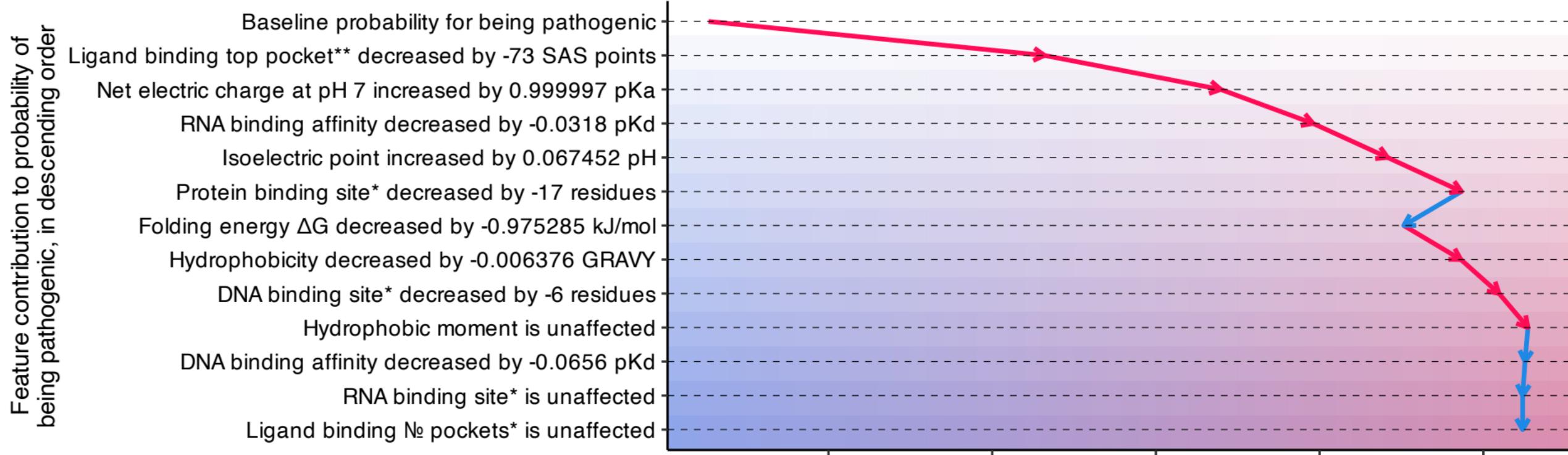


# DAVE1 decision plot for GA554R in gene SLCO2A1 (Q92959, ENST00000310926), GRCh38 3:133938459C>T

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



\* = if any, one or more    \*\* = if any

Cumulative probability heuristic for SHAP values, benign/path. threshold is 0.286  
Final probability for being pathogenic is 0.724, variant is estimated to be pathogenic