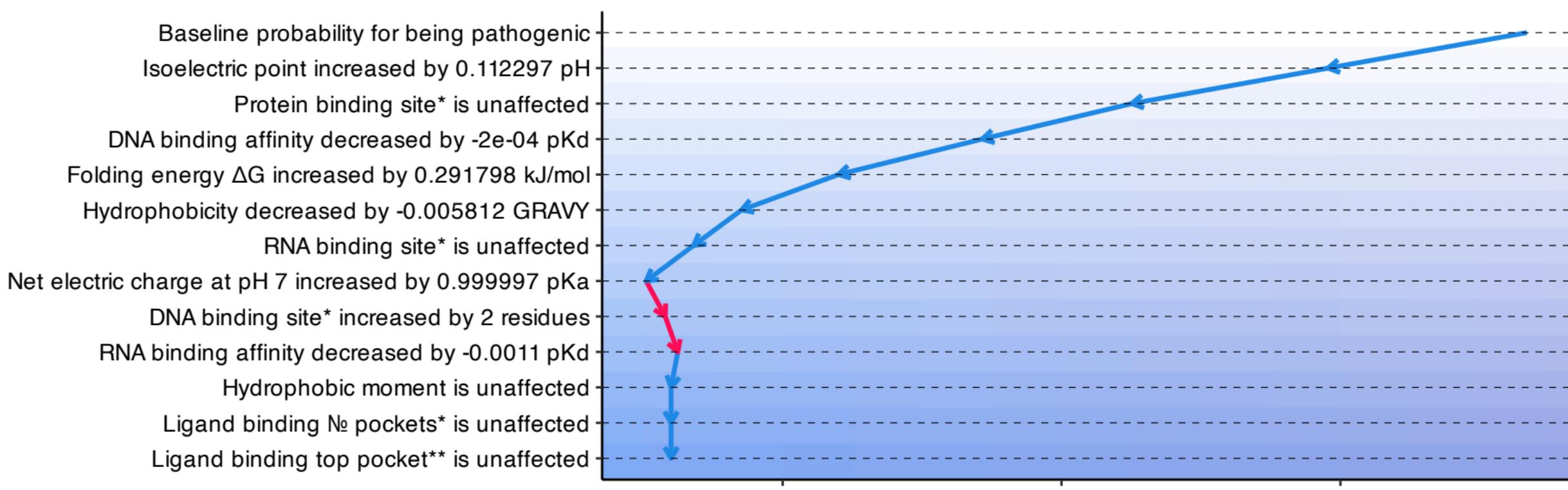# DAVE1 decision plot for PA443R in gene LIPC (P11150, ENST00000299022), GRCh38 15:58563663C>G

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

Feature contribution to probability of being pathogenic, in descending order

- Baseline probability for being pathogenic
- Isoelectric point increased by 0.112297 pH
- Protein binding site* is unaffected
- DNA binding affinity decreased by -2e-04 pKd
- Folding energy ΔG increased by 0.291798 kJ/mol
- Hydrophobicity decreased by -0.005812 GRAVY
- RNA binding site* is unaffected
- Net electric charge at pH 7 increased by 0.999997 pKa
- DNA binding site* increased by 2 residues
- RNA binding affinity decreased by -0.0011 pKd
- Hydrophobic moment is unaffected
- Ligand binding № pockets* is unaffected
- Ligand binding top pocket** is unaffected

Cumulative probability heuristic for SHAP values

0.12   0.16   0.20

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

Final probability for being pathogenic is 0.104, variant is estimated to be benign