	-----VVDGEPCLSLNITWYLSKADCYNEIYNFKAEVELYLEKLEKRLSGSKYQT
mmElkin1_iso1	61	RNTTILLKFDGEPCLSLNITWYLSKADCYNEIYNFKAEELSYLENLKKGLSGRYQT
hsElkin1_iso1	121	SSKLFQNCSELFKTQTTFSGDFMHLPLLGKQEKENGNTNLTFTIGDKTAMHEPLQTWQDA
hsElkin1_iso3	60	SSKLFQNCSELFKTQTTFSGDFMHLPLLGKQEKENGNTNLTFTIGDKTAMHEPLQTWQDA
mmElkin1_iso1	121	SSRLFQNCSELYKAQSFSGDFTHRLPLLGKQEKENATNVTFTIGDKIAMHEPLQTWQDA
hsElkin1_iso1	181	PYIFIVHIGISSKESKENSLSNLFMTTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
hsElkin1_iso3	120	PYIFIVHIGISSKESKENSLSNLFMTTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
mmElkin1_iso1	181	PYIFIVHIGISSKESKENSLSNLFMTTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
hsElkin1_iso1	241	GVLWLAWSAACYWRDLLRIQFWIGAVIFLGMIEKAVFYAEFQNIYKGESVQCALILAELL
hsElkin1_iso3	180	GVLWLAWSAACYWRDLLRIQFWIGAVIFLGMIEKAVFYAEFQNIYKGESVQCALILAELL
mmElkin1_iso1	241	GVLWLAWSAACYWRDLLRIQFWIGAVIFLGMIEKAVFYAEFQNIYKGESVQCALILAELL
hsElkin1_iso1	301	SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
hsElkin1_iso3	240	SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
mmElkin1_iso1	301	SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
hsElkin1_iso1	361	SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRNIVKLSLYRHFTNTLILAVAASIVFII
hsElkin1_iso3	300	SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRNIVKLSLYRHFTNTLILAVAASIVFII
mmElkin1_iso1	361	SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRNIVKLSLYRHFTNTLILAVAASIVFII
hsElkin1_iso1	421	WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMVLWRPSANNQRFASFPLSEEEEE
hsElkin1_iso3	360	WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMVLWRPSANNQRFASFPLSEEEEE
mmElkin1_iso1	421	WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMVLWRPSANNQRFASFPLSEEEEE
hsElkin1_iso1	481	DEQKEPMLKESFEGMKMRSTKQEPNGNSKVNKAQEDDLKWVEENVPSSVTDVALPALDLS
hsElkin1_iso3	420	DEQKEPMLKESFEGMKMRSTKQEPNGNSKVNKAQEDDLKWVEENVPSSVTDVALPALDLS
mmElkin1_iso1	481	DEQKEPMLKESFEGMKMRSTKQEPNGNSKVNKAQEDDLKWVEENVPSSVTDVALPALDLS
hsElkin1_iso1	541	DEERMITHFERSKME
hsElkin1_iso3	480	DEERMITHFERSKME
mmElkin1_iso1	541	DEERMITHFERSKME



**B**



**Figure 4- figure supplement 1: Sequence alignment of human and mouse Elkin1 protein and the effect of N-terminal deletions on *hsElkin1* 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 *hsElkin1*-iso3 versus *hsElkin1* truncation mutants. Note that function is only lost once the first predicted TM domain is disrupted.