Figure S10. Binding isotherms generated by plotting the change in ^{1}H and ^{15}N chemical shifts ($\Delta\delta$) as a function of peptide concentration. Titration data were fit by a one-site binding model. As indicated by the K_d values, FasDD peptides bind much weaker to isolated domains of Ca^{2+}/CaM than that of the full-length protein (15-268 vs. 0.3 and 1.1 µM). Data also show that both peptides have higher affinity to Ca^{2+}/CaM-C than Ca^{2+}/CaM-N.