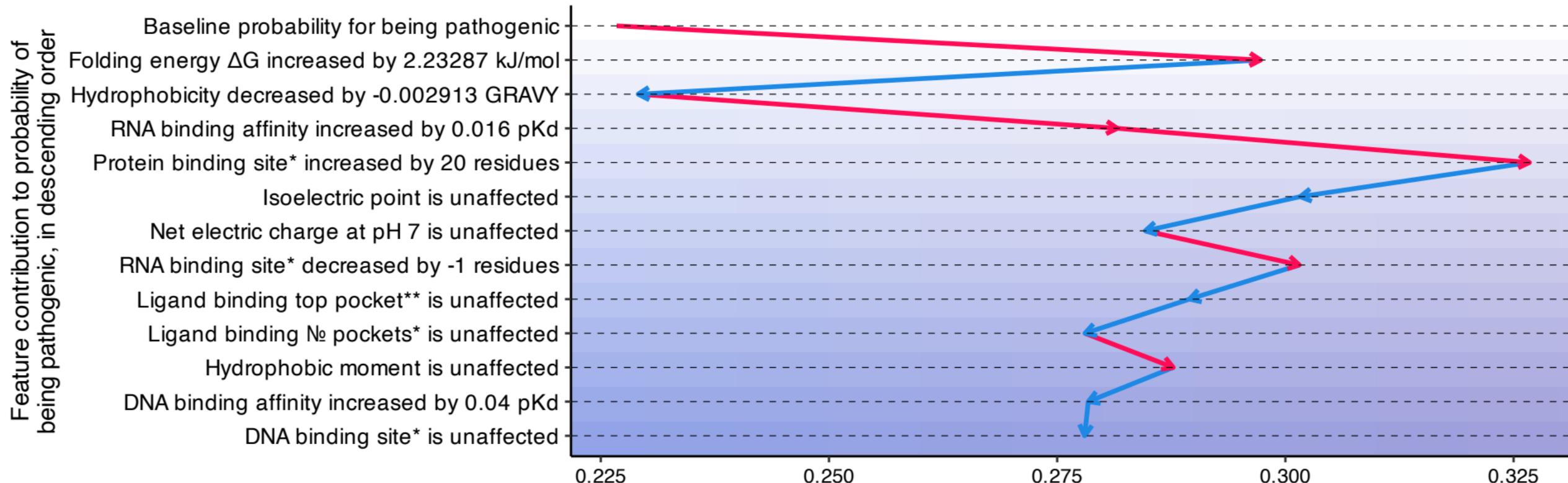


DAVE1 decision plot for LA622Q in gene CACNA1A (O00555, ENST00000360228), GRCh38 19:13308168A>T

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
Final probability for being pathogenic is 0.278, variant is estimated to be benign