1. Full mutational scan of c259 around epitope SLLMWTQ**C** is recorded elsewhere from PMID: 37607971 (also the source of the TCR sequence), where the TCR is recorded as “1G4”. The current data is from “[Generation of T cells with reduced off-target cross-reactivities by engineering co-signalling receptors](https://www.biorxiv.org/content/10.1101/2024.10.25.620274v1.full)”, Fig 5C killing heatmap, where the scan is around SLLMWITQ**V.**
2. We record the killing data corresponding to Fig 5C in the paper. The raw data is not available, neither are the heatmaps in vector graphics format. So we save the heatmaps as jpg files, read pixel-wise RGB values using a Python code and then map the RGB values to killing values using the colorbar. Cysteine is excluded in the scan at all positions. Killing data for mutations at position 9 broadly matches with the IFN values for the same mutants found in the other source (e.g., higher activity for substituted amino acids A, I, L, M).