1. We record the normalized -log10(EC50) fitted values for mutant peptides, found in Source Data Extended Data Fig. 6, where EC50 is named the fit parameter “K\_a”. Following the main text “The inferred EC50’s were further clipped to the range of 1E-4 mu g/mL to 1E+4 mu g/mL”, we do the same. So, first we calculate a=-log10(EC50) for all mutant peptides for a given TCR, then clip the values (including +-Inf) to [-4,4] and then use the MATLAB command normalize(a(:),"range") to have all the mutant activities between [0,1] for a given TCR.
2. The TCR V alpha and V beta sequences are in Extended Data Fig. 4