

SHAP decision plot for AA302P in gene APOA5 (Q6Q788), GRCh38 11:116790325C>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 increased by 3.64413

Net electric charge at pH 7 is unchanged

Isoelectric point is unchanged

DNA binding affinity pKd increased by 7e-05

Ligand binding top SAS points is unchanged

Hydrophobic moment is unchanged

Hydrophobicity decreased by -0.00929

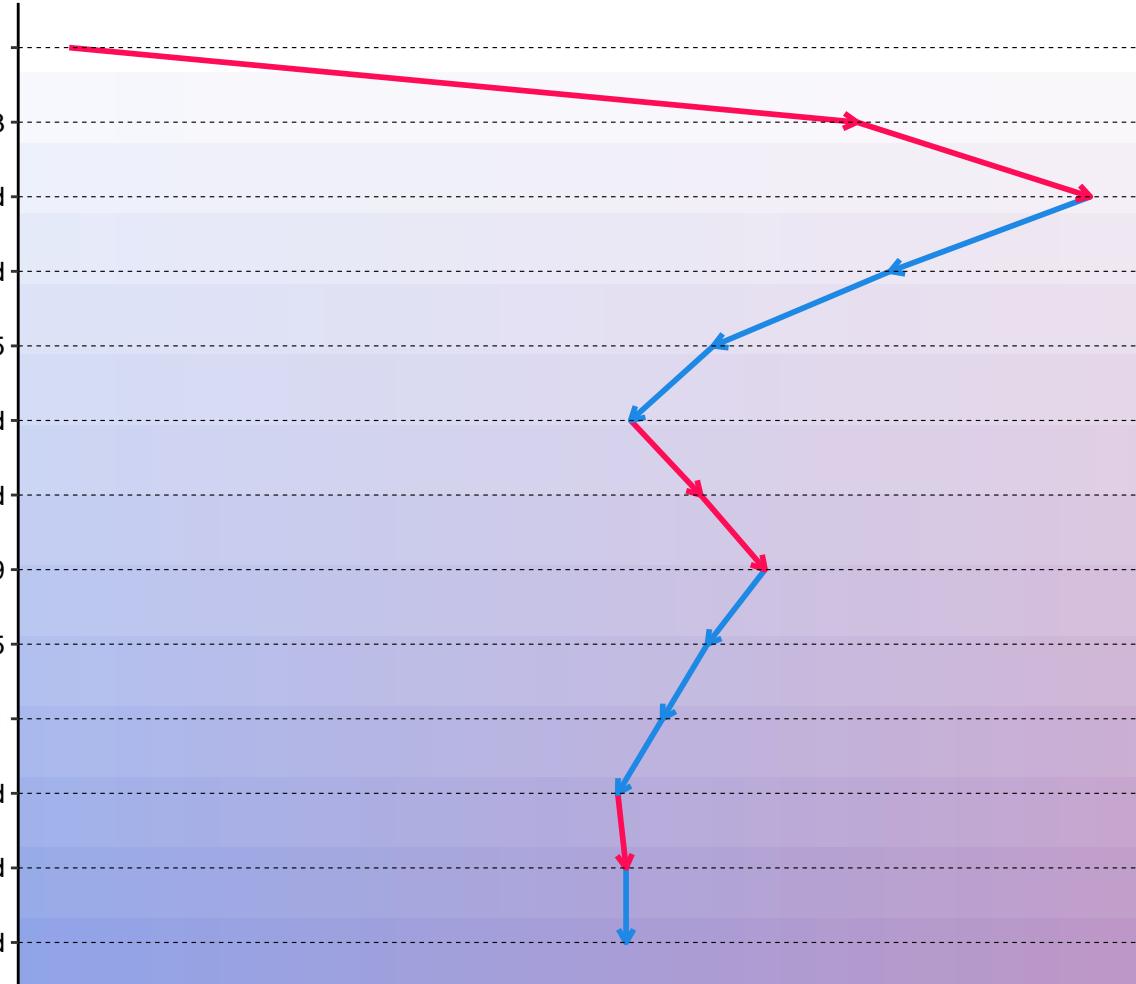
RNA binding affinity pKd decreased by -1e-05

Protein binding site binarized per residue decreased by -1

DNA binding site binarized per residue is unchanged

RNA binding site binarized per residue is unchanged

Ligand binding pockets is unchanged



Cumulative probability heuristic for SHAP values
Final probability for being pathogenic is 0.386