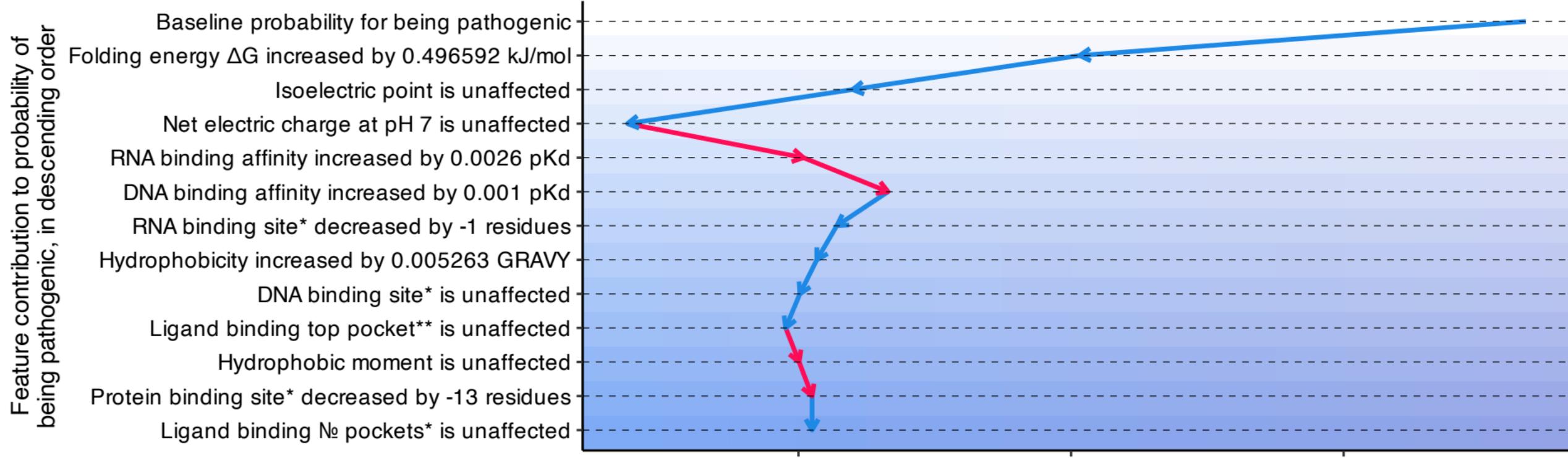# DAVE1 decision plot for TA379A in gene LPL (P06858, ENST00000650287), GRCh38 8:19959376A>G

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
- Folding energy ΔG increased by 0.496592 kJ/mol
- Isoelectric point is unaffected
- Net electric charge at pH 7 is unaffected
- RNA binding affinity increased by 0.0026 pKd
- DNA binding affinity increased by 0.001 pKd
- RNA binding site* decreased by -1 residues
- Hydrophobicity increased by 0.005263 GRAVY
- DNA binding site* is unaffected
- Ligand binding top pocket** is unaffected
- Hydrophobic moment is unaffected
- Protein binding site* decreased by -13 residues
- Ligand binding № pockets* 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 0.122, variant is estimated to be benign