Schematic single-residue scanning of reactive peptides.

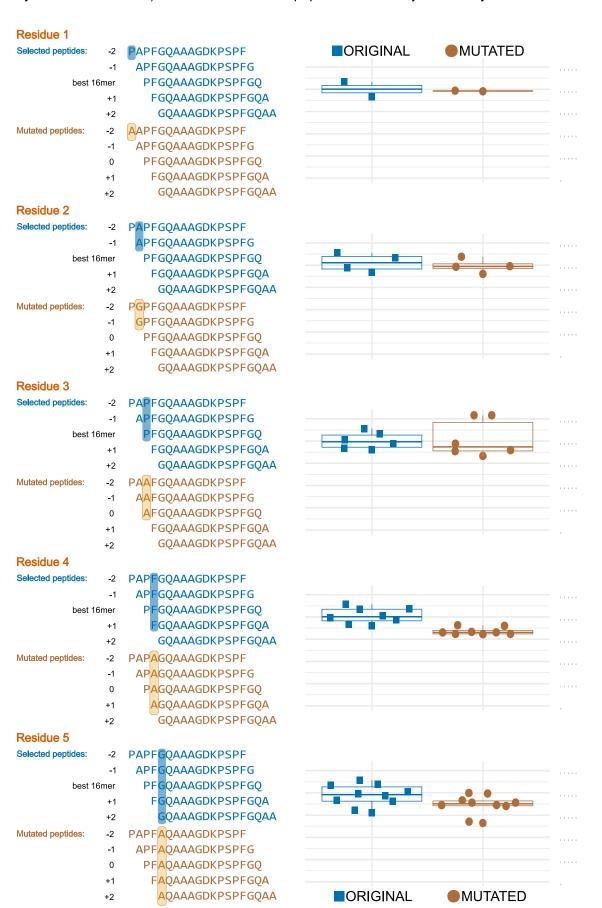
Example Using CA-2/Ag2 Antigen | TcCLB.508831.140 (repetitive)

repetitive unit

Protein sequence: PFGQAAAGDKPA[PFGQAAAGDKPS]PFGQAAAGDKPA...

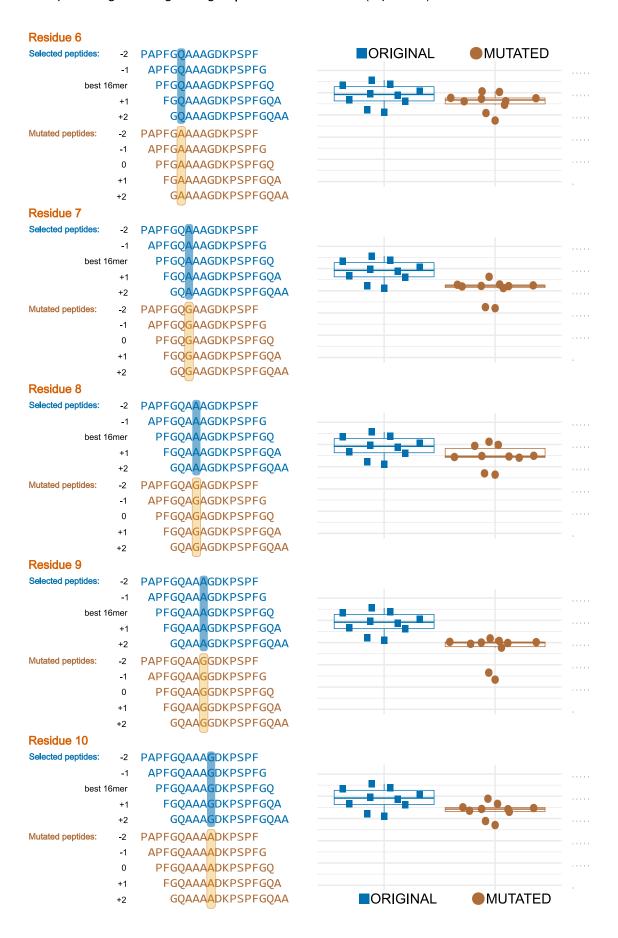
best 16me

Given a selected 16mer (most reactive peptide in an antibody-binding peak), the mutational scanning assessment analyzed the antibody-binding (reactivity) of 5 unmutated peptides, and 3 to 5 mutated peptides per residue position (see figure below). Unmutated peptides correspond to peptides starting at -2, -1, +1, and +2 with respect to the 1st residue of the selected 16mer. Mutations were always to an Alanine, except where the original residue was an Alanine (it was substituted for a Glycine in these cases). A total of 74 mutated peptides were analyzed for any selected 16mer.



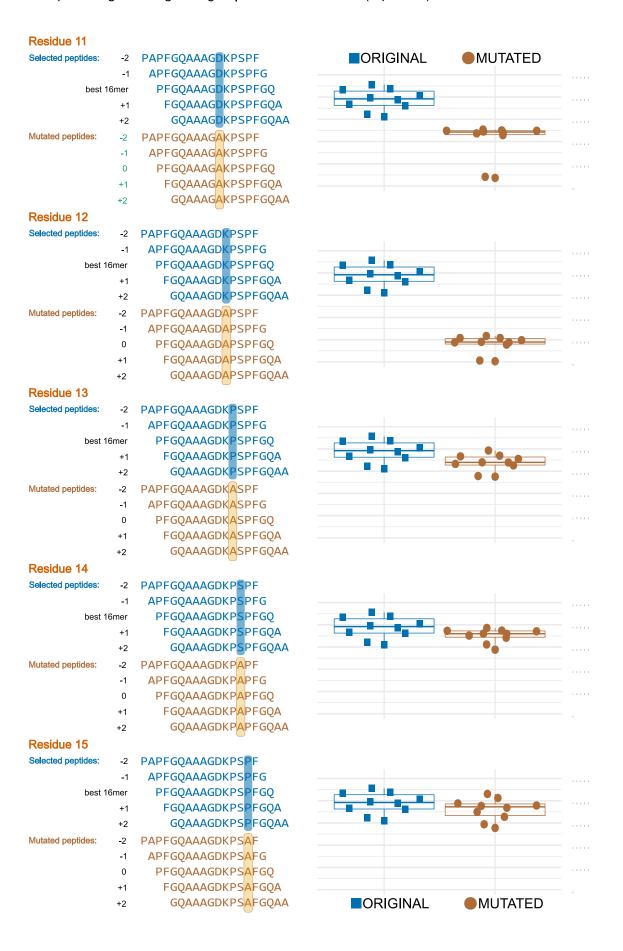
Schematic single-residue scanning of reactive peptides (continued)

Example Using CA-2/Ag2 Antigen | TcCLB.508831.140 (repetitive)



Schematic single-residue scanning of reactive peptides (continued)

Example Using CA-2/Ag2 Antigen | TcCLB.508831.140 (repetitive)



Schematic single-residue scanning of reactive peptides (continued) Example Using CA-2/Ag2 Antigen | TcCLB.508831.140 (repetitive) Residue 16 Selected peptides: -2 PAPFGQAAAGDKPSPFG -1 APFGQAAAGDKPSPFGQ -1 PFGQAAAGDKPSPFGQA +1 FGQAAAGDKPSPFGQA +2 GQAAAGDKPSPFGQAA

