

Disruption of the IS6-AID linker affects voltage-gated calcium channel inactivation and facilitation

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Volume 133, No. 3, March 2, 2009. Pages 327–343.

Please note that in the original Fig. 2, “10³” was missing from the y axes. The correct figure appears below.

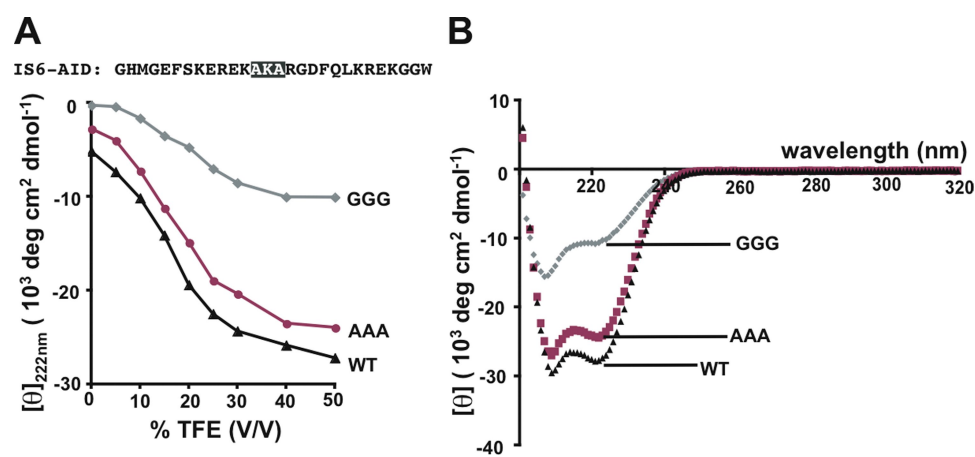


Figure 2. Glycine substitution in IS6-AID linker disrupts helical structure. (A) Mean residue ellipticity at 222 nm for IS6-AID linker peptide, and AAA and GGG mutant peptides as a function of TFE concentration. Peptide sequence is shown. Black highlights the site of the GGG and AAA mutations. (B) IS6-AID linker peptide CD spectra at a peptide concentration of 50 μM in 50% TFE.