

Supplementary Material

Figure S1. 8% (w/v) 8 M urea native-PAGE demonstrating the result of the positional scanning library (Ac-TX₂AF-NH₂; X₂ = A, H, I, L, M, F, T, V, W and Y). The screening was performed with a 100-fold molar excess of each individual peptide (lane 1 to 10: Ac-TVAF-NH₂, Ac-TIAF-NH₂, Ac-TFAF-NH₂, Ac-TYAF-NH₂, Ac-TTAF-NH₂, Ac-TWAF-NH₂, Ac-THAF-NH₂, Ac-TLAF-NH₂, Ac-TAAF-NH₂ and Ac-TMAF-NH₂) against M-AT at 37 °C for 2 h. The peptide Ac-TTAF-NH₂ annealed to M-AT under the same condition as Figure 1A in reference 55, indicating the peptide itself was sufficient to form binary complex. Note there were other 99 peptides in the sub-library of Ac-TTX₃X₄-NH₂ that may or may not bind to M-AT. In addition, the result also showed that a greater tolerance of amino acid at the X₂ position, as 7 out of the 10 selected amino acids were able to form intense binary complex.

