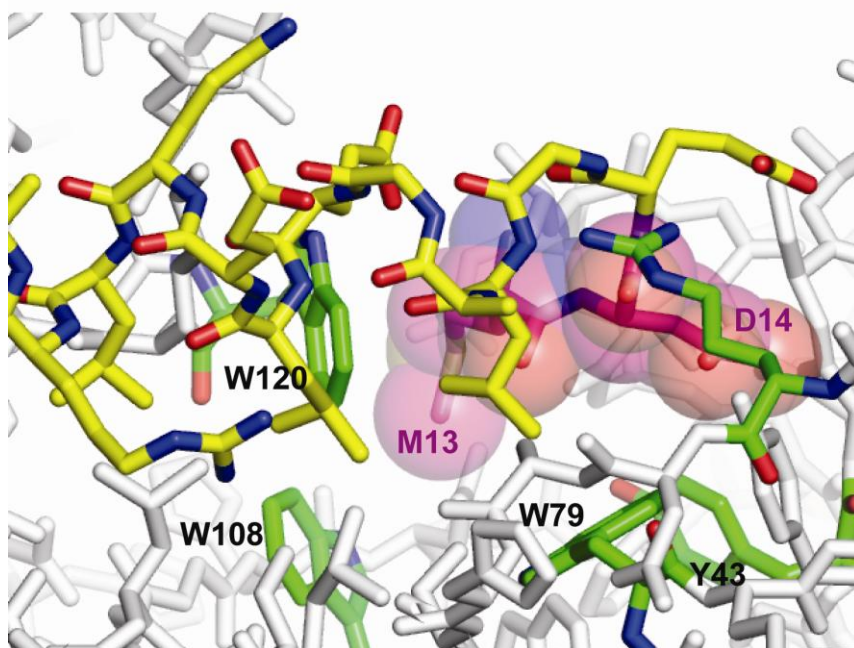
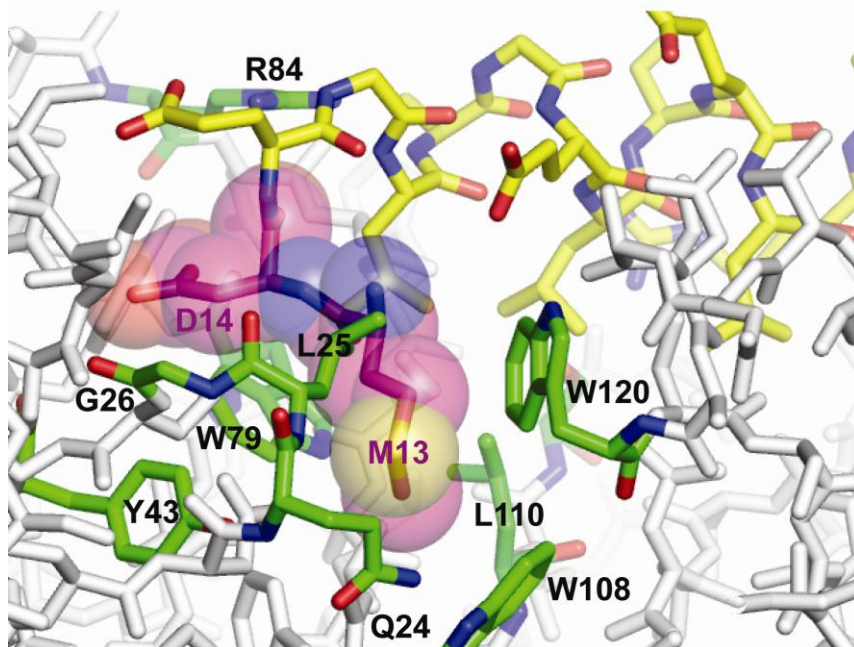


Supplementary Material

A



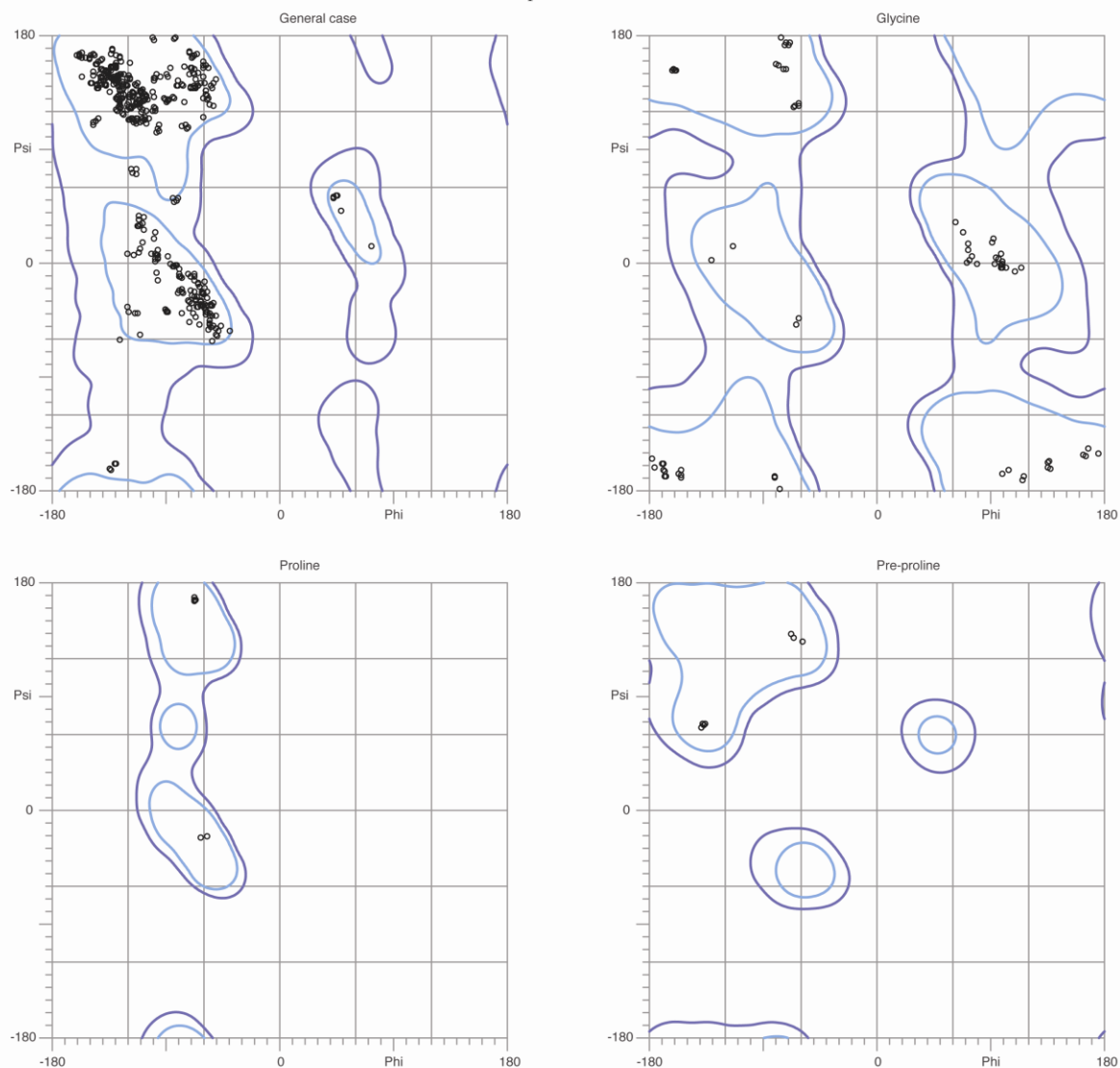
B



Supplementary Figure 1. Model of the N1 mutant showing how the replacement of the “HV” motif with “MD” can potentially form stabilizing interactions with the biotin-binding pocket of SAV. (A) “Front” and (B) “back” views are drawn from the same viewpoints used to create Figs. 3(a) and 3(b).

MolProbity Ramachandran analysis

r9a.pdb, model 1



97.9% (507/518) of all residues were in favored (98%) regions.
100.0% (518/518) of all residues were in allowed (>99.8%) regions.

There were no outliers.

<http://kinemage.biochem.duke.edu>

Lovell, Davis, et al. Proteins 50:437 (2003)

Supplementary Figure 2. Ramachandran plots showing the distribution of main-chain torsion angles as calculated by *MolProbity*.