M47 is a SVM based predictor for the effects of Mutation on protein stability. To decrease the number of model parameters and to improve the generalization potential, we calculated amino acid contact energy (CE) change for point variations using a structure-based coarse-grained model. Based on the CE change and further physicochemical properties of amino acids as input features, we developed the support vector machine classifier with 47 input features.

To meet the format of CAGI challenge, we normalized Prediction result from 0-2. We cannot predict wild type or mutation containing X, so these are marked as “\*”.

For the “Standard\_Deviation” column, we have no idea how to define the value for each mutation, just leave “\*” for all mutations. We think each protein can has one SD value for all mutations’ prediction result, which is 0.388 for PTEN, and 0.456 for TPMT.

The tool can be downloaded from <http://structure.bmc.lu.se/PPSC/>

The work was published in 2013:

Yang Y, Chen B, Tan G, et al. Structure-based prediction of the effects of a missense variant on protein stability.[J]. Amino Acids, 2013, 44(3):847-855.