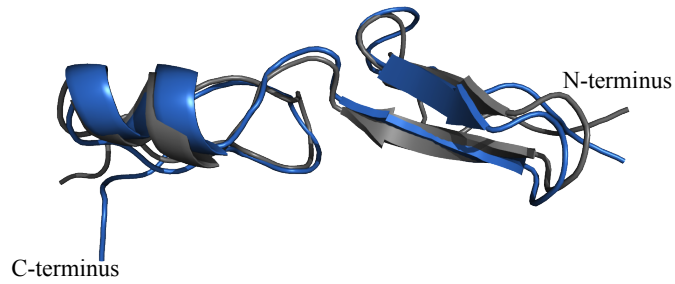
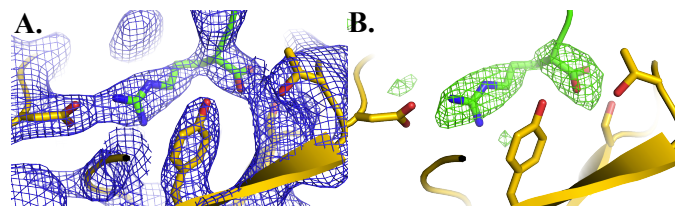


SUPPLEMENTAL FIGURES



Supplemental Figure 1: The VEGF-A HBD structure. The VEGF-A HBD solution structure (gray, PDB=1KMX) shares a similar structural architecture with the current Nrp1 bound HBD structure (blue).



Supplemental Figure 2: Binding of the C-terminal arginine into the conserved Nrp1-b1 binding pocket reveals a conserved binding mode between both molecules in the asymmetric unit. (A) 2Fo-Fc electron density map contoured at 1.0 and (B) Fo-Fc omit electron density map contoured at 3.0 for R164 chain B.