SHAP decision plot for HA553R in gene PCSK9 (Q8NBP7), GRCh38 1:55059640A>G, VKGL April 2024: VUS

SHAP values do not correlate with feature values, but instead capture feature contributions based on the interactions among all features uniquely for this prediction

Features affecting probability by >0% in descending order of impact:

- Global model base probability
- Total energy decreased by −0.284796
- Ligand binding pockets decreased by −1
- Protein binding site binarized per residue decreased by −1
- Net electric charge at pH 7 increased by 0.909088
- Isoelectric point increased by 0.034492
- RNA binding site binarized per residue is unchanged
- RNA binding affinity pKd increased by 1e−04
- Hydrophobicity decreased by −0.001879
- DNA binding site binarized per residue decreased by −1
- Hydrophobic moment is unchanged
- DNA binding affinity pKd increased by 0.00074
- Ligand binding top SAS points is unchanged

Cumulative probability heuristic for SHAP values
Final probability for being pathogenic is 0.13