A Conformational Investigation of Propeptide Binding to the Integral Membrane Protein γ-Glutamyl Carboxylase Using Nanodisc Hydrogen Exchange Mass Spectrometry

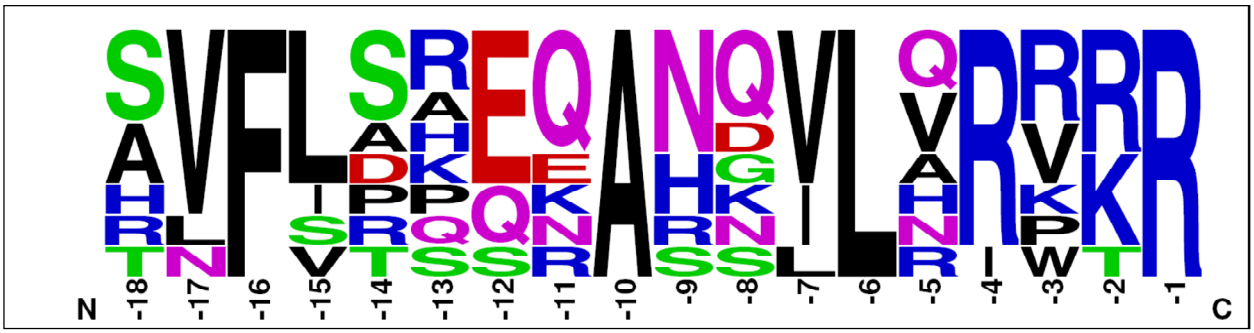
Christine H. Parker,[,†] Christopher R. Morgan,[§,#] Kasper D. Rand,[§,⊥] John R. Engen,[§] James W. Jorgenson,[†] and Darrel W. Stafford[‡]*

Supporting Information

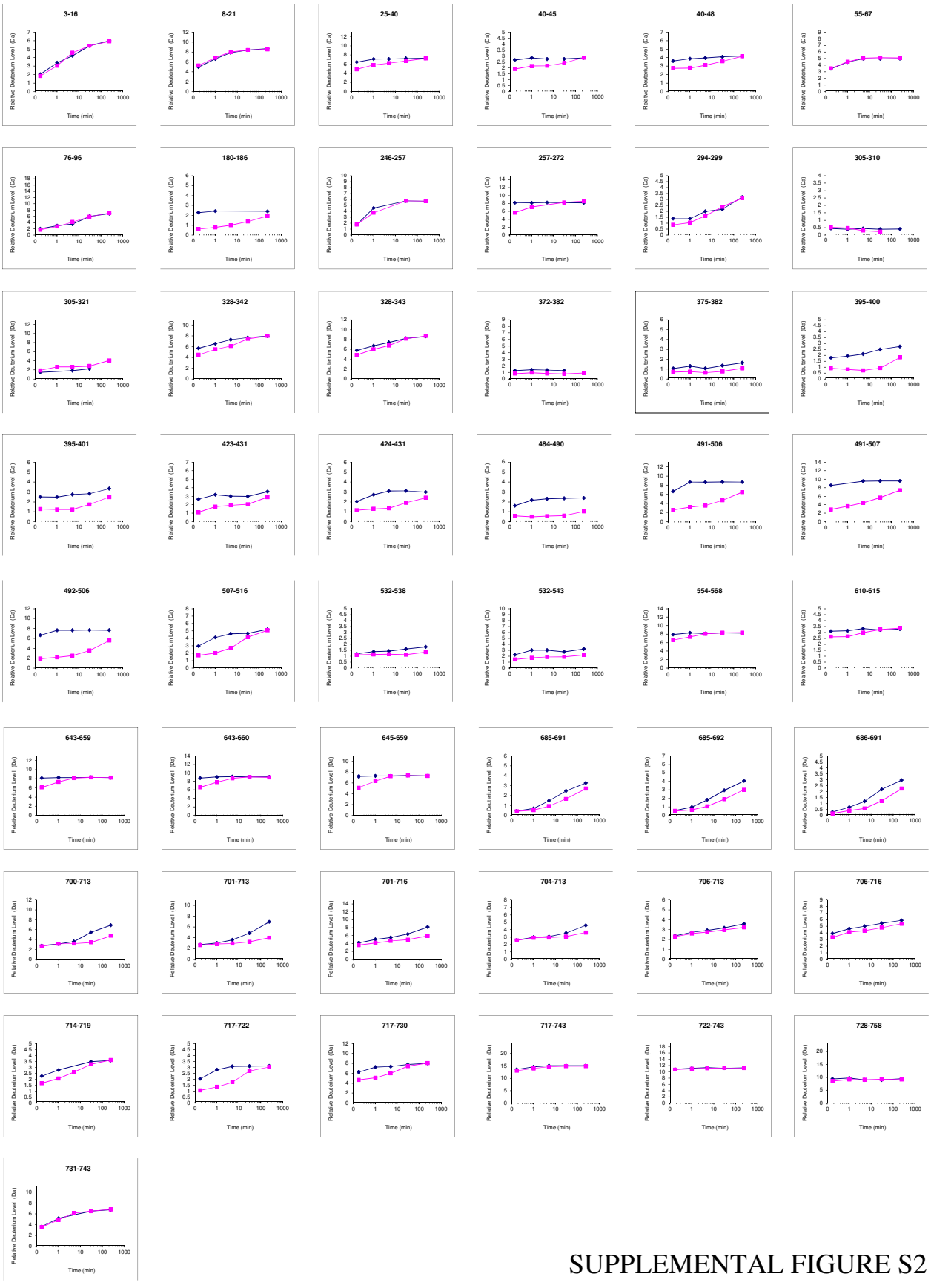
SUPPORTING INFORMATION FIGURE LEGENDS

Supplemental Figure S1 – Graphical representation of propeptide multiple sequence alignment using WebLogo[5, 6] for human vitamin K-dependent proteins: consensus propeptide, factor VII, factor IX, factor X, protein C, protein S, protein Z, and prothrombin. Alignment is presented as a stack of symbols corresponding to individual positions within the propeptide sequence. The overall height of the symbols within the stack indicates the relative frequencies of each amino acid. Propeptide alignment indicates highly conserved amino acid positions at phenylalanine –16, alanine –10, leucine –6, and arginine –1.

Supplemental Figure S2 – Deuterium uptake curves for all identified GGCX peptides matched in both biological sample preparations for GGCX-nanodiscs (blue) and GGCX-pCon-nanodiscs (pink). Deuterium uptake curves are constructed by plotting the relative change in deuterium incorporation as a function of label time. The y-axis maximum represents the maximum amount of deuterium that could be incorporated into each peptide, based on sequence.



SUPPLEMENTAL FIGURE S1



SUPPLEMENTAL FIGURE S2