1. Supplementary data has barplots from mutational scan data. We opened them in Adobe Illustrator and noted the height of the bars in pixels and converted them into actual values (see the MATLAB code for details). In “max heights” columns for lower and upper bars, I used the index peptide amino acid bars at each position as the standard
2. The TCR CDR sequences are taken from a companion article: “[Selection of a Clinical Lead TCR Targeting Alpha-Fetoprotein-Positive Liver Cancer Based on a Balance of Risk and Benefit](https://www.frontiersin.org/articles/10.3389/fimmu.2020.00623/full)” Fig 1A. We designate the region “CAAS….” Or “CASS….” Before “GXG” as CDR3 regions and do UniProt search for the rest part to assign alleles