hsElkin1_iso1	1 MAAAAWLQVLPVILLLLGAHPSPLSFFSAGPATVAAADRSKWHIPIPSGKNYFSFGKILF
hsElkin1_iso3	1 MAHSDT
mmElkin1_iso1	1 MAVAAWLQVSPVIFLLLGAQPFPLSFLGAGPAPVFAADRSKWHIPMPSGKGYFNFGKILF
- hsElkin1_iso1 hsElkin1_iso3 mmElkin1_iso1	61 RNTTIFLKFDGEPCDLSLNITW <mark>Y</mark> LKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQT 7VVDGEPCDLSLNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQT 61 RNTTILLKFDGEPCD <mark>Q</mark> SLNITWFLKSADCYNEIYNFKADEIES <mark>YLEN</mark> LKGKKGLSGRYQT
hsElkin1_iso1	121 SSKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIGDKTAMHEPLQTWQDA
hsElkin1_iso3	60 SSKLFQNCSELFKTQTFSGDFMHRLPLLGEKQEAKENGTNLTFIGDKTAMHEPLQTWQDA
mmElkin1_iso1	121 SSRLFQNCSELYKAQSFSGDFTHRLPLLGEKQEAKENATNVTFTGDKIAMHEPLQTWQDA
hsElkin1_iso1	181 PYIFIVH <mark>I</mark> GISSSKES <mark>S</mark> KEN <mark>S</mark> LSNLFTMTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
hsElkin1_iso3	120 PYIFIVHIGISSSKES <mark>S</mark> KEN <mark>S</mark> LSNLFTMTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
mmElkin1_iso1	181 PYIFIVH <mark>V</mark> GISSSKES <mark>P</mark> KEN <mark>A</mark> LSNLFTMTVEVKGPYEYLTLEDYPLMIFFMVMCIVYVLF
hsElkin1_iso1	241 GVLWLAWSACYWRDLLRIQFWIGAVIFLGMLEKAVFYAEFQNIRYKGESVQGALILAELL
hsElkin1_iso3	180 GVLWLAWSACYWRDLLRIQFWIGAVIFLGMLEKAVFYAEFQNIRYKGESVQGALILAELL
mmElkin1_iso1	241 GVLWLAWSACYWRDLLRIQFWIGAVIFLGMFEKAVFYAEFQNIRYKGESVQNALVLAELL
hsElkin1_iso1	301 SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
hsElkin1_iso3	240 SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
mmElkin1_iso1	301 SAVKRSLARTLVIIVSLGYGIVKPRLGVTLHKVVVAGALYLLFSGMEGVLRVTGAQTDLA
hsElkin1_iso1	361 SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRRNIVKLSLYRHFTNTLILAVAASIVFII
hsElkin1_iso3	300 SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRRNIVKLSLYRHFTNTLILAVAASIVFII
mmElkin1_iso1	361 SLAFIPLAFLDTALCWWIFISLTQTMKLLKLRRNIVKLSLYRHFTNTLILAVAASIVFII
hsElkin1_iso1	421 WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMVLWRPSANNQRFAFSPLSEEEEE
hsElkin1_iso3	360 WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMVLWRPSANNQRFAFSPLSEEEEE
mmElkin1_iso1	421 WTTMKFRIVTCQSDWRELWVDDAIWRLLFSMILFVIMILWRPSANNQRFAFSPLSEEDEE
hsElkin1_iso1	481 DEQKEPMLKESFEGMKMRSTKQEPNG <mark>N</mark> SKVNKAQEDDLKWVEENVPSSVTDVALPALLDS
hsElkin1_iso3	420 DEQKEPMLKESFEGMKMRSTKQEPNGNSKVNKAQEDDLKWVEENVPSSVTDVALPALLDS
mmElkin1_iso1	481 DEQKEPMLKESFEGMKMRSTKQEPNG <mark>T</mark> SKVNKAQEDDLKWVEENVPSSVTDVALPALLDS
hsElkin1_iso1	541 DEERMITHFERSKME
hsElkin1_iso3	480 DEERMITHFERSKME
mmElkin1_iso1	541 DEERMITHFERSKME
Conservative residue change	Predicted TM region B Deflection (nm) 1 0 1 0 1 0 1 0 1 0 0 1 0 0 0 0 0 0 0
Non-conservative residue change	in this study
	Elkin1 $\Delta 0.207$
	Elkin1 ∆0-207 Elkin1 ∆0-269 → hsElkin1 ∆0-269 → hsElkin1 ∆0-269 (5 cells) → hsElkin1 ∆0-269 (5 cells)

## 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.