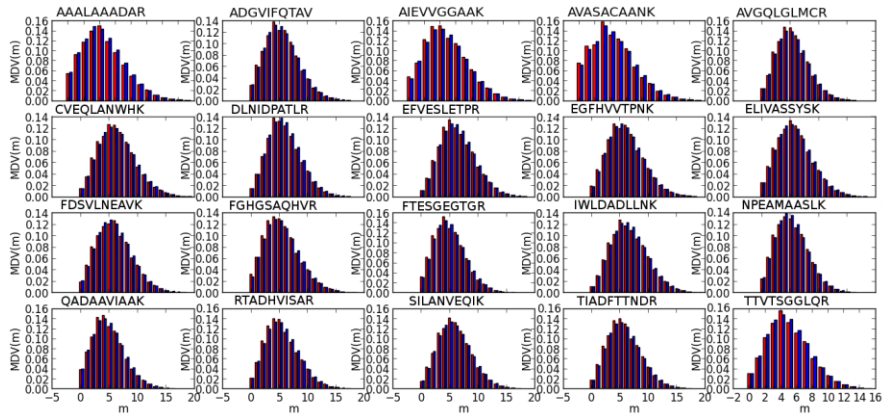
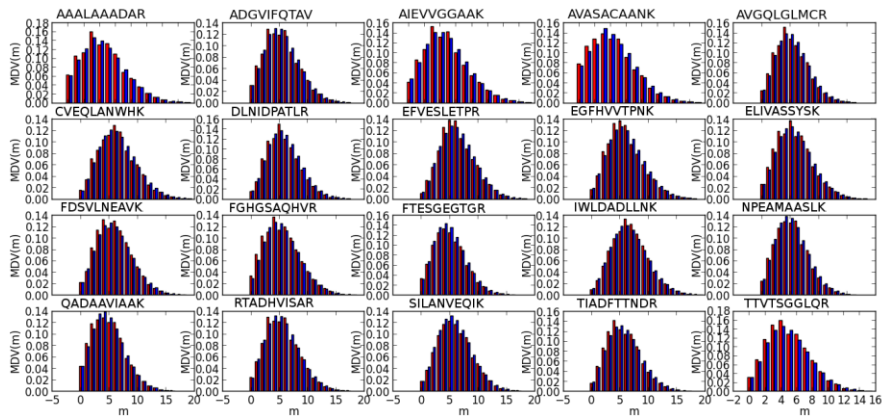


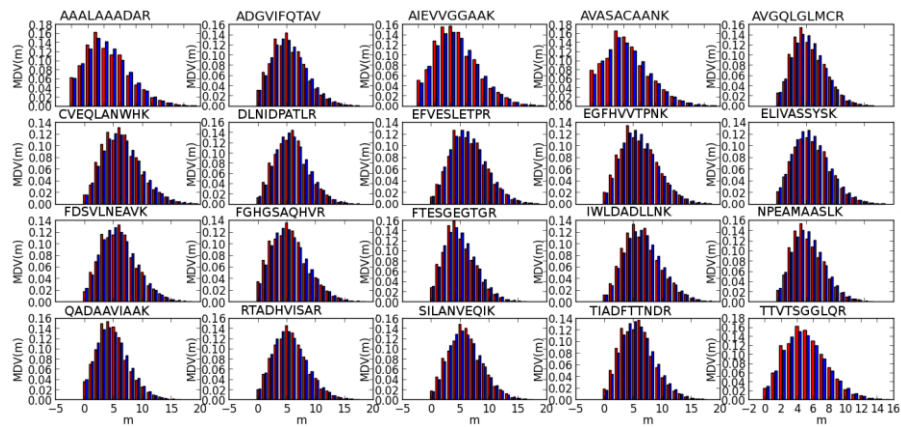
(a)

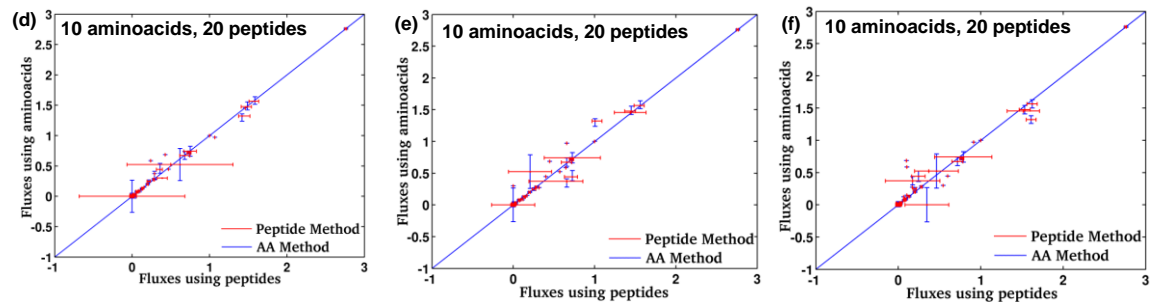


(b)



(c)





**Figure S4.** Peptide labeling data fit for *E. coli* rf05 strain for 20 peptides and 10 aminoacids. Fits were obtained for experimentally measured peptide MDV's with following error rates (a) 0.05, (b) 0.08 and (c) 0.10. Red denotes the MDV for experimentally measured data, blue columns are the fit. Comparison between flux profiles measured through  $^{13}\text{C}$  MFA using aminoacids and peptides, and fits were obtained for experimentally measured peptide MDV's with following error rates (d) 0.05, (e) 0.08 and (f) 0.10. The performance of the peptide-based method deteriorates strongly for  $\delta \geq 0.08$ .