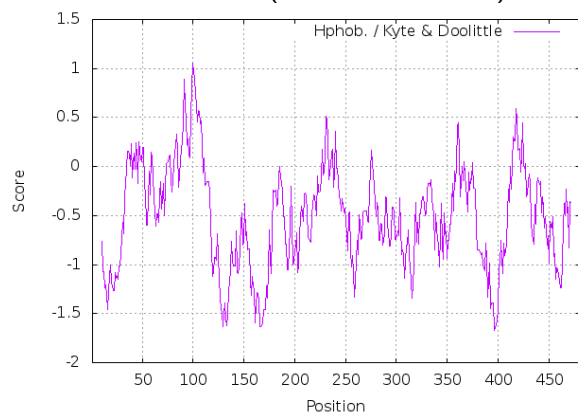
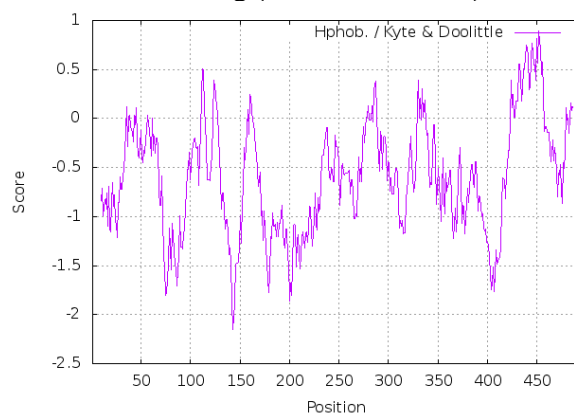


ADDITIONAL FILE 1

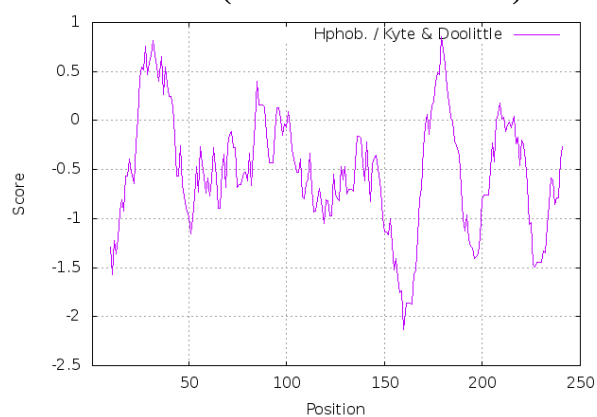
A-MatN (CHAP- ami2-SH3)



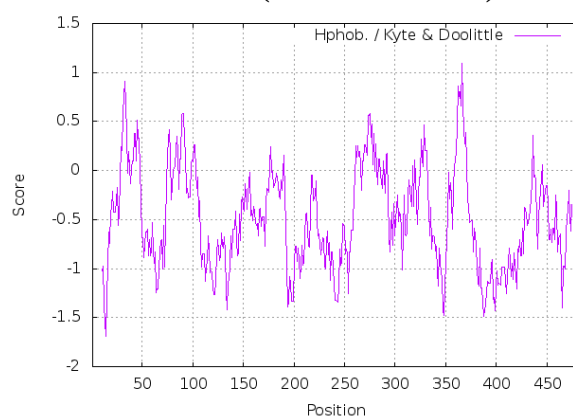
B-Cg (CHAP-ami2-SH3)



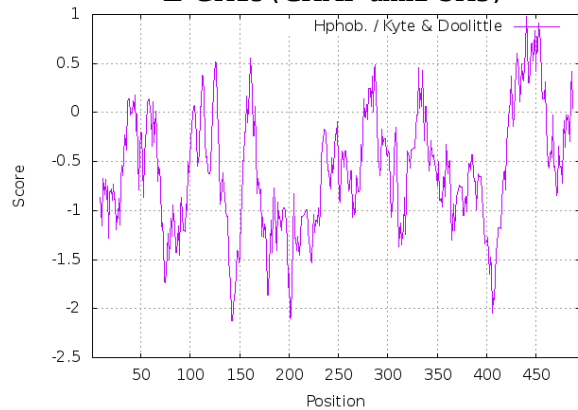
C-308 (CHAP – CBD non-SH3)



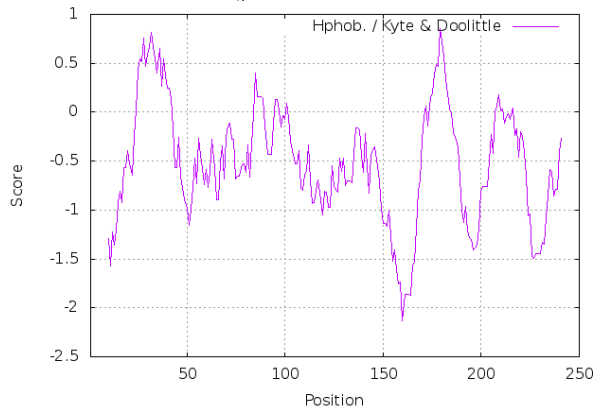
D-320 (CHAP- ami3-SH3)



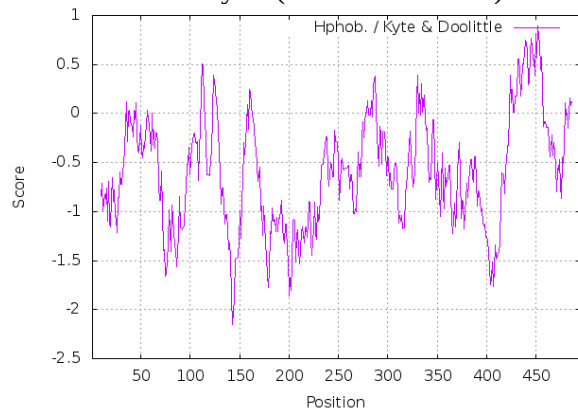
E-GH15 (CHAP-ami2-SH3)



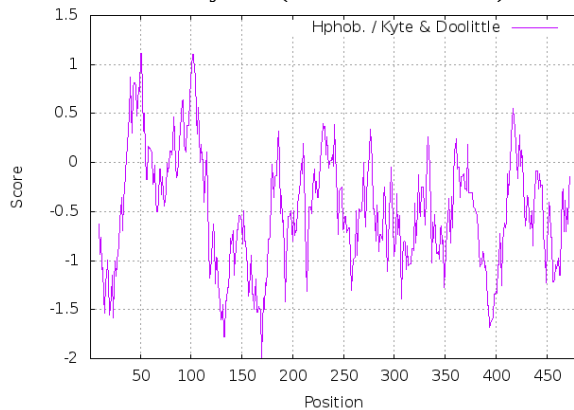
F-PlyGRCS: CHAP-SH3



G-LysK (CHAP-ami2-SH3)



H-LysH5 (CHAP-ami2-SH3)



Hydrophobicity plots of endolysins. Kyte-Doolittle plot predicts whether different protein segments would interact with or reside in a membrane. Hydrophobic regions achieve positive values of at least 1.6 at their centers. The online tool ProtScale (<https://web.expasy.org/protscale/>) was used for the construction of plots. Protein sequences (A-D) were from phage endolysins sequenced in our laboratory (Suárez *et al*, submitted to Microbiology Spectrum, Spectrum00334-22) or reported in the literature (E-H) [17,29,14,18]. Endolysin domain composition is shown between brackets.