



Figure S1. Machine learning-based identification of AMP-like epitopes (Ampitopes) in three subtypes Influenza hemagglutinin (HA) proteins. Thousands HA proteins from three subtypes influenza strains (1510 H1N1, 3303 H3N2 and 122 IBV) are scanned with an AMP classifier for peptide sequences sharing the physiochemical features with natural AMP. Each query sequence is assigned a σ score. The first amino acid in each sequence is colored based on the score to reflect AMP-ness of this query sequence. A large, positive σ score suggest high probability of being AMP. Sequences with $\sigma < 0$ (non-AMP) is labeled as deep blue.